



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/12, C07K 14/47, 16/18, G01N 33/566, C12Q 1/68, C12N 15/11, 15/62, A01K 67/027, A61K 38/00</b>	<b>A2</b>	<b>(11) International Publication Number: WO 00/58473</b>  <b>(43) International Publication Date: 5 October 2000 (05.10.00)</b>																											
<b>(21) International Application Number: PCT/US00/08621</b> <b>(22) International Filing Date: 31 March 2000 (31.03.00)</b>  <b>(30) Priority Data:</b> <table border="0"> <tr> <td>60/127,607</td> <td>31 March 1999 (31.03.99)</td> <td>US</td> </tr> <tr> <td>60/127,636</td> <td>2 April 1999 (02.04.99)</td> <td>US</td> </tr> <tr> <td>60/127,728</td> <td>5 April 1999 (05.04.99)</td> <td>US</td> </tr> <tr> <td>09/540,763</td> <td>30 March 2000 (30.03.00)</td> <td>US</td> </tr> </table> <b>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications</b> <table border="0"> <tr> <td>US</td> <td>60/127,607 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>31 March 1999 (31.03.99)</td> </tr> <tr> <td>US</td> <td>60/127,636 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>2 April 1999 (02.04.99)</td> </tr> <tr> <td>US</td> <td>60/127,728 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>5 April 1999 (05.04.99)</td> </tr> <tr> <td>US</td> <td>09/540,763 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>30 March 2000 (30.03.00)</td> </tr> </table> <b>(71) Applicant (for all designated States except US): CURAGEN CORPORATION (US/US); 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).</b>	60/127,607	31 March 1999 (31.03.99)	US	60/127,636	2 April 1999 (02.04.99)	US	60/127,728	5 April 1999 (05.04.99)	US	09/540,763	30 March 2000 (30.03.00)	US	US	60/127,607 (CIP)	Filed on	31 March 1999 (31.03.99)	US	60/127,636 (CIP)	Filed on	2 April 1999 (02.04.99)	US	60/127,728 (CIP)	Filed on	5 April 1999 (05.04.99)	US	09/540,763 (CIP)	Filed on	30 March 2000 (30.03.00)	<b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only): SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US).</b>  <b>(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).</b>  <b>(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</b>  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
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<b>(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"</b>  <b>(57) Abstract</b>  <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>																													

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## NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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## BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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## SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORF polypeptides encoded by an ORF nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORF polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORF polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORF antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a  
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORF polypeptide by providing a cell containing a ORF nucleic acid, *e.g.*, a vector that includes a ORF nucleic  
15 acid, and culturing the cell under conditions sufficient to express the ORF polypeptide encoded by the nucleic acid. The expressed ORF polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORF polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORF polypeptide or nucleic  
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORF polypeptide by contacting ORF polypeptide with a compound and determining whether the ORF polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORF polypeptide activity identified by contacting a ORF polypeptide with the compound and determining whether the compound modifies activity of the ORF polypeptide, binds to the ORF polypeptide, or binds to a nucleic acid molecule encoding a ORF polypeptide.

30 In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORF-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORF polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is  
5 preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

10 In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a  
15 control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which  
20 such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention  
25 belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and  
30 examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

### DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF<sub>n</sub> according to the invention (wherein *n* is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2*n*-1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2*n*. For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected.

Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

### **Amylases**

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

### 5      **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

### **Angiopoeitin**

Members of the angiopoietin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

### 25      **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5           **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

**Colony-stimulating factor-related proteins**

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

**Complement-related proteins**

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

### **Cytochrome**

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

### **Kinesins**

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

### **Cytokines, Interferon, Interleukin**

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

### **G-protein coupled receptors**

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.



**Thioesterases**

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_ma_bind	DNA/RNA binding protein/factor
	dna_ma_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
10	reductase	reductase
	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM	similar
	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
	struct	structural associated protein
20	sulfotransferase	sulfotransferase
	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
25	tgf	transforming growth factor
	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
40	ubiquitin	ubiquitin
	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are  
 5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to  
 10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

### ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the  
 25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as  
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is  
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and  
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a  
20 vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism  
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular  
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any  
5 of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2<sup>nd</sup> Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

10 A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an  
15 automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or  
20 complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be  
25 chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence  
30 shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5           As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.

10       Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

          Moreover, the nucleic acid molecule of the invention can comprise only a portion of the  
15       nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,  
20       and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but  
25       differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild-type.

          Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or  
30       analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified



oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);  
 5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be  
 10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides  
 15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX  
 20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4:

## 25 ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of  
 30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at  $T_m$ , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein  $n = 1$  to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

#### Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 $n$  (wherein  $n = 1$  to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 $n$ -1 for the corresponding  $n$ , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 $n$ -1 (wherein  $n = 1$  to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

#### Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

#### Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are



carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

### ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

#### **Determining homology between two or more sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

#### **Chimeric and fusion proteins**

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5       For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10       In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15       In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20       In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of  
30       ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

#### ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one



embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

#### Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can  
5 be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

### Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as  $F_{ab}$  or  $(F_{ab})_2$ , that bind immunospecifically to any of the proteins of the invention.

10 An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in  
15 any of SEQ ID NO:2n (wherein n = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6  
20 contiguous amino acids of any of SEQ ID NO:2n (wherein n = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example,  
25 the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as  
30 immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)}_2$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND  
 5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see *e.g.*, Huse, *et al.*,  
 10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F<sub>ab</sub> fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by  
 15 techniques known in the art including, but not limited to: (i) an F<sub>(ab)<sub>2</sub></sub> fragment produced by pepsin digestion of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab)<sub>2</sub></sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized  
 20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent  
 25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*  
 30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

### ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can  
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are  
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the  
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the  
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation  
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons  
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,  
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,  
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*  
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,  
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.



In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews—Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

## 5           **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences  
10   have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal  
15   includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous  
20   recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding  
25   nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to  
30   the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G<sub>0</sub> phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

### Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder  
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated  
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible  
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as  
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.



It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

#### **Additional Uses and Methods of the Invention**

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5           This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

#### Screening Assays

          The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,  
10   peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

          In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained  
15   using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are  
20   applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

          Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)  
25   *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

          Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),  
30   plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding  
5 of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct  
10 binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular  $\text{Ca}^{2+}$ , diacylglycerol,  $\text{IP}_3$ , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the  
15 induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test  
20 compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test  
25 compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein  
30 or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton<sup>®</sup> X-100, Triton<sup>®</sup> X-114, Thesit<sup>®</sup>, Isotridecypoly(ethylene glycol ether)<sub>n</sub>, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

5 In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also  
10 likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene  
15 encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor  
20 are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

25 This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

#### Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For  
30 example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.



### **Predictive Medicine**

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

### **Use of Partial ORFX Sequences in Forensic Biology**

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: \_\_ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

### Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

#### **Diagnostic Assays**

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX  
5 nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological  
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid  
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or  
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as  
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include  
5 Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test  
10 subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable  
15 of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological  
20 sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

### 25 Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a  
30 disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for  
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained  
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder  
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample  
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a  
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion  
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a  
10 sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through  
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one  
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*  
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA



heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5        The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10        Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

#### Pharmacogenomics

15        Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be  
20        considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate  
25        dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30        Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a  
5 common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic  
10 polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor  
15 metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic  
20 response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation  
25 content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus  
30 enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

### Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

#### Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

#### **Determination of the Biological Effect of a Therapeutic**

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

#### **Malignancies**

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,



but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models,  
5 in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

#### 10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or  
15 suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number  
20 in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the  
25 epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

### Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

### Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

### Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

### Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5           A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),  
10   transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein  
15   (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for  
20   example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

          Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be  
25   treated or prevented by administration of a Therapeutic that modulates activity.

#### **Cytokine and Cell Proliferation/Differentiation Activity**

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,  
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+ ), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing  
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or  
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells  
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,  
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

### Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the



immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;  
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which  
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins  
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by  
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.  
30

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

#### **Hematopoiesis Regulating Activity**

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5         Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*  
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,  
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.  
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

#### **Tissue Growth Activity**

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for  
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation  
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

### Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in 10 these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may 15 also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

### Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of 30 wounds and other trauma to tissues, as well as in treatment of localized infections. For example,



attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,  
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

- 20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for  
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

#### Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor  
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and  
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and  
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell  
interactions and their ligands (including without limitation, cellular adhesion molecules (such as  
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,  
10 antigen recognition and development of cellular and humoral immune responses). Receptors and  
ligands are also useful for screening of potential peptide or small molecule inhibitors of the  
relevant receptor/ligand interaction. A protein of the present invention (including, without  
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of  
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the  
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:  
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and  
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions  
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*  
*Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,  
*J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The  
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the  
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,  
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory  
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production  
of other factors which more directly inhibit or promote an inflammatory response. Proteins  
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

### **Tumor Inhibition Activity**

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

### **Other Activities**

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

## 10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395[emb CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	284636
2	80248091 (3, 4)	Novel Protein sim. GBank gij282508[sp P71559]SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	284907, 284800, 284602, 284762, 284769, 284889, 284638, 284587
3	80415924 (5, 6)			UNCLASSIFIED	284910, 284604, 284634, 284805, 284638, 284691, 284907, 284892, 284829
4	82018837 (7, 8)			UNCLASSIFIED	284908, 284909, 284760, 284628, 284635
5	79970035 (9, 10)			UNCLASSIFIED	22278002, 284563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	284908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415926[gb AAD20157] - (AC008282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 284508, 284509, 284905, 284908, 284907, 284908, 284909, 284511, 285008, 284512, 285009, 284910, 284595, 284598, 284758, 284603, 284604, 284760, 284762, 284683, 284766, 284787, 284889, 35695917, 284690, 284892, 284693, 33657109, 284628, 284629, 35698423, 55811578, 35695855, 284630, 284631, 284632, 284634, 284636, 284637, 284638, 284639, 18108385, 284563, 284564, 284566, 284488
8	56824278 (15, 16)	Novel Protein sim. GBank gij565582[sp Q06456]NIRB_KLEPN - NITRITE REDUCTASE [NAD(P)H] LARGE SUBUNIT		reductase	284907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	284908
11	20414027 (21, 22)			UNCLASSIFIED	284605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145[emb CAA9987.1] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	284259, 285007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	284556, 284537, 284584
14	95105114 (27, 28)	Novel Protein sim. GBank gij2832761[emb CAA12845] - (A225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696298, 35696052, 284510, 35695917, 284691, 284628, 35698423, 284555, 284558, 284559, 83373044
15	20456307 (29, 30)	Novel Protein sim. GBank gij1710781[sp Q10234]RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	284604
16	20760356 (31, 32)				284555

17	20292744 (33, 34)	Novel Protein sim. GBank gll117484[sp]P44391[URE1_HAEN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)]	Contains protein domain (PF00449) - Urease		284600
18	80246804 (35, 36)	Novel Protein sim. GBank gll2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]			28331827, 284555, 284557, 284638, 284558
19	80076824 (37, 38)	Novel Protein sim. GBank gll2508112[sp]P43672[UUP - ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP]		UNCLASSIFIED transport	22276898, 284907, 284910, 284600, 284693
20	20724558 (39, 40)	Novel Protein sim. GBank gll1730203[sp]P50442[GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)]		UNCLASSIFIED	22276895, 284908, 285008, 285010, 285011, 284602, 284605, 284768, 284688, 21906764, 284891, 18108376, 284636, 18108387, 284486
21	80417554 (41, 42)	Novel Protein sim. GBank gll1873209[emb]CAB070771 - (Z82771) lade25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase		284885
22	11705858 (43, 44)	Novel Protein sim. GBank gll4803369[emb]CAB42783.11 - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]		UNCLASSIFIED	284488, 284907, 284909, 284600, 284602, 284603, 284605, 284682, 284768, 32833866, 284636, 284486
23	80419178 (45, 46)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e		284593
24	20291897 (47, 48)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	Contains protein domain (PF00365) - Phosphofructokinase		284593
25	80253774 (49, 50)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
26	80253384 (51, 52)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284601, 284762, 284766, 284768, 284636
27	80235795 (53, 54)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
28	79483581 (55, 56)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
29	82448765 (57, 58)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
30	78189333 (59, 60)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
31	19848158 (61, 62)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
32	82448485 (63, 64)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
33	79587628 (65, 66)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
34	87467657 (67, 68)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
35	95005170 (69, 70)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
36	82448485 (63, 64)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638
37	20369215 (73, 74)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]		UNCLASSIFIED	284638

38	20468334 (75, 76)	Novel Protein sim. GBank gl 3605970 emb CAA06231  - (AJ004833) periplasmic nitrate reductase, large subunit [Rhodospirillum rubrum sp.]		reductase	284605	
39	94300715 (77, 78)	Novel Protein sim. GBank gl 1929449 (L63543) - endodermis [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	284905, 284908, 284907, 68712502, 284908, 284909, 284511, 285009, 284910, 55812038, 284758, 285011, 284782, 284682, 284783, 284784, 284786, 285022, 284693, 284628, 284631, 284634, 284635, 284555, 284638, 18108381, 284558, 18108385, 284482	
40	20535825 (79, 80)			UNCLASSIFIED	284592	
41	80023287 (81, 82)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			284591, 35595917	
42	20724566 (83, 84)			UNCLASSIFIED	284602	
43	20467069 (85, 86)	Novel Protein sim. GBank gl 3820584 (AF086781) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	284605	
44	13085287 (87, 88)	Novel Protein sim. GBank gl 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	284769, 284636	
45	39384711 (89, 90)	Novel Protein sim. GBank gl 1861738 (U98888) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	284769, 284510, 284508	
46	95003398 (91, 92)			ngf	284566	
47	11898624 (93, 94)			UNCLASSIFIED	284689	
48	79407218 (95, 96)				18108385, 284635, 284628	
49	21659844 (97, 98)			UNCLASSIFIED	284603	
50	80503868 (99, 100)				284508, 284603, 284769, 284689, 284638, 284558, 284488	
51	80255569 (101, 102)	Novel Protein sim. GBank gl 3411177 (AF078240) - MccC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	284593, 18108387	
52	79208528 (103, 104)	Novel Protein sim. GBank gl 3814992 sp Q28284 SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struct	284634	
53	36966970 (105, 106)	Novel Protein sim. GBank gl 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	284762	
54	79570887 (107, 108)					
55	80202703 (109, 110)	Novel Protein sim. GBank gl 1833572 (U52064) - Herpesvirus salmout ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]		UNCLASSIFIED	284630, 284909, 284766	
56	8758408 (111, 112)	Novel Protein sim. GBank gl 4321560 gb AAD15785  - (AF050114) euginate lyase [Pseudomonas sp. W7]			28331824, 284102, 285018, 18108376	
57	11223368 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284604	

58	91227508 (115, 116)	Novel Protein sim. GBank gij15016074jgb AAD45616.1AF08194 - (AF08194) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	58182575, 284259, 60432049, 35696052, 68712502, 284908, 285008, 285010, 285011, 284891, 29148784, 35695917, 60170615, 284891, 284692, 284693, 18108374, 35696423, 58182323, 80432113 284600, 284689, 284638
59	80077371 (117, 118)	Novel Protein sim. GBank gij1172820isp P45830RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00853) - Glycosyl transferase	transferase	
60	12958341 (119, 120)				
61	80426808 (121, 122)	Novel Protein sim. GBank gij1710218 (U78260) - unknown [Homo sapiens]		glycoprotein	284689 284766
62	13504966 (123, 124)				284630
63	18474553 (125, 126)			UNCLASSIFIED	285019
64	20724578 (127, 128)	Novel Protein sim. GBank gij420845ipr JA47041 - transposase homolog (insertion element [SAE1] - Alcaligenes eutrophus		UNCLASSIFIED	284602
65	78326308 (129, 130)	Novel Protein sim. GBank gij3122312ip O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	284563
66	46854384 (131, 132)	Novel Protein sim. GBank gij3282723jemb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278986, 284558
67	78952543 (133, 134)	Novel Protein sim. GBank gij231985isp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	285021
68	79817382 (135, 136)				284909
69	79841764 (137, 138)				284908
70	79871328 (139, 140)			UNCLASSIFIED	284908
71	85897458 (141, 142)				284908, 284908
72	87734977 (143, 144)	Novel Protein sim. GBank gij4415928jgb AAD201571 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	284602, 285021
73	80025241 (145, 146)			UNCLASSIFIED	284488, 284903, 284906, 284907, 284908, 284511, 285008, 284910, 284758, 87168474, 284682, 284766, 284888, 284889, 35695917, 285021, 60170615, 284891, 33657023, 284692, 284693, 284629, 284631, 284639, 22279000
74	20377410 (147, 148)			UNCLASSIFIED	60424179, 284508, 284908, 285007, 284603, 284687, 284889, 284692, 18108387
75	11818032 (149, 150)	Novel Protein sim. GBank gij2853098jemb CAA189141 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	284605 284689
76	95105303 (151, 152)	Novel Protein sim. GBank gij4468811jemb CAB38212 - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	
77	10144718 (153, 154)	Novel Protein sim. GBank gij854065jemb CAA58337 - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	83373044, 284908, 284557
78	8758258 (155, 156)			UNCLASSIFIED	284683 284604



79	94140180 (157, 158)	Novel Protein sim. GBank gl 5689453 db BAA83010.1  - (AB028881) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00189) - PH domain		35698288, 22278998, 29331822, 29331824, 29331825, 29331827, 284905, 284906, 284907, 66712502, 284908, 284909, 285008, 285009, 284910, 60170831, 55812038, 33108954, 285017, 285018, 284288, 284768, 56181582, 21908785, 21908789, 29148784, 265020, 284690, 284691, 284692, 284693, 80431528, 35898423, 284631, 284632, 284634, 284636, 284639, 83373044, 284564, 284568, 284567
80	82314840 (159, 160)			UNCLASSIFIED	284768, 284801, 265008, 284910, 284604, 284605, 284634, 284635, 284605, 284762, 284637, 284592, 284628, 284807, 284691, 284908, 284567, 284909, 284768, 284605
81	20467247 (161, 162)	Novel Protein sim. GBank gl 1723442 sp Q10258 YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C8F8.10 IN CHROMOSOME 1		reductase	284567
82	16331388 (163, 164)	Novel Protein sim. GBank gl 2885868 (AF045770) - methylmalonate semi-aldehyde dehydrogenase (Oriza sativa)		dehydrogenase	284567
83	94741180 (165, 166)	Novel Protein sim. GBank gl 3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 284508, 284509, 284905, 284908, 284909, 284511, 284591, 284593, 284594, 284595, 284596, 284738, 284603, 284780, 284681, 18108351, 284762, 284682, 284784, 284684, 284768, 284686, 284632, 284637, 284557, 284638, 284639, 18108385, 284568
84	80355375 (167, 168)	Novel Protein sim. GBank gl 173384 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)		transport	284508, 284908, 284907, 284908, 284909, 284910, 284760, 284783, 284764, 284768, 284768, 284769, 35898555, 284636, 284637
85	80488600 (169, 170)	Novel Protein sim. GBank gl 2120898 pir S70882 - glycosyltransferase homolog - Bordetella pertussis		transferase	284605, 284762, 284687, 284769, 18108374, 284636, 284488
86	39559043 (171, 172)	Novel Protein sim. GBank gl 3256023 emb CAA17228.1  - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			284910
87	13658808 (173, 174)			UNCLASSIFIED	284093

88	95344718 (175, 176)	Novel Protein sim. GBank gij559703[dbj BAA07552] - (D38548) ha1025 is new [Homo sapiens]		52844507, 52846365, 18108398, 85274572, 58182575, 58994075, 35886288, 22278997, 22278998, 22278999, 284092, 284093, 284094, 284095, 284259, 29331822, 29331824, 58182181, 68714117, 29331825, 29331826, 80432289, 29331827, 29331828, 35886052, 33656970, 284105, 284508, 284905, 284908, 284907, 284908, 29331830, 68712502, 52844045, 58182435, 285007, 285009, 284910, 60170831, 284592, 60431735, 60433358, 33657402, 284757, 60433438, 58182038, 284758, 21908754, 52846317, 33109954, 52844286, 87168474, 285011, 87168559, 284801, 285017, 265018, 284604, 265018, 264448, 284369, 284288, 284788, 52844229, 21908786, 21908787, 21908788, 21908789, 5811957, 35885917, 285020, 285021, 265022, 60170815, 52844150, 33657023, 65274820, 33657109, 27486281, 27486284, 33657349, 35885763, 284828, 283972, 18108374, 55810764, 35888423, 55811578, 65274791, 35885855, 60431850, 284636, 52844332, 58182323, 60170394, 83373044, 18108385, 18108387, 18108388, 58528486, 87168518, 60432113, 22279000, 22279002, 284482, 284584, 284488, 284600
89	80077389 (177, 178)	Novel Protein sim. GBank gij1710383[sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115998 (179, 180)			
91	78908950 (181, 182)	Novel Protein sim. GBank gij2489881[sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED protease	284760 285008
92	79554871 (183, 184)	Novel Protein sim. GBank gij3387754[emb CAA20079] - (AL031155) hypothetical protein SC3A7.18c [Streptomyces coelicolor]	UNCLASSIFIED	284891
93	80496778 (185, 186)	Novel Protein sim. GBank gij2885095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase_associated	284807, 284808, 284910, 285008, 284605, 284789
94	79848649 (187, 188)	Novel Protein sim. GBank gij1171919[sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - transport CBS domain	284908
95	11080238 (189, 190)			264594

98	94322125 (191, 192)	Novel Protein sim. GBank gj4589550jdbjBAA76802.1] - (AB023175) KIAA0958 protein (Homo sapiens)	UNCLASSIFIED	22278995, 22278999, 264259, 28331822, 29331826, 35686052, 29148499, 284509, 284806, 284807, 284808, 284809, 285007, 285008, 284910, 285008, 284593, 285010, 285017, 284604, 285019, 18108351, 284288, 284786, 284788, 284789, 21906765, 21906767, 21906769, 285020, 284892, 33857182, 35885783, 264828, 284829, 18108379, 284631, 284638, 18108381, 284559, 18108382, 83373044, 22279002, 284508
97	79605200 (193, 194)	Novel Protein sim. GBank gj4583559jembjCAB40388.1] - (AJ005255) OxyR [Erwinia chrysanthemii]	UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gj1001693jdbjBAA10430] - (DB4002) hypothetical protein [Synecococcus sp.]	UNCLASSIFIED	284809
99	20466524 (197, 198)	Novel Protein sim. GBank gj1168479jspjP43925jEFG_HAEIN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	284805
100	79640113 (199, 200)	Novel Protein sim. GBank gj480897jprjS37485 - gene ms91 protein - mouse	UNCLASSIFIED	284693
101	80203298 (201, 202)	Novel Protein sim. GBank gj2894186jembjCAA11773.1] - (AJ223998) PCZA381.18 [Amycolatopsis orientalis]	UNCLASSIFIED	285020, 284102, 263972
102	20467258 (203, 204)	Novel Protein sim. GBank gj173104jspjP54509jYQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	synthase	284605
103	20466368 (205, 206)	Novel Protein sim. GBank gj173104jspjP54509jYQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Helicases conserved C-terminal domain	284605
104	80247572 (207, 208)	Novel Protein sim. GBank gj1854085jembjCAA56337] - (X83413) U88 [Human herpesvirus 8]	UNCLASSIFIED	284591, 284595, 284602
105	79605206 (209, 210)	Novel Protein sim. GBank gj17685117 (U70770) - furrowed [Drosophila melanogaster]	complement	284508
106	28382058 (211, 212)	Novel Protein sim. GBank gj1705505jspjP54729jBS4_MOUSE - BS4 PROTEIN	UNCLASSIFIED	284511, 285008
107	80057791 (213, 214)	Novel Protein sim. GBank gj4887229jgbjAAD32244.1jAF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	ATPase-associated	28331824, 284591, 21908754, 265019
108	80237938 (215, 216)	Novel Protein sim. GBank gj263577jembjCAB15264] - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35685917, 22278996, 284113, 284800, 284602, 284603, 285017, 284910, 284908, 284638, 284786
109	95194148 (217, 218)	Novel Protein sim. GBank gj2330781jembjCAB11265] - (Z98601) carboxypeptidase a precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	284758, 284603, 284630, 284636, 284637
110	79532823 (219, 220)			284687
111	39565458 (221, 222)			284564
112	79856038 (223, 224)		UNCLASSIFIED	284908
113	17959439 (225, 226)		UNCLASSIFIED	285007
114	80502101 (227, 228)		UNCLASSIFIED	284769

115	80251003 (228, 230)	Novel Protein sim. GBank glj2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52845156, 52845080, 33856970, 284592, 21906754, 27486264, 18108379, 35698423, 284635, 52844332, 18108382
116	81288888 (231, 232)				284605, 284908, 284907, 284908, 284909, 284910, 284758, 285010, 284783, 284682, 284784, 284766, 284685, 284688, 284788, 284789, 33657023, 284693, 33657109, 284628, 18108374, 284631, 284632, 284634, 284636, 284637, 284638, 284639, 56526488, 284585, 284568
117	78636895 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	284639, 284693
118	80222170 (235, 236)				283974
119	91013071 (237, 238)	Novel Protein sim. GBank glj732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278986, 29331824, 60432289, 265007, 60433438, 284603, 284605, 18108351, 284789, 284689, 265020, 284534, 27486281, 284558, 83373044, 18108385, 284564
120	8756481 (239, 240)	Novel Protein sim. GBank glj2131219 (pirj[S50157] - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)	kinase		284603
121	80028153 (241, 242)				284585
122	20457820 (243, 244)	Novel Protein sim. GBank glj2052147 (embj[CAB08137] - (284752) ksgA [Mycobacterium tuberculosis])	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	284605
123	8758278 (245, 246)				284604
124	79104017 (247, 248)	Novel Protein sim. GBank glj2833385 (spj[Q43134]UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 285008, 265007, 285008, 285010, 285011, 18108355, 18108378, 18108380, 18108384
125	87797888 (249, 250)	Novel Protein sim. GBank glj475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	284508, 284908, 265009, 284596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank glj5102785 (embj[CAB45200.1] - (AL078308) putative transcriptional regulator [Streptomyces coelicolor]			284511
127	20467287 (253, 254)				284605
128	80248473 (255, 256)	Novel Protein sim. GBank glj130120 (spj[P23820]PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	284907, 284909, 284910, 284600, 284601, 284603, 284605, 18108351, 284683, 284557
129	95290543 (257, 258)	Novel Protein sim. GBank glj2508493 (spj[P38036]YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35698423, 35695855, 284600, 284602, 284603, 284604, 284605, 284508, 284908, 284564, 284628, 284682, 284585, 284683
130	80085583 (259, 260)	Novel Protein sim. GBank glj84065 (embj[CAB38337] - (X83413) U88 [Human herpesvirus 6])			284634
131	94985022 (261, 262)	Novel Protein sim. GBank glj1076036 (pirj[S54860] - ABC transporter PstC-2 chain - Mycobacterium tuberculosis)	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 284789, 29331828, 284689, 22278986, 285021, 284600, 284511, 284601, 284602, 284605, 284905, 284636

132	10887892 (263, 264)	Novel Protein sim. GBank glj1877340[embjCAB07088] - (Z82771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	284638 284805, 284689
133	94630883 (265, 266)				
134	78834660 (267, 268)	Novel Protein sim. GBank glj4585838[embjCAB40932.1] - (AL048630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	284905, 284605, 285021
135	18885057 (269, 270)	Novel Protein sim. GBank glj1460074[embjCAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			284634
136	78846083 (271, 272)	Novel Protein sim. GBank glj2125896[embjCAA7331.1] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	284508
137	78819770 (273, 274)				
138	78835971 (275, 276)	Novel Protein sim. GBank glj5420387[embjCAB46878.1] - (AJ243459) proteophosphoglycan [Leishmania major]			284683, 284685, 284686, 284691, 284692, 284693
139	86686078 (277, 278)	Novel Protein sim. GBank glj5689912[embjCAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	18108374, 18108385, 33657109, 33657182, 285010, 22278988, 285008, 285007, 285008, 285009, 284693
140	78825758 (279, 280)				22278988, 285007, 284810, 60433356, 285010, 284602, 284605, 284768, 284688, 284769, 284693, 32833986, 18108374, 18108387
141	20700094 (281, 282)				18108387
142	80028104 (283, 284)	Novel Protein sim. GBank glj3581916[embjCAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284808
143	11072274 (285, 286)			nuclease	284602, 285017
144	95009102 (287, 288)	Novel Protein sim. GBank glj3334127[spP87303]BAC2 MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)			
145	80027058 (289, 290)	Novel Protein sim. GBank glj3757569[embjCAA21315] - (AL031883) 1-evidence-predicted by content; 1-method=genefinder084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			284600
146	13085682 (281, 292)	Novel Protein sim. GBank glj140807[spP24538]Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase		283978, 284600, 284910, 284632, 284508, 284553, 284584, 284591, 284558, 284908, 284628, 284639
147	94320386 (293, 294)	Novel Protein sim. GBank glj2827608[embjCAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	284805, 284908, 284809, 284510, 285009, 60433356, 284600, 284601, 284604, 284605, 284887, 284769, 18108385, 85274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank glj2918947[embjCAA17585] - (AL021999) hypothetical protein Rv0888 [Mycobacterium tuberculosis]		transport	285009, 285010, 284600, 284602, 284603, 284604, 284605, 284693, 33657109, 284636

149	80249373 (297, 298)	Novel Protein sim. GBank gij172073jipj11040Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - ABC transporter	transport	285010, 284600, 284601, 284603, 284604, 27486285, 284638
150	20284748 (289, 300)	Novel Protein sim. GBank gij3724125[emb]CAA11805] - (AJ224340) maltosephosphorylase [Lactobacillus santfrancisco]			284600
151	20726388 (301, 302)	Novel Protein sim. GBank gij729312jipjP07651]DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	284602
152	95002877 (303, 304)	Novel Protein sim. GBank gij2497852jipjP55687]Y4TM_RHIN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	284602
153	80258685 (305, 306)	Novel Protein sim. GBank gij3123021jipjQ80509]VT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	284583
154	82305888 (307, 308)	Novel Protein sim. GBank gij1418897]pirjJUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	284910, 284782, 284691, 284634 284605
155	20429859 (309, 310)	Novel Protein sim. GBank gij828710]pirjS41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	284585
156	39564742 (311, 312)	Novel Protein sim. GBank gij3695013 (AF052588) - CtrA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HnfC family	hydrolase	284691
157	10358887 (313, 314)	Novel Protein sim. GBank gij1073072]pirjC55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	284805
158	79761936 (315, 316)	Novel Protein sim. GBank gij1073072]pirjC55543 - cmaU protein - Pseudomonas syringae pv. syringae	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	285003 284605
159	78890376 (317, 318)	Novel Protein sim. GBank gij1173023]jipjP48789]RL30_STRCO - 80S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomalprot	22278996, 284600, 284603, 35695917, 32833986, 35698423, 284638
160	11075119 (319, 320)	Novel Protein sim. GBank gij5304859]embjCAB46028.1] - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	284112, 284532, 22278002
161	80055007 (321, 322)	Novel Protein sim. GBank gij1173023]jipjP48789]RL30_STRCO - 80S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	284639
162	80016371 (323, 324)	Novel Protein sim. GBank gij5304859]embjCAB46028.1] - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	UNCLASSIFIED	284905, 284907, 284600 284891
163	11692308 (325, 326)	Novel Protein sim. GBank gij2681891]embjCAA15785] - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	284805, 284488
164	80077802 (327, 328)	Novel Protein sim. GBank gij4418478]gbjAAD20378] - (AF125988) transposase [Mycobacterium avium]		UNCLASSIFIED	285010
165	10856067 (329, 330)	Novel Protein sim. GBank gij78177]pirjQCECT - hypothetical 38.8k protein (fla 5' region) - Escherichia coli		UNCLASSIFIED	284600
166	88095003 (331, 332)	Novel Protein sim. GBank gij78177]pirjQCECT - hypothetical 38.8k protein (fla 5' region) - Escherichia coli			284558, 284557, 284558, 284559

170	79612384 (339, 340)	Novel Protein sim. GBank gi 140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLD8 INTERGENIC REGION (F139)	Contains protein domain (PF01810) - LysE type translocator	264908 264596, 264604	
171	95283073 (341, 342)				
172	37787007 (343, 344)	Novel Protein sim. GBank gi 4210905 gb AAD12048.1  - (AF045809) AgIG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	264769	
173	57529660 (345, 346)	Novel Protein sim. GBank gi 132854 sp P02387 RL2_ECOLI - 60S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	264769	
174	95283078 (347, 348)	Novel Protein sim. GBank gi 1881350 db BAA18371  - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693	
175	79758270 (348, 350)	Novel Protein sim. GBank gi 2072722 emb CAB08328  - (Z85121) manA [Mycobacterium tuberculosis]	isomerase	264565	
176	80058898 (351, 352)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	264907, 264910, 264681, 264558	
177	86864652 (353, 354)	Novel Protein sim. GBank gi 2328738 emb CAB10952  - (Z88268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	264768, 60424179, 264687, 264688, 264768, 29331828, 60432289, 18108376, 264689, 18108387, 32833988, 22278998, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264782, 264636, 264908, 264664, 264637, 264638, 264486, 60433356, 264768	
178	79559528 (355, 356)	Novel Protein sim. GBank gi 1806596 (U81768) - kinesin-73 [Drosophila melanogaster]	struct	264693, 33857109, 264635	
179	20263112 (357, 358)		UNCLASSIFIED	264593	
180	80488658 (359, 360)	Novel Protein sim. GBank gi 1168367 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE	helicase	264769	
181	79585369 (361, 362)	Novel Protein sim. GBank gi 3170615 (AF059485) - DOC4 [Mus musculus]	UNCLASSIFIED	21908767, 264635, 264639, 18108384	
182	80577899 (363, 364)		UNCLASSIFIED	264259, 35696052, 56182435, 264511, 285018, 33857109, 264555, 264566 264690	
183	11614017 (365, 366)	Novel Protein sim. GBank gi 1078627 pir jS64172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED		
184	10174167 (367, 368)	Novel Protein sim. GBank gi 4371280 gb AAD18138  - (AC008280) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264510	

185	21660322 (369, 370)	Novel Protein sim. GBank gl 300817 emb CAA18398.1  - (AL022304) putative nima transport regulator [Schizosaccharomyces pombe]	UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gl 2828802 sp P94408 YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SPF-GERKA INTERGENIC REGION	transport	264595
187	80186811 (373, 374)	Novel Protein sim. GBank gl 3150280 emb CAA18170  - (AL023634) cyclin [Schizosaccharomyces pombe]	UNCLASSIFIED	264389
188	20484942 (375, 376)	Novel Protein sim. GBank gl 2145853 pir J572938 - hix protein - Mycobacterium leprae	kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gl 1881244 db BAA18271  - (AB001486) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	UNCLASSIFIED	35686032, 264602, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264565
190	80086621 (379, 380)	Novel Protein sim. GBank gl 120226 sp P28725 FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)	synthase	264563
191	88095012 (381, 382)	Novel Protein sim. GBank gl 4980892 gb AAD3474.1 AE00171 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]	isomerase	264508, 264604, 264605, 264768, 264555
192	16333378 (383, 384)	Novel Protein sim. GBank gl 1705481 sp P3358 BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	transport	264587
193	78810127 (385, 386)	Novel Protein sim. GBank gl 3122305 sp Q27778 K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)		264605
194	20484949 (387, 388)	Novel Protein sim. GBank gl 1781203 emb CAB06110  - (Z83899) and [Mycobacterium tuberculosis]		264638
195	13518389 (389, 390)	Novel Protein sim. GBank gl 3122305 sp Q27778 K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)	gaba	264600, 264688, 264638
196	95005568 (391, 392)	Novel Protein sim. GBank gl 3122305 sp Q27778 K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)	kinase	264602, 264682, 264692, 18108374
197	80248665 (393, 394)	Novel Protein sim. GBank gl 3122305 sp Q27778 K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)		264638
198	78163635 (395, 396)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		265008
199	78890715 (397, 398)	Novel Protein sim. GBank gl 289437 emb CAA74911.1  - (Y14573) ring finger protein [Hordeum vulgare]	UNCLASSIFIED	264585, 264596
200	79413848 (399, 400)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]	UNCLASSIFIED	29331828, 265007, 264512, 33657402
201	86945624 (401, 402)	Novel Protein sim. GBank gl 289437 emb CAA74911.1  - (Y14573) ring finger protein [Hordeum vulgare]	UNCLASSIFIED	264596, 265017, 18108351, 264682, 264683, 264787, 264829, 55610764, 264634, 264635, 58182323, 80432113, 22278000



202	70588046 (403, 404)	Novel Protein sim. GBank, g1j231772[sp]P30598[CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)]	Contains protein domain (PF01844) - synthase Chitin synthase	284600
203	78843927 (405, 406)	Novel Protein sim. GBank g1j1504042[dj]BAA132201 - (D86984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 28331822, 28331825, 28331827, 284908, 21908754, 284883, 21908786, 21908789, 35986423, 284558
204	78855188 (407, 408)	Novel Protein sim. GBank g1j2833808[emb]CAB133101 - (Z88111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	284809
205	10090583 (409, 410)	Novel Protein sim. GBank g1j2134381[pri]S60878 - polydrome 1 protein - chicken	transport	284909
206	8758473 (411, 412)	Novel Protein sim. GBank	UNCLASSIFIED	284604
207	20764522 (413, 414)	Novel Protein sim. GBank g1j2134381[pri]S60878 - polydrome 1 protein - chicken	UNCLASSIFIED	284556
208	20288281 (415, 416)	Novel Protein sim. GBank		284605
209	80071089 (417, 418)	g1j2501040[sp]O05814[SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)]		284605, 284689
210	80188800 (419, 420)			284905, 284907, 284908, 284786, 284687, 284891, 284628, 18108374, 284638
211	80034539 (421, 422)	Novel Protein sim. GBank		263878
212	82442474 (423, 424)	g1j5031809[trf]NP_005538.1[psLR - Immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	284508, 284905, 284908, 284907, 284908, 284600, 284782, 284534, 284632, 284634, 284635, 284639, 284486
213	80248562 (425, 426)	Novel Protein sim. GBank g1j3122358[sp]O33123[LEU2_MYCLE - 3-ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	22278996, 284508, 284600, 284602, 284603, 284605, 33657023, 284565, 284486
214	80079381 (427, 428)	Novel Protein sim. GBank g1j118236[sp]P18421[CH80_COX8U - 60 KD CHAPERONIN (PROTEIN CPN80) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)]	Contains protein domain (PF00118) - TCP-1/cpn80 chaperonin family	284600, 284693
215	14973283 (429, 430)	Novel Protein sim. GBank g1j3417287 (AC002310) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	284629
216	80177716 (431, 432)	Novel Protein sim. GBank g1j2608924[sp]P49754[VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)]	dna_rna_bind	284448
217	78603634 (433, 434)	Novel Protein sim. GBank		284508
218	80258475 (435, 436)	Novel Protein sim. GBank g1j1173288[sp]P38108[RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	mapolymerase	284594
219	20438787 (437, 438)	Novel Protein sim. GBank g1j1781087[emb]CAB082311 - (Z83864) g1jB [Mycobacterium tuberculosis]	synthase	284604
220	13499572 (439, 440)	Novel Protein sim. GBank g1j284703 (AF052427) - unknown [Trypanosoma cruzi]	nucleaseinhib	284689
221	11267498 (441, 442)	Novel Protein sim. GBank g1j4587313[db]BAA78708.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	UNCLASSIFIED	284555

222	79862802 (443, 444)	Novel Protein sim. GBank gl 1877268 emb CAB07049  - (Z82770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]	UNCLASSIFIED	284805, 284769, 35698423
223	83033668 (443, 446)		UNCLASSIFIED	284808, 284907, 284603
224	79557920 (447, 448)		UNCLASSIFIED	284884, 284693
225	78559541 (448, 450)		UNCLASSIFIED	284892
226	78172397 (451, 452)	Novel Protein sim. GBank gl 2274851 db BAA21515  - (D84159) 3-7 gene product [Homo sapiens]	UNCLASSIFIED	22278998, 284112, 33657023, 283981
227	81777198 (453, 454)	Novel Protein sim. GBank gl 868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]	UNCLASSIFIED	35695917, 284636, 284907
228	79872285 (455, 456)		UNCLASSIFIED	284768, 284907, 284908, 284692, 284593, 284639
229	78838268 (457, 458)		UNCLASSIFIED	284908, 284910
230	11013208 (459, 460)		UNCLASSIFIED	284831
231	20822207 (461, 462)	Novel Protein sim. GBank gl 1835114 emb CAA17133  - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]	UNCLASSIFIED	284908, 284600, 284603, 284692
232	80055035 (463, 464)		UNCLASSIFIED	284600, 284603, 284605, 284687, 284769
233	80083054 (465, 466)	Novel Protein sim. GBank gl 2842340 (AF032970) - imidazole propionate hydrolase [Pseudomonas putida]	UNCLASSIFIED	284604
234	7523968 (467, 468)	Novel Protein sim. GBank gl 3510505 (AF030881) - polypeptide [Fugu rubripes]	UNCLASSIFIED	284369
235	80203871 (469, 470)		UNCLASSIFIED	284108
236	78940001 (471, 472)	Novel Protein sim. GBank gl 2104609 emb CAB08805  - (Z95398) PckA [Mycobacterium leprae]	UNCLASSIFIED	284805
237	11755273 (473, 474)		UNCLASSIFIED	284681
238	78481401 (475, 476)		UNCLASSIFIED	284839
239	82435180 (477, 478)	Novel Protein sim. GBank gl 2485817 sp Q57252 YDIJ_HAEIN - HYPOTHETICAL PROTEIN H11783	UNCLASSIFIED	284908, 285010, 284603, 284782, 284682, 284636, 284638, 284486
240	21635575 (479, 480)	Novel Protein sim. GBank gl 3183458 sp P75788 YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA	transport	284259, 284769
241	80377307 (481, 482)	Novel Protein sim. GBank gl 3875920 emb CAB04111  - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D8888 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284908, 284809, 284784, 284639
242	82148454 (483, 484)		UNCLASSIFIED	284489, 284907, 284808, 284511, 284760, 284784, 284692, 284635, 284637
243	79833207 (485, 486)	Novel Protein sim. GBank gl 2624302 emb CAA15575  - (AL008862) ald [Mycobacterium tuberculosis]	UNCLASSIFIED	284908
244	80248682 (487, 488)	Novel Protein sim. GBank gl 2820825 (AF044499) - vgrG protein [Escherichia coli]	UNCLASSIFIED	284600, 284602, 284605, 284768, 284689
245	78883543 (488, 490)		UNCLASSIFIED	284907, 284758
246	79162828 (491, 492)	Novel Protein sim. GBank gl 5420387 emb CAB46879.1  - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284637, 18108381, 18108387, 284585

247	78873185 (493, 494)	Novel Protein sim. GBank g j1839006 emb CAB0648  - (Z85982) argB [Mycobacterium tuberculosis]		Kinase	264809, 264691, 35696423, 18108387
248	80488983 (495, 498)	Novel Protein sim. GBank g j186574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 264907, 284511, 264602, 264768, 264688, 285021, 35695959, 18108385
249	78784845 (497, 498)			UNCLASSIFIED	264907, 284910, 265011, 264782, 264638
250	78818980 (499, 500)				21808786, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645156, 26331822, 26331824, 52644045, 265018, 21908785, 21908788, 265020, 27486281, 27486285, 35695763, 18108376, 264556, 264559, 264585
252	78737758 (503, 504)	Novel Protein sim. GBank g j327166 db BAA31651  - (AB014576) KIAA0878 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 508)	Novel Protein sim. GBank g j3036880 emb CAA18513  - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank g j3915488 sp O34891 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COIT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264806, 264602, 264687, 265021, 264488
255	11388316 (509, 510)	Novel Protein sim. GBank g j1865720 db BAA04134  - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank g j465787 sp P34422 YL31, CAEEL - HYPOTHETICAL 88.0 KD PROTEIN F4488.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank g j1172039 sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA-3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA-3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459484 (515, 516)	Novel Protein sim. GBank g j3127838 emb CAA18902  - (AL023498) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	78910152 (517, 518)			collagen	264681, 264688, 264692
260	20378437 (519, 520)			UNCLASSIFIED	264682, 264556
261	20285683 (521, 522)	Novel Protein sim. GBank g j123781 sp P42422 HJTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264389
263	88095045 (525, 528)	Novel Protein sim. GBank g j3924708 emb CAA84846  - (Z35597) Weak similarity with sea squirt nitrogen precursor protein (blast score 71); cDNA EST EMBL:702089 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264458, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264804, 265019, 264605, 264760, 18108351, 264763, 264784, 264288, 264788, 264789, 264789, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	37370826 (527, 528)	Novel Protein sim. GBank g j3043734 db BAA25531  - (AB011177) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264608, 21908754, 265018, 265019, 265020

265	95355648 (529, 530)	Novel Protein sim. GBank gl 4589624 gb BAA78034.1  - (AB023207) KIAA0990 protein [Homo sapiens]		kinase	284488, 35896286, 29331824, 56182181, 35898052, 264508, 264905, 264908, 264907, 68712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264596, 55811388, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21908765, 21908787, 21908789, 265020, 264891, 33857023, 33857109, 33857182, 264828, 35898423, 35898555, 264830, 264831, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526486, 87168518, 264564, 264566, 264486
266	78588076 (531, 532)				264600
267	11382222 (533, 534)			UNCLASSIFIED	264828
268	78809568 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84381144 (539, 540)	Novel Protein sim. GBank gl 4507387 ref NP_003182.1 pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)	Novel Protein sim. GBank gl 4980738 gb AAD35331.1 AE001707 - glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		UNCLASSIFIED	264909, 264693
272	9874778 (543, 544)	Novel Protein sim. GBank gl 1188224 sp P44589 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		synthase	264908
273	12840684 (545, 546)			UNCLASSIFIED	264688
274	39524248 (547, 548)	Novel Protein sim. GBank gl 3253159 (AF005335) - Translation initiation factor eIF2C [Oryctolagus cuniculus]			264564
275	82787041 (549, 550)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	264807, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	66871073 (551, 552)	Novel Protein sim. GBank gl 128021 sp P20864 OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN			265008, 60432229
277	80079735 (553, 554)	Novel Protein sim. GBank gl 128021 sp P20864 OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN		ribosomal prot	264600, 18108387
278	12886847 (555, 556)	Novel Protein sim. GBank gl 79839 pir J03812 - uvrB protein - Micrococcus luteus		UNCLASSIFIED	264689
279	95282719 (557, 558)			nuclease	264508, 264604, 21806784, 264638, 264557, 264404
280	5603817 (559, 560)				264259
281	80249598 (561, 562)	Novel Protein sim. GBank gl 3123160 sp Q18884 YLN2 CAEEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 264634, 264555, 264556, 264557, 264558
282	18598882 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (587, 588)	Novel Protein sim. GBank gi2428094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696032, 29331828, 284508, 284905, 284600, 284602, 284605, 284682, 284784, 56181582, 21908784, 18108378, 284636, 284559, 18108387
285	8757940 (569, 570)	Novel Protein sim. GBank gi2072674 (emb CAB08305  - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	284603
286	80503235 (571, 572)	Novel Protein sim. GBank gi1785323 (bba1157678 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]; silkworms, Peptide Partial, 633 aa) [Bombyx mori]		UNCLASSIFIED	284688
287	12745921 (573, 574)	Novel Protein sim. GBank gi1870009 (emb CAB08680  - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis])	Contains protein domain (PF00440) - Bacterial regulatory proteins, tetR family	UNCLASSIFIED	284557
288	20756502 (575, 576)	Novel Protein sim. GBank gi2506864 (sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	284601
289	80043804 (577, 578)	Novel Protein sim. GBank gi1625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	284605
290	80430175 (579, 580)	Novel Protein sim. GBank gi1718085 (sp P53528 UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase	UNCLASSIFIED	284909, 284605, 284687, 284689, 284692
291	20747431 (581, 582)	Novel Protein sim. GBank gi117422 (sp P10040 CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696032, 284906, 265011, 284628, 55811576
292	80052555 (583, 584)	Novel Protein sim. GBank gi1181819 (dbj BAA11565  - (D82384) a variant of TSC-22 [Gallus gallus]			52644507, 29331822, 264592, 265020, 284639
293	80082519 (585, 586)	Novel Protein sim. GBank gi3849789 (dbj BAA33403  - (AB012228) SecA [Vibrio alginolyticus]		synthase	284508
294	79830303 (587, 588)	Novel Protein sim. GBank gi5889867 (emb CAB52004.1  - (AL109683) putative membrane protein [Streptomyces coelicolor A3(2)])	UNCLASSIFIED	UNCLASSIFIED	284905, 284687, 264638
295	79444180 (589, 590)				
296	79807078 (591, 592)				
297	79831297 (593, 594)				
298	80418868 (595, 596)				

298	95293298 (597, 598)	Novel Protein sim. GBank gij220637[dbj BA014771] - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	264488, 263984, 56994075, 22278997, 22278998, 22278999, 20281099, 28931824, 28331825, 29331826, 60432289, 28331827, 28331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264595, 264596, 264759, 33657084, 87188558, 265018, 265019, 264764, 264288, 264768, 264687, 58181562, 264769, 21908765, 21908768, 21908769, 33657023, 264692, 33657109, 27486281, 18108370, 264628, 264629, 53811578, 35685855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108387, 87168518, 22279000, 22279002, 264565, 264588, 264587
300	20711340 (598, 600)	Novel Protein sim. GBank gij145922 (M20981) - Iron diferrate transport protein precursor [Escherichia coli]		UNCLASSIFIED
301	13511332 (601, 602)	Novel Protein sim. GBank gij1174881[sp P44594 TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]		transport
302	9875280 (603, 604)	Novel Protein sim. GBank gij1728887[sp P40802 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264687
303	79574895 (605, 608)	Novel Protein sim. GBank gij67885[pir J HNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus		264908
304	20711344 (607, 608)	Novel Protein sim. GBank gij728887[sp P40802 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264689
305	80412520 (609, 610)	Novel Protein sim. GBank gij1657554[gb AA818082.1] - (U73857) hypothetical protein [Escherichia coli]	helicase	264602
306	8515878 (611, 612)	Novel Protein sim. GBank gij1657554[gb AA818082.1] - (U73857) hypothetical protein [Escherichia coli]		264783
307	80222801 (613, 614)	Novel Protein sim. GBank gij170812[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	UNCLASSIFIED	263978
308	80064303 (615, 616)	Novel Protein sim. GBank gij170812[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	UNCLASSIFIED	265010, 21908768, 265020, 18108374, 263977
309	80504138 (617, 618)	Novel Protein sim. GBank gij8420387[emb CAB46878.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01351) - Ribonuclease HII	284910, 284600, 264805, 264687, 264689, 264638, 18108387
310	80053818 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]		264769
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264603
312	80054347 (623, 624)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]		264602
313	80046768 (625, 626)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	UNCLASSIFIED	264566
				264603, 264567

314	187645112 (627, 628)	Novel Protein sim. GBank gll3661583 (AF092175) - Ikaros (Dantio reflo)	Contains protein domain (PF00320) - GATA zinc finger	dna_mg_bind	264259, 60432289, 26331828, 264805, 264908, 264908, 264908, 264908, 264910, 60432229, 33637402, 60433438, 33109854, 265011, 265017, 264803, 265018, 264288, 264768, 264692, 35695763, 264628, 264629, 264639, 60170394, 22279002, 264589
315	82356091 (629, 630)	Novel Protein sim. GBank gll1652620(dj)BAA17540] - (D80907) pyridine nucleotide transhydrogenase beta subunit [Synecococcus sp.]			264508, 264600, 264762, 264687, 264768, 52844229, 264769, 264689, 264636, 264636, 264486
316	79811071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	264683
317	20468844 (633, 634)	Novel Protein sim. GBank gll118244]sp]P24176]DAPE. ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)		UNCLASSIFIED	264605
318	94141836 (635, 636)	Novel Protein sim. GBank gll468022]p]b]AAD27583.1(AF11827) Dnb-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostellum (slime mold) repeats	transport	264908, 264908, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21908769, 264691, 264693, 264628, 63274791, 264635, 264636, 264638, 83373044, 22279002, 264589
319	17289360 (637, 638)	Novel Protein sim. GBank gll1149693]emb]CAA60220] - (X86498) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gll2811033]sp]O05314]GLGC. MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gll1680718 (U68234) - all-trans-retinoic acid 4-hydroxylase [Dantio reflo]		cyto450	264508, 264908, 264907, 264908, 265009, 264596, 264784, 264628, 264634, 264635, 264638, 264639, 83373044, 264587
322	68489053 (643, 644)	Novel Protein sim. GBank gll1180355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265008, 264593, 264628, 264635
324	78174383 (647, 648)			UNCLASSIFIED	264687
325	78882691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gll451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264488, 264905, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	
329	10173821 (657, 658)			UNCLASSIFIED	264592
330	86597787 (659, 660)	Novel Protein sim. GBank gll4181358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	264510
331	79754888 (661, 662)	Novel Protein sim. GBank gll80741]p]r]S20912 - regulatory protein whiB - Streptomyces coelicolor		UNCLASSIFIED	264259, 264908
332	80071440 (663, 664)	Novel Protein sim. GBank gll114049]sp]P19480]AHPE_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		transcriptfactor	264910, 264687, 264689, 264638, 264587
333	13008555 (665, 666)			reductase	35698423, 264636, 264638, 264585
					264687

334	80230771 (667, 668)	Novel Protein sim. GBank glj322228[pir][S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	264905, 264600, 264604, 264486
335	80057028 (669, 670)	Novel Protein sim. GBank glj219393[embj][CA808602] - (Z98800) glpQ2 [Mycobacterium tuberculosis]	esterase	264907, 264603, 264683, 18108374, 264636, 18108387
336	80414318 (671, 672)		UNCLASSIFIED	265009, 264768, 264686
337	11090829 (673, 674)			264602
338	95413134 (675, 676)	Novel Protein sim. GBank glj5454074[ref][NP_008303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	264568, 18108397, 22278988, 26331822, 20281099, 29331824, 56182181, 68714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87186599, 265017, 265018, 265019, 264760, 55811150, 264681, 264782, 18108351, 264882, 264764, 264788, 264685, 264688, 264768, 52644228, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35698423, 35695855, 264635, 264555, 264638, 264558, 264837, 264957, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87186518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713[dbj][BAA35087.1] - (AB015879) DnaK [Porphyrromonas glighalis]	eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank glj2842699[spj][Q82353][UBPC - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)]	ubiquitin	264905, 265019, 264768, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank glj2688380 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	isomerase	264605
342	80054198 (683, 684)	Novel Protein sim. GBank glj1684738[embj][CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]	Contains protein domain (PF00280) - Tryptophan synthase alpha chain	264603, 264604
343	20468782 (685, 686)			
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117275[embj][CA809104] - (Z95818) hypothetical protein Rv0807 [Mycobacterium tuberculosis]	UNCLASSIFIED	264605, 264605, 264768, 18108370, 18108374, 35695855
345	80258653 (689, 690)	Novel Protein sim. GBank glj3023317[epj][Q48935][APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE]	histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glj4239787[embj][CAA75437] - (Y15168) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	264905



347	79158195 (693, 694)	Novel Protein sim. GBank gij731675jip138785jYH4. YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	285008, 285008, 285010, 285016, 263987, 283981
348	80020208 (695, 696)	Novel Protein sim. GBank gij1073810jip1347672 - ugpB protein - Escherichia coli		transport	284602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank gij3261598jembICAB009171 - (Z77137) hypothetical protein Rv1277 (Mycobacterium tuberculosis)		nuclease	285007
350	80502370 (699, 700)	Novel Protein sim. GBank gij295936jembICAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	285009, 284769, 284689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gij295936jembICAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	284769, 284805, 284808
352	11611585 (703, 704)	Novel Protein sim. GBank gij4416302jgbJAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	284595
353	80081853 (705, 706)	Novel Protein sim. GBank gij1174887jip142873jURE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	284604
354	56626130 (707, 708)	Novel Protein sim. GBank gij115157jip16574jBVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	284628
355	80046344 (709, 710)	Novel Protein sim. GBank gij115157jip16574jBVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED	284909, 284595, 284683, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gij115157jip16574jBVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		transcriptfactor	284909, 284591, 284592
357	80070566 (713, 714)	Novel Protein sim. GBank gij497637 (J03839) - cytochrome oxidase d subunit 1 [Escherichia coli]		oxidase	284605
358	37032756 (715, 716)	Novel Protein sim. GBank gij2280990 (AF006000) - Big 1 [Bordetella pertussis]		UNCLASSIFIED	284768
359	80501488 (717, 718)	Novel Protein sim. GBank gij3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		UNCLASSIFIED	284604, 284769
360	80026748 (719, 720)	Novel Protein sim. GBank gij3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		UNCLASSIFIED	284594
361	80584075 (721, 722)	Novel Protein sim. GBank gij3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		transferase	22278996, 284259, 29331822, 29331824, 284605, 55811957, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gij113764jip125718jAMY1 - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	284688
363	79750145 (725, 726)	Novel Protein sim. GBank gij22829818jip185171jNUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)			284588
364	82443593 (727, 728)	Novel Protein sim. GBank gij22829818jip185171jNUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	284769, 284602, 284604, 284508, 284762, 284638, 284488

365	88040288 (729, 730)	Novel Protein sim. GBank gi 4929268 gb AAD33924.1  - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	284488, 21906788, 21906787, 55811576, 21906769, 29146629, 22278995, 22278996, 265020, 265022, 284634, 284691, 284593, 33857023, 33857402, 284693, 284639, 284594, 29331824, 284758, 18108385, 28331827, 87168559, 285018, 22279000, 265019, 284482, 284761, 264681, 18108351, 265017, 284757
366	81821838 (731, 732)			
367	95357471 (733, 734)	Novel Protein sim. GBank gi 4503843 ref NP_003908.1 pG2AD - UNKNOWN	Contains protein domain (PF01602) - Glycoprotein Adaplin N terminal region	60424179, 65274572, 56182375, 22278994, 56994075, 22278998, 284259, 29331822, 29331824, 56182181, 60424289, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 284805, 284828, 56182435, 285008, 284512, 265008, 284591, 55812038, 55811388, 285010, 87168559, 285017, 285018, 284604, 265019, 55811150, 284448, 284389, 284288, 284888, 284788, 56181562, 21906788, 21906788, 55811957, 35895917, 285022, 60170815, 33857023, 65274820, 18108385, 283987, 33857109, 33857349, 35895763, 264828, 18108376, 55811576, 65274791, 35895856, 56182323, 83373044, 60432113, 284563, 284584, 284587, 284509
368	78607269 (735, 736)	Novel Protein sim. GBank gi 3913029 sp P84987 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	284508, 284604, 284605, 284636
369	95262917 (737, 738)			
370	88090868 (739, 740)	Novel Protein sim. GBank gi 3249559 (AF018261) - EH domain binding protein Epain [Rattus norvegicus]		284805, 284592, 284605, 284766, 284691
371	95292599 (741, 742)	Novel Protein sim. GBank gi 2995299 emb CAA18328  - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - transferase IPP transferase	284805, 284908, 284510, 284600, 284601, 284802, 284603, 265018, 284604, 284605, 285021, 284892, 284636, 284584
372	80021107 (743, 744)	Novel Protein sim. GBank gi 2506393 sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN		284584
373	78663768 (745, 746)			
374	78947568 (747, 748)	Novel Protein sim. GBank gi 3341840 emb CAA13184  - (AJ231122) z81 [Vibrio cholerae]	UNCLASSIFIED	284809
375	91230181 (749, 750)	Novel Protein sim. GBank gi 5458834 gb AA043716.1  - (AF182322) prolodaderin gamma A2 [Homo sapiens]	UNCLASSIFIED	284905, 284808
376	80505214 (751, 752)	Novel Protein sim. GBank gi 1805409 dbj BAA08970  - (D50453) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 284259, 28331828, 56182435, 60433358, 60433438, 284757, 55812038, 284758, 55811957, 284690, 33857023, 284769
377	10339083 (753, 754)		UNCLASSIFIED	284808

376	80056153 (755, 756)	Novel Protein sim. GBank gl 1076013 pir A48930 - carb	Contains protein domain (PF00289) - synthase	UNCLASSIFIED	265008, 264555
378	80503437 (757, 758)	protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Carbamoyl-phosphate synthase (CPSase)		264769
380	80060937 (759, 760)	Novel Protein sim. GBank gl 216558 dbj BAA02174  - (D12851) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - dehydrogenase		264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gl 3327136 dbj BAA31636  - (AB014581) KIAA0681 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87168518, 22278002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 26331822, 60432289, 29331827, 264286, 264766, 263987, 65274791, 35695855, 263981, 83373044, 264567
385	10237678 (769, 770)				264692
386	79633434 (771, 772)	Novel Protein sim. GBank gl 1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00485) - dehydrogenase		264906
387	17960637 (773, 774)	Novel Protein sim. GBank gl 1460074 emb CA01048  - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gl 4240169 dbj BAA74863.1  - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - homeobox		35696286, 264905, 66712502, 60432229, 264593, 60433356, 264688, 264688, 21908765, 264891, 22278000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278986, 264630, 264556, 22278002
390	80078949 (778, 780)			UNCLASSIFIED	264600
391	7657302 (781, 782)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			264482
392	79786056 (783, 784)				
393	33206031 (785, 786)	Novel Protein sim. GBank gl 3378523 emb CAA08867  - (AJ009832) cyclomaltoextrinase glucanotransferase [Thermotoga neapolitana]	UNCLASSIFIED		264908
			synthase		264602, 21806764
394	10104463 (787, 789)				
395	80228010 (789, 790)				
396	20436224 (791, 792)	Novel Protein sim. GBank gl 2677780 (U70327) - unknown [Paratropus polyactis]	UNCLASSIFIED		264693
397	80417014 (793, 794)	Novel Protein sim. GBank gl 4507809 ref NP_000388.1 pWAS  - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Contains protein domain (PF00047) - struct		264508, 264563
			Immunoglobulin domain		264556
398	91230517 (795, 796)	Novel Protein sim. GBank gl 1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - transport		265007, 265009, 264508, 264556, 264629, 264766
			Mitochondrial carrier proteins		18108398, 22278985, 22278998, 56994075, 22278999, 264289, 26331824, 26331828, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264286, 264766, 21908765, 21908766, 21908767, 265020, 265021, 33657023, 33657109, 264628, 3588423, 35895855, 264952, 18108380, 264587, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gi 3358091 dbj BAA31995  - (AB016974) glycerol kinase [Pseudomonas toleosa]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	284592, 284595
400	94117490 (799, 800)	Novel Protein sim. GBank gi 728835 epi P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278999, 284259, 29331824, 285006, 265007, 265009, 60432229, 33657402, 21908754, 285010, 285017, 285018, 285019, 18108351, 18108357, 21908765, 265021, 285022, 284691, 284692, 33657023, 18108370, 65274791, 284634, 284636, 60170394, 56182323, 284594
401	11397491 (801, 802)	Novel Protein sim. GBank gi 4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	
402	95420284 (803, 804)	Novel Protein sim. GBank gi 5689487 dbj BAA83027.1  - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	- phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 284093, 284259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 284908, 284907, 284909, 285008, 284511, 285007, 265008, 284910, 284591, 33657402, 60433356, 60433438, 284596, 21908754, 52844288, 285010, 285011, 87188559, 265017, 285018, 285019, 284681, 18108351, 284682, 284448, 284288, 284684, 284766, 284767, 284688, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 285020, 285021, 285022, 284690, 284693, 65274620, 35695763, 284628, 18108370, 284629, 18108378, 35898423, 55811576, 284635, 284636, 284557, 284639, 18108365, 22279002, 284593, 284594, 284595, 284596, 284768, 284632, 284639, 284563, 284682, 285008, 284682
403	80439913 (805, 806)			UNCLASSIFIED	
404	1180865 (807, 808)				
405	79471280 (809, 810)	Novel Protein sim. GBank gi 2661649 emb CAA15755  - (AL009198) dnaE2 [Mycobacterium tuberculosis]		polymerase	
406	79634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 284693
407	80478229 (813, 814)				
408	80079958 (815, 816)			UNCLASSIFIED	284769
409	5040527 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058918) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		UNCLASSIFIED	284600
				helicase	284259

410	95357406 (819, 820)	Novel Protein sim. GBank gij475016[dbj BAA08184] - (D28601) Unknown [Mus musculus]		UNCLASSIFIED	284488, 52846365, 52846842, 58181686, 35898288, 52845080, 29331822, 29331824, 58182181, 28331825, 60424289, 35898052, 33656970, 284508, 284509, 284905, 284908, 284907, 284908, 52844045, 284909, 284510, 285007, 284512, 285008, 284910, 33657402, 284758, 52846317, 55811386, 285010, 285011, 285017, 284804, 285018, 55811150, 284782, 284784, 284786, 284887, 284788, 284788, 52844229, 21908786, 285020, 285021, 284534, 52844150, 284692, 33657023, 85274820, 33657109, 33657182, 27486261, 35895783, 284828, 284629, 60431528, 18108378, 283978, 35898423, 35898655, 284632, 284634, 284635, 284637, 284638, 284558, 284639, 56182323, 284559, 60432113, 22279002, 284563, 284565, 284486
411	80501670 (821, 822)			UNCLASSIFIED	284769
412	80241662 (823, 824)	Novel Protein sim. GBank gij3261784[embj CAB08997] - (Z8559) htpX [Mycobacterium tuberculosis]		eph	284807, 284910, 283873, 22279002, 284605
413	11076446 (825, 826)	Novel Protein sim. GBank gij128038[sp P20707 ODO1_AZOV1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)]		dehydrogenase	18108374, 284760, 284769, 284602, 284638, 284603, 284909, 284605
414	82050554 (827, 828)	Novel Protein sim. GBank gij4888350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	284908, 87168518
415	84453144 (829, 830)	Novel Protein sim. GBank gij2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	284488, 284800, 284802, 284764, 284636
416	80402775 (831, 832)	Novel Protein sim. GBank gij170917[sp P3231 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		284605
417	20153787 (833, 834)	Novel Protein sim. GBank gij328165[embj CAB03751] - (Z81388) hypothetical protein Rv2419c [Mycobacterium tuberculosis]		UNCLASSIFIED	284689, 284693
418	84125841 (835, 836)			collagen	284908, 284910, 284784, 284639
419	85314273 (837, 838)			phosphatase	284769
420	37036349 (839, 840)	Novel Protein sim. GBank gij291694[embj CAA17580] - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	284908, 284600, 284601, 284603, 284604, 284760, 284769
421	95282842 (841, 842)	Novel Protein sim. GBank gij231752[sp Q00787 CHB1_STRAL - 80 KD CHAPERONIN 1 (PROTEIN CPN80 1) (GROEL-PROTEIN 1) (HSP58)]	Contains protein domain (PF00118) - TCP-1/cpn80 chaperonin family	eph	22278896, 284682, 18108376, 18108387
422	76471263 (843, 844)			UNCLASSIFIED	284509
423	79604648 (845, 846)			UNCLASSIFIED	284509

424	78866557 (847, 848)	Novel Protein sim. GBank glj4828614[re]NP_004977.1 pKTN1 - kinesin 1 (kinesin receptor)		struct	285019
425	80431450 (849, 850)	Novel Protein sim. GBank glj1703707 bbs178482 - KRP5-kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	struct	284908, 285007, 55811386, 284768, 55810764
426	80084522 (851, 852)				284605, 284559
427	80057232 (853, 854)	Novel Protein sim. GBank glj231828 pP28929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	284803, 284636
428	79487788 (855, 856)	Novel Protein sim. GBank glj128126 pJ522897 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	284883
429	80081232 (857, 858)	Novel Protein sim. GBank glj1808154 emb CAB08451 - (284385) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase	UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 284584, 284782
430	80504182 (859, 860)	Novel Protein sim. GBank glj1808154 emb CAB08451 - (284385) hypothetical protein Rv0688 [Mycobacterium tuberculosis]			284508, 284905, 284509, 284908, 284909, 285008, 284600, 284687, 284789, 284889, 284636, 284638, 18108385, 284486
431	20824249 (861, 862)				284568
432	16525372 (863, 864)				285020
433	81494303 (865, 866)	Novel Protein sim. GBank glj3123552 emb CAA18608 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0268 LIKE) [Homo sapiens]		UNCLASSIFIED	284907, 284908, 284909, 284910, 284592, 284595, 284758, 284804, 284780, 284762, 284763, 284638, 284837, 22278002
434	84326323 (867, 868)	Novel Protein sim. GBank glj2495272 sp Q88828 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696052, 55810784, 55811578, 65274781, 35695855, 60432113, 55811150, 284636, 284768
435	80502738 (869, 870)	Novel Protein sim. GBank glj114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	284595, 264769
436	41085853 (871, 872)			UNCLASSIFIED	265020, 22278002
437	11389281 (873, 874)			UNCLASSIFIED	284593
438	11773835 (875, 876)			UNCLASSIFIED	284886
439	80019485 (877, 878)	Novel Protein sim. GBank glj3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			284905, 284800, 284802, 284604
440	78841062 (879, 880)	Novel Protein sim. GBank glj2281232 gb AAB8531.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 284905, 284908, 284909, 265011, 35698423
441	20386835 (881, 882)	Novel Protein sim. GBank glj5638946 gb AAD45904.1 AF16132 - (AF161328) histidine kinase CuiS [Corynebacterium diphtheriae]			284805
442	85281058 (883, 884)	Novel Protein sim. GBank glj1184780 (U46088) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 284909
443	82458427 (885, 886)	Novel Protein sim. GBank glj5686993 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 284508, 284908, 284512, 284604, 284782, 284769, 284689, 284636
444	11385887 (887, 888)	Novel Protein sim. GBank glj1783249 gb BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	284591

445	79552708 (889, 890)	Novel Protein sim. GBank gij5531272[emb]CAB50897.1] - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	284893 284509
446	79810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcript factor	284788, 55811578
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542814[emb]CAB02185] - (Z80109) fms [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	284508, 284600, 284603, 284605, 284682, 284788, 18108362, 284634, 18108387
448	80238110 (895, 896)	Novel Protein sim. GBank gij118784[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284605, 284559
449	20460834 (897, 898)	Novel Protein sim. GBank gij4589508[db]BAA78775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	65274572, 22278998, 29331824, 29331826, 284906, 284910, 284592, 52846317, 285017, 21908787, 55811957, 58528486, 22279002
451	21433609 (901, 902)			UNCLASSIFIED	284486
452	10287278 (903, 904)	Novel Protein sim. GBank gij2850814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	284692 284907, 284800
453	52560098 (905, 906)	Novel Protein sim. GBank gij2493000[sp]Q09450[SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		transferase	284603
454	38523922 (907, 908)				
455	13089692 (909, 910)	Novel Protein sim. GBank gij446889[emb]CAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	284887
456	79563081 (911, 912)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	UNCLASSIFIED	284691 284905
457	79831273 (913, 914)				
458	79581227 (915, 916)	Novel Protein sim. GBank gij4508075[ref]NP_002733.1[ppRKC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	55812038, 285010, 285018, 284681
459	80567359 (917, 918)	Novel Protein sim. GBank gij113158[sp]P25516[ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		kinase	22278997, 284259, 29331826, 285018, 284448, 284369, 21808765, 35696423
460	79245880 (919, 920)	Novel Protein sim. GBank gij1168574[sp]P42494[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		UNCLASSIFIED	284906
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[sp]P42494[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	284602, 284605, 284768, 284768, 285021, 33857023, 284559

462	79808589 (923, 924)	Novel Protein sim. GBank gi 1346891 sp P45597 PTF1_XANCP. (CONTAINS: PHOSPHORYL TRANSFER PROTEIN (MTP) PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00381) - PEP-utilizing enzymes	UNCLASSIFIED	284807
463	79768417 (925, 926)	Novel Protein sim. GBank gi 83413 U88 [Human herpesvirus 6]		UNCLASSIFIED	284905, 284906, 284908, 284909, 284910, 284991, 284995, 285011, 284632, 284635, 284636, 284637, 284638, 284639
464	82340151 (927, 928)	Novel Protein sim. GBank gi 5689776 emb CA852137.1  - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00848) - Calpain family cysteine protease	UNCLASSIFIED	284634
465	83005730 (929, 930)	Novel Protein sim. GBank gi 1808175 emb CA808470  - (Z64395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	285017, 21906784, 285020
466	20460845 (931, 932)	Novel Protein sim. GBank gi 1808175 emb CA808470  - (Z64395) rpsC [Mycobacterium tuberculosis]		UNCLASSIFIED	284605, 284659
467	80408035 (933, 934)	Novel Protein sim. GBank gi 548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	284784
468	52562208 (935, 936)	Novel Protein sim. GBank gi 2114024 emb CA808957  - (Z85958) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	284692
469	19520327 (937, 938)	Novel Protein sim. GBank gi 2809459 emb CAA17347  - (AL021929) cbbQ [Mycobacterium tuberculosis]		UNCLASSIFIED	284488
470	80502758 (939, 940)	Novel Protein sim. GBank gi 14921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	synthase		284602, 284769
471	17937351 (941, 942)	Novel Protein sim. GBank gi 14921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	transport		265019
472	80047458 (943, 944)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284596, 284685, 284557
473	20558793 (945, 946)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284369
474	80593365 (947, 948)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	22278997, 284692, 284288
475	82454665 (949, 950)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284907, 284908, 284511, 265008, 284762, 284448, 284636, 284638
476	84143657 (951, 952)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 60432048, 284259, 284508, 52844045, 55812038, 284758, 265011, 284288, 284686, 52844228, 65274791, 284638, 284596
477	79175833 (953, 954)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284638
478	79833483 (955, 956)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284690, 284693
479	80189746 (957, 958)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	collagen		284688, 35685855, 285008, 284631, 284810, 284632, 284638, 285018, 284369, 284909
480	79390729 (959, 960)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachococcus baikalensis]	mapolymerase		264369
481	78624578 (961, 962)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachococcus baikalensis]		UNCLASSIFIED	284683
482	83050611 (963, 964)	Novel Protein sim. GBank gi 4083042 (AF068065) - GP800; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	284909, 284688, 284768, 284693, 55811576, 56182323, 18108395



483	20203308 (965, 968)	Novel Protein sim. GBank gij2104303jemb[CAB08632] - (Z95387) hypothetical protein Rv2810c [Mycobacterium tuberculosis]	Contains protein domain (PF00634) - Glycosyl transferases group 1	284600
484	11618046 (967, 968)	Novel Protein sim. GBank gij34-50883 (AF083334) - fibroin [Antheraea pernyi]	UNCLASSIFIED	284584
485	80191234 (969, 970)	Novel Protein sim. GBank gij5042272jemb[CAB44528.1] - (AL078616) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	UNCLASSIFIED	284604
486	80059042 (971, 972)	Novel Protein sim. GBank gij5724778jgb[AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	dehydrogenase	284638
487	11813338 (973, 974)	Novel Protein sim. GBank gij3882223jdb[BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]	kinase	284638
488	91222383 (975, 976)	Novel Protein sim. GBank gij82091jpi[A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)]	collagen	284688, 68714117, 284768, 18108385, 55911576, 265008, 265008, 265009, 265019, 22279002, 264259, 16108370, 284907, 284784, 56182323, 264288, 284693
489	10887710 (977, 978)	Novel Protein sim. GBank gij2894206jemb[CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]	UNCLASSIFIED	284639
490	95381124 (979, 980)	Novel Protein sim. GBank gij5282605jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	22278996, 29331822, 28331828, 264107, 284908, 284110, 265009, 284592, 284593, 60433356, 264288, 264683, 263974, 263976, 20281071, 60432113
491	80498412 (981, 982)	Novel Protein sim. GBank gij2894206jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284768
492	87421264 (983, 984)	Novel Protein sim. GBank gij2894206jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284600
493	11692842 (985, 986)	Novel Protein sim. GBank gij2894206jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284638
494	87726604 (987, 988)	Novel Protein sim. GBank gij2894206jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284489, 35898286, 60432289, 28331828, 35898052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 265008, 284910, 33857402, 264762, 264764, 264768, 284769, 284888, 21908785, 21908789, 35898917, 265020, 284893, 33857109, 284629, 35898423, 35695855, 284634, 284638
495	80028598 (989, 990)	Novel Protein sim. GBank gij2781517jemb[CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	284602, 284682, 284638
496	78985624 (991, 992)	Repressor (Amino-Terminal Domain) (R1-68)	Contains protein domain (PF01381) - Helix-turn-helix	284601, 265021
497	78848681 (993, 994)	Novel Protein sim. GBank gij128738jpi[P28225]PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)	oxidase	265006

488	88095408 (995, 996)	Novel Protein sim. GBank gl 1145789 (U41662) - neuroigin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	284259, 29331826, 35698052, 284508, 284509, 284805, 284808, 284907, 284908, 284909, 284510, 284511, 285008, 284910, 284591, 33657402, 284758, 285010, 285011, 284800, 284801, 284805, 284883, 284784, 284788, 284787, 284788, 284887, 284789, 21808787, 33657023, 284893, 284828, 284829, 35698423, 284630, 284832, 284834, 284835, 284837, 284838, 284558, 284839, 18108385, 284583, 284584, 284565, 284566, 284587
499	20438222 (997, 998)	Novel Protein sim. GBank gl 97480 pir S18739 - Integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	284805
500	11076810 (999, 1000)				284805
501	13418034 (1001, 1002)	Novel Protein sim. GBank gl 5708250 emb CAB52363.1] - (AL108747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gl 4488678 emb CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 285011, 284802, 284605, 284635
503	20284463 (1005, 1006)			UNCLASSIFIED	284564
504	10887321 (1007, 1008)			UNCLASSIFIED	284687
505	95003068 (1009, 1010)			UNCLASSIFIED	284389
506	16454282 (1011, 1012)	Novel Protein sim. GBank gl 4033509 sp P02589 CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	285010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gl 2501089 sp Q48127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	284604
508	78841424 (1015, 1016)	Novel Protein sim. GBank gl 468089 sp P34818 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1238.2 IN CHROMOSOME III		UNCLASSIFIED	284808
509	11776388 (1017, 1018)				284638
510	83373465 (1019, 1020)			UNCLASSIFIED	284887, 284639
511	16523578 (1021, 1022)				285007
512	20398484 (1023, 1024)	Novel Protein sim. GBank gl 2497418 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	284565
513	78457404 (1025, 1026)	Novel Protein sim. GBank gl 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	284683, 284689, 35698423, 284639
514	78813805 (1027, 1028)	Novel Protein sim. GBank gl 1184780 (U46088) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 284909
515	79462591 (1029, 1030)				22278999, 284690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gl 2127400 pir S65770 - maltotigosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q38)		amylase	284910

517	95262994 (1033, 1034)	Novel Protein sim. GBank gll2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264585
518	8491831 (1035, 1036)	Novel Protein sim. GBank gll854085[emb]CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91877888 (1037, 1038)	Novel Protein sim. GBank gll5689365[db]BAA83073.1 - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	- dna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645080, 29331824, 66714117, 60424269, 29331826, 35696052, 264905, 29331830, 86712502, 264511, 265007, 264591, 80432229, 33657402, 80433438, 21908754, 33109954, 52644296, 87168474, 37168859, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21908765, 21908766, 21908787, 21908769, 265021, 80170815, 33657023, 264692, 52645128, 33657109, 27486262, 27486264, 35695783, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56528488, 80432113
520	78669188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gll1169128[sp]P46839[CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80433608 (1043, 1044)	Novel Protein sim. GBank gll1172689[sp]P44331[RBKS_HAEIN - RIBOKINASE	Contains protein domain (PF00284) - pRb family carbohydrate kinase	- kinase	264805, 264768
523	16356013 (1045, 1046)	Novel Protein sim. GBank gll2132243[pir]S81028 - hypothetical protein YPL238c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261605 (1047, 1048)	Novel Protein sim. GBank gll4033608[db]BAA351361 - (AB012308) B2HC [Anthracidaria crassipine]		ATPase_associated	264092, 264596, 265011
525	79810048 (1049, 1050)				264807
526	38627630 (1051, 1052)	Novel Protein sim. GBank gll4106610[emb]CAA213651 - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fasta scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)				
528	85484134 (1055, 1056)			UNCLASSIFIED	264769
529	17936810 (1057, 1058)	Novel Protein sim. GBank gll731088[sp]P24215[UXXA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	56182575, 265017, 265018
530	10687336 (1059, 1060)	Novel Protein sim. GBank gll42144[emb]CAA2520[ - (X00513) NusA protein (nusA) [Escherichia coli]		hydrolase	265019
531	80226576 (1061, 1062)			UNCLASSIFIED	264687
532	80933444 (1063, 1064)	Novel Protein sim. GBank gll3262840[emb]CAB45758.1 - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00822) - SPRY domain	UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
				UNCLASSIFIED	264488, 264490, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1085, 1088)	Novel Protein sim. GBank gij483839 gb AAD31583.1 AF11229 - (AF11229) Integral inner nuclear membrane protein MANT [Homo sapiens]			284907, 284809, 284768, 35695917, 284630, 284555
534	82388284 (1087, 1088)	Novel Protein sim. GBank gij2895352 emb CAA04808.1  - (A001208) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		284905, 265011, 284601, 284602, 284805, 284782, 284788, 285020, 284893, 284838
535	78841850 (1089, 1070)	Novel Protein sim. GBank gij3878638 emb CAA88953  - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:700719 comes from this gene; cDNA EST yk485d8.3 comes from this gene; cDNA EST yk485d8.5 comes from this gene; cDNA EST yk48214.3 comes from this gene; cDNA EST Y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase associated	284906
536	79807207 (1071, 1072)	Novel Protein sim. GBank gij2498628 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KO PROTEIN IN BIOA 5 REGION	reductase		18108376, 284905, 284906, 284907, 284909
537	84147448 (1073, 1074)				
538	87821863 (1075, 1076)	Novel Protein sim. GBank gij134820 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen		285008, 284605, 65274781 28331822, 28331824, 28331825, 28331826, 28331827, 284908, 52844045, 33857402, 285017, 284782, 284883, 284288, 284885, 21908785, 35885783, 284558, 80170394, 284558, 22279002
539	28398288 (1077, 1078)	Novel Protein sim. GBank gij2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		284602, 265019
540	79837077 (1079, 1080)				
541	87782288 (1081, 1082)	Novel Protein sim. GBank gij3882241 db BAA34480.1  - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor		284893 18108394, 22278997, 22278998, 284259, 284112, 265009, 33857402, 55812038, 52846317, 285017, 21908785, 284893, 55811576, 284635, 58528488, 284588
542	85285638 (1083, 1084)	Novel Protein sim. GBank gij5042272 emb CAB44528.1  - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		284910, 285018, 284889, 284638, 284486
543	79786290 (1085, 1086)				
544	20437181 (1087, 1088)	Novel Protein sim. GBank gij2791398 emb CAA15994  - (AL021184) hypothetical protein Rv1484 [Mycobacterium tuberculosis]	UNCLASSIFIED		284602, 284908
545	80434504 (1089, 1090)		UNCLASSIFIED		284605
546	80249016 (1091, 1092)	Novel Protein sim. GBank gij4887211 gb AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			284768, 284634, 284907, 284592, 284909 284800, 284602, 21908785
547	11077563 (1093, 1094)	Novel Protein sim. GBank gij1350855 sp P18176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase		284604
548	82114938 (1095, 1096)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		284488, 284905, 284910, 284780, 284693, 284639, 284563, 284584

549	95421904 (1097, 1098)	Novel Protein sim. GBank gll4337460[gb AAD18133] - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278998, 22278997, 22278998, 22278999, 264259, 29331824, 68714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264888, 264888, 21906765, 21908788, 21908787, 21908788, 21908789, 265020, 264691, 33657023, 264692, 264693, 65274620, 52845129, 33657109, 27486261, 27486262, 27488264, 33657348, 55811576, 18108387, 60432113, 22278002
550	10886616 (1098, 1100)	Novel Protein sim. GBank		UNCLASSIFIED	264688
551	80439980 (1101, 1102)	gll3122893[sp P94085]SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	264908, 264909, 264768
552	84672870 (1103, 1104)	Novel Protein sim. GBank		UNCLASSIFIED	264689, 264639, 264563
553	80106002 (1105, 1106)	protein [Drosophila melanogaster]	Contains protein domain (PF00008) - EGF-like domain	glycoprotein	55811957, 264628
554	79818378 (1107, 1108)	Novel Protein sim. GBank		kinase	264908
555	78986347 (1109, 1110)	gll13151[sp P02808]PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank		transcriptfactor	284508, 284605, 284559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gll5042273[emb CAB44527.1] - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	284488
558	20724429 (1115, 1116)	Novel Protein sim. GBank		UNCLASSIFIED	284602
559	80084353 (1117, 1118)	Novel Protein sim. GBank		UNCLASSIFIED	284634

560	80088533 (1119, 1120)	Novel Protein sim. GBank gi2492585 sp Q53183 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF000005) - ABC transporter	transport	18108386, 284908, 284602, 284604, 18108374
561	20283187 (1121, 1122)			UNCLASSIFIED	284800
562	11688161 (1123, 1124)			UNCLASSIFIED	284889
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi4104925 (AF042276) - poly(hydroxycarboxylate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	284910, 284691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi2792310 (AF040570) - unknown [Amycolatopsis mediterranei]		dehydrogenase	284582
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi3449284 gb BAA32482  - (AB011532) MEGF9 [Rattus norvegicus]	Contains protein domain (PF000008) - EGF-like domain	synthase	285010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi4538568 emb CAB38487.1  - (AL035638) putative helicase [Streptomyces coelicolor]		helicase	284908, 284510, 285008, 284910, 284758, 284900, 284602, 284604, 284605, 284768, 284687, 284689, 35695917, 284693, 85274620, 284488
567	78560955 (1133, 1134)	Novel Protein sim. GBank gi100506 pi S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria trichervia (fragment)	Contains protein domain (PF003380) - Malic enzyme	UNCLASSIFIED	284881, 284691, 284593
568	94881793 (1135, 1136)	Novel Protein sim. GBank gi3915843 sp Q31212 IRS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF003318) - Ribosomal protein S2	ribosomal prot	284565
569	39508897 (1137, 1138)	Novel Protein sim. GBank gi118122 sp P21827 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		UNCLASSIFIED	18108378, 18108387, 284565
570	78375927 (1139, 1140)	Novel Protein sim. GBank		transport	284907, 284909
571	79783961 (1141, 1142)	Novel Protein sim. GBank gi118122 sp P21827 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		UNCLASSIFIED	284762
572	36988838 (1143, 1144)	Novel Protein sim. GBank gi4539222 emb CAB3888.1  - (AL049487) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	285007, 284601
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		UNCLASSIFIED	284638
574	13521592 (1147, 1148)	Novel Protein sim. GBank gi118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284687
575	13078416 (1149, 1150)	Novel Protein sim. GBank gi118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi45457625 emb CAB49116.1  - (AJ248283) PAB2227 [Pyrococcus abyssi]			284605
577	68727102 (1153, 1154)	Novel Protein sim. GBank gi5042274 emb CAB44528.1  - (AL078618) nuod, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF003346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35696052, 284638
578	11804477 (1155, 1156)	Novel Protein sim. GBank gi11723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	284638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi11723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	284682, 284559

580	80059417 (1159, 1180)				22278999, 35696052, 264555, 264556, 264558, 264559
581	78230833 (1181, 1182)			UNCLASSIFIED	265008, 264584
582	80049617 (1183, 1184)		Contains protein domain (PF00047) - immunoglobulin domain	struct	265021, 264555, 264557
583	78321382 (1185, 1186)			transport	264584
584	78845024 (1187, 1188)				
585	78581454 (1189, 1170)			UNCLASSIFIED	264488, 264908, 264788, 264887, 35698423
586	38277486 (1171, 1172)			UNCLASSIFIED	265018, 264684, 21806769
587	80497359 (1173, 1174)			UNCLASSIFIED	264808, 265007
588	78557239 (1175, 1176)			hydrolase	264600, 264602, 264605, 264769, 264690, 264557
589	78805828 (1177, 1178)			UNCLASSIFIED	265020, 264692
590	78815629 (1179, 1180)			UNCLASSIFIED	22278998, 264907, 264909, 264510, 265009, 265010, 264687, 264788, 35695917, 18108376, 264634, 264638, 264638
591	10313540 (1181, 1182)			UNCLASSIFIED	264808, 264909
592	13889767 (1183, 1184)			mapolymerase	264691
593	82348899 (1185, 1186)			MHC	263872
594	20212382 (1187, 1188)			dehydrogenase	264511, 264782, 264769, 264488
595	10064084 (1188, 1190)			UNCLASSIFIED	264605
596	13085170 (1191, 1192)				264769
597	80259003 (1193, 1194)			UNCLASSIFIED	264638
598	94140218 (1195, 1196)			UNCLASSIFIED	264592
599	20385137 (1197, 1198)			UNCLASSIFIED	264758, 65810784, 264555, 264558, 264637, 83373044
600	10357883 (1199, 1200)			UNCLASSIFIED	264603
601	78810404 (1201, 1202)			UNCLASSIFIED	264808
					264510

802	78250602 (1203, 1204)	Novel Protein sim. GBank gij3522981gpbAAC34243.1] - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	265007	
803	11466087 (1205, 1206)		UNCLASSIFIED	284595	
804	81675420 (1207, 1208)			284758	
805	20436657 (1209, 1210)	Novel Protein sim. GBank gij11753222spjP44917Y883_HAEIN - HYPOTHETICAL PROTEIN H0883	UNCLASSIFIED	284605	
806	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284gbiAAD38043.1JAF15138 - (AF151383) Cdc42 GTPase-activating protein [Mus musculus]	UNCLASSIFIED	284764	
807	95381508 (1213, 1214)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]	UNCLASSIFIED	284508, 284908, 85658542, 284682, 284687, 284689, 284534, 18108378, 35998423, 284638, 284555, 284638	
808	11810888 (1215, 1216)		UNCLASSIFIED	284682	
809	80064775 (1217, 1218)	Novel Protein sim. GBank gij2498701spjP55552Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	284605	
810	79629413 (1219, 1220)			284692	
811	87586205 (1221, 1222)			284508, 284908, 284907, 284908, 284909, 284511, 284910, 284758, 284604, 284684, 284786, 284888, 284892, 284628, 284635, 284636, 284837, 284558	
812	95287851 (1223, 1224)	Novel Protein sim. GBank gij18773861embjCAB07118] - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease 284600, 284601, 284604, 284789, 284558, 284565	
813	7523475 (1225, 1226)		UNCLASSIFIED	284389	
814	78969348 (1227, 1228)	Novel Protein sim. GBank gij5114231gbiAAD40238.1JAF13870 - (AF138709) histidine kinase YycG [Staphylococcus aureus]	kinase	18108372, 284563	
815	39586888 (1229, 1230)	Novel Protein sim. GBank gij1339850dbjBAA12741] - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	synthase	284600, 284602, 284629	
816	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387spjP35673GALE_ERWAM - UDP-GLUCOSE 4- EPIMERASE (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE)	isomerase	284603	
817	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498907spjO60789TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	52845158, 21806765, 35698423, 21806768, 21808769, 22278994, 35698286, 22278998, 285020, 285021, 285007, 285008, 284638, 52844150, 33657023, 284692, 284693, 28931822, 28931824, 55812038, 83373044, 58182181, 60424269, 68714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35698052, 28931828, 27486262, 33657349, 56528468, 285018, 285019, 22279002, 284482, 284448, 28931830, 68712502, 284909	



618	20632843 (1235, 1236)	Novel Protein sim. GBank gl 5459388 emb CAB50746.1  - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603
619	91227224 (1237, 1238)				56994075, 29331826, 33656970, 265008, 33657402, 33108954, 87188559, 264448, 18108374, 83373044
620	61183143 (1239, 1240)	Novel Protein sim. GBank gl 46433 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 [DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1]		phosphatase	29148498, 264756, 284389, 29148627
621	80239251 (1241, 1242)	Novel Protein sim. GBank gl 2633557 emb CAB13060  - (Z99110) yjdF [Bacillus subtilis]		UNCLASSIFIED	264556, 264558, 264639
622	20458427 (1243, 1244)	Novel Protein sim. GBank gl 1857710 gb AAB48482  - (U87224) contactin associated protein [Rattus norvegicus]		UNCLASSIFIED	264605
623	10131798 (1245, 1246)	Novel Protein sim. GBank gl 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK	Contains protein domain (PF00054) - laminin G domain	laminin	264908
624	19534127 (1247, 1248)	Novel Protein sim. GBank gl 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596
625	13084619 (1249, 1250)	Novel Protein sim. GBank gl 2894252 emb CAA17114.1  - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688
626	88082803 (1251, 1252)	Novel Protein sim. GBank gl 416592 sp P32323 JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 284805, 264808, 33657023, 33657109, 264558
627	80255457 (1253, 1254)	Novel Protein sim. GBank gl 3098418 (AF040844) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635
628	80077086 (1255, 1256)	Novel Protein sim. GBank gl 1711643 sp P50528 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600
629	79851602 (1257, 1258)	Novel Protein sim. GBank gl 1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264808, 264807
630	39565158 (1259, 1260)	Novel Protein sim. GBank gl 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490
631	20598718 (1261, 1262)	Novel Protein sim. GBank gl 140687 sp P11686 YQGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978
632	27843690 (1263, 1264)			UNCLASSIFIED	264808, 264800, 264605, 264768, 264689, 264486
633	80477772 (1265, 1266)			UNCLASSIFIED	264769
634	17938808 (1267, 1268)			UNCLASSIFIED	265019
635	78574508 (1269, 1270)			UNCLASSIFIED	264889
636	78810981 (1271, 1272)			UNCLASSIFIED	264586, 264782, 264693

637	82455798 (1273, 1274)	Novel Protein sim. GBank g 2328739 emb CAB10953  - (Z98288) recN [Mycobacterium tuberculosis]		nuclease	284908, 284907, 284510, 284511, 284601, 284602, 284603, 284604, 284605, 18108351, 284762, 284766, 284687, 284789, 284688, 35895917, 284693, 284634, 284638, 284639, 284559, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank g 4678662 emb CAB41074.1  - (AL049845) putative large ATP-binding protein [Streptomyces coelicolor]			284636
639	80204210 (1277, 1278)	Novel Protein sim. GBank g 458828 db BAA76836.1  - (AB023209) KIAA0992 protein [Homo sapiens]		struct	284112, 283974
640	17928578 (1278, 1280)	Novel Protein sim. GBank g 1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]		Contains protein domain (PF01466) - napolymerase Skp1 family	285009, 285010
641	79836398 (1281, 1282)			UNCLASSIFIED	284693
642	19898737 (1283, 1284)			UNCLASSIFIED	284565
643	81516220 (1285, 1286)			UNCLASSIFIED	284908, 284908, 284758, 284288, 284632, 284635, 284638, 284584
644	11751367 (1287, 1288)			UNCLASSIFIED	284684
645	85010807 (1289, 1290)			UNCLASSIFIED	284908, 284762, 284693, 284639, 284559
646	80089083 (1291, 1292)			UNCLASSIFIED	284595, 284588
647	80257085 (1293, 1294)	Novel Protein sim. GBank g 4507813 ref NP_003738.1 pTNKS - TANKYRASE		transcriptfactor	284909, 284591
648	80077428 (1295, 1296)	Novel Protein sim. GBank g 1044863 bbs 169646 - protamine [Monodonta turbinata, gonads, Peptide, 108 aa]		UNCLASSIFIED	284600
649	80247447 (1297, 1298)			UNCLASSIFIED	283978
650	11798316 (1299, 1300)			UNCLASSIFIED	284886
651	11776832 (1301, 1302)	Novel Protein sim. GBank g 1346916 sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			284802, 284638
652	85516704 (1303, 1304)	Novel Protein sim. GBank g 1722977 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	284805, 284907, 284909, 283978, 284637
653	82124947 (1305, 1306)			UNCLASSIFIED	22278998, 284510, 284511, 284512, 284593, 21906754, 284803, 284760, 18108376, 284558
654	95010589 (1307, 1308)	Novel Protein sim. GBank g 130327 sp P28647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)		UNCLASSIFIED	284908, 284595, 284632
655	79320892 (1309, 1310)			transferase	284592
656	80418739 (1311, 1312)			Contains protein domain (PF01553) - Acyltransferase	
657	20811010 (1313, 1314)			UNCLASSIFIED	284602, 284605, 284766, 284691
				UNCLASSIFIED	284557, 284558

659	87761915 (1315, 1316)	Novel Protein sim. GBank gij5689483jdbj BAA83030.1  - (AB029001) KIAA1078 protein [Homo sapiens]	UNCLASSIFIED	22278986, 60432049, 29331822, 29331824, 29331826, 285007, 285009, 33657402, 33657084, 285017, 264448, 21908785, 21908786, 283987, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872jprj 48724 - zinc finger protein PZF - mouse	transcription factor	22278989, 60432049, 66714117, 29331827, 285007, 284786, 56181562, 18108359, 18108365, 18108370, 18108381
660	81897822 (1319, 1320)	Novel Protein sim. GBank	UNCLASSIFIED	284787
661	80026023 (1321, 1322)	gij134180jprj 15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTI-TERMINATOR	UNCLASSIFIED	284510, 265009, 284600, 284602, 284603, 284604, 284605, 3283386, 18108376, 284636, 18108387, 22278000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gij4548229jpbj AD22450.1 AF11818 - (AF118183) SecA homolog [Actinobacillus actinomycetemcomitans]	UNCLASSIFIED	284605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gij5689250jdbj BAA82881.1  - (AB024335) similar to orf3 [Comamonas testosteroni]	dehydrogenase	284789
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij1852848jdbj BAA17768  - (D90909) DNA photolyase [Synechocystis sp.]	isomerase	284600
665	80078053 (1329, 1330)	Novel Protein sim. GBank gij116841jprj P21640 COBJ_PSEDE - PRECORRIN-3 C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE)	glycoprotein	284907, 265007
666	78603142 (1331, 1332)	Novel Protein sim. GBank gij3261829jemb CAB10927  - (Z98280) hypothetical protein Rv1230c [Mycobacterium tuberculosis]	UNCLASSIFIED	284689, 284602, 284593
667	84631802 (1333, 1334)	Novel Protein sim. GBank gij5688851jdbj BAA82702.1  - (AB017438) Orf5 [Streptomyces coelicolor]	UNCLASSIFIED	284905, 284906, 284908, 284600, 284601, 284603, 284605, 284760, 284689, 284636, 284638, 284639
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853jemb CAA20808  - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	UNCLASSIFIED	284637
669	12987154 (1337, 1338)	Novel Protein sim. GBank gij2582531 (AF028444) - 2-isopropylmalate synthase [Streptomyces coelicolor]	synthase	284905, 284906, 284908, 284601, 284762, 284786, 284689, 284638, 18108365, 284486
670	80238549 (1339, 1340)	Novel Protein sim. GBank gij4589285jpbj AD26430.1 AF13515 - (AF135154) feric alkaligin aldophore receptor [Bordetella pertussis]	UNCLASSIFIED	284690, 284692, 284693, 284636, 18108387
671	79601388 (1341, 1342)	Novel Protein sim. GBank gij2114430 (U92703) - Oil-1/EBF-like-3 transcription factor [Mus musculus]	transcription factor	284910, 265017
672	79834371 (1343, 1344)	Novel Protein sim. GBank gij4589285jpbj AD26430.1 AF13515 - (AF135154) feric alkaligin aldophore receptor [Bordetella pertussis]	transcription factor	284769
673	82285788 (1345, 1346)	Novel Protein sim. GBank gij4589285jpbj AD26430.1 AF13515 - (AF135154) feric alkaligin aldophore receptor [Bordetella pertussis]	UNCLASSIFIED	284629
674	79189259 (1347, 1348)	Novel Protein sim. GBank gij4589285jpbj AD26430.1 AF13515 - (AF135154) feric alkaligin aldophore receptor [Bordetella pertussis]	UNCLASSIFIED	284629

675	67895970 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AA035347.1 AE001708 - (AE001708) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	284488, 22278999, 68714117, 284508, 284511, 285008, 60433438, 284600, 284601, 284602, 284603, 284604, 284605, 284782, 284687, 284769, 60431602, 18108374, 284636, 284638 285010
676	78898807 (1351, 1352)	Novel Protein sim. GBank gi 1723568 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C8.07		ATPase-associated	284591, 284632
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 687208 (U03976) - dynein heavy chain isoform 5C [Tripneustes gratilis]			
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 158827 lpr j2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284758, 284682, 284557
679	79888855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22218  - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278998, 284693
680	20728424 (1359, 1360)	Novel Protein sim. GBank gi 5174483 ref NP_008050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284600, 284602 284102, 284907, 284908, 285006, 284693, 283872, 83373044, 284566
682	11392478 (1363, 1364)	Novel Protein sim. GBank gi 4756208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VHI-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	UNCLASSIFIED phosphatase	284595 284634
683	80083680 (1365, 1366)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]			284605
685	80248735 (1369, 1370)				284809, 283987, 283981
686	79208608 (1371, 1372)				284631
687	80085629 (1373, 1374)				284693, 284635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688982 (AF027768) - LepA (Serratia marcescens)		peptidase	284807, 284638
689	68084258 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif (e.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284908, 284907, 285007, 285009, 60433438, 21908754, 284760, 18108358, 21908766, 21908769, 285021, 18108361, 283974, 18108379, 284557, 18108385, 22278002 284510, 284511, 284764, 284769
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A86)		UNCLASSIFIED	
691	81854392 (1381, 1382)				284757
692	83088038 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1  - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED UNCLASSIFIED	55812038, 55811957, 285018, 55811150, 18108351, 284908, 60431528, 284594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U68 [Human herpesvirus 6]		UNCLASSIFIED	284635
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi 267327 sp Q01033 VC48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278998, 284510, 284602, 284603, 284762, 284687, 284769, 284693

685	94147849 (1389, 1390)	Novel Protein sim. GBank glj4468339[emb]CAB38059.1]- (AJ010801) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	55182575, 284508, 284905, 284907, 29331830, 284908, 284909, 284511, 285007, 284910, 284758, 284784, 284288, 85274791
686	78830882 (1391, 1392)	Novel Protein sim. GBank glj2848950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	284905, 284595
687	11767869 (1393, 1394)	Novel Protein sim. GBank glj1731343[sp]Q10894[YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY48.25]	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	284682
688	66695852 (1395, 1396)			UNCLASSIFIED	284888, 35695917
689	79582558 (1397, 1398)			UNCLASSIFIED	284682
700	78830898 (1399, 1400)				284693
701	80230242 (1401, 1402)	Novel Protein sim. GBank glj1001238[db]BAA104771 - (DB4003) hypothetical protein [Synchocystis sp.]		UNCLASSIFIED	284488, 284510, 284511, 284602, 284605, 284689
702	78814789 (1403, 1404)	Novel Protein sim. GBank glj2498935[sp]Q46338[SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT]		UNCLASSIFIED	284909
703	20446820 (1405, 1406)	Novel Protein sim. GBank glj3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	oxidase	UNCLASSIFIED	284604
704	84312224 (1407, 1408)	Novel Protein sim. GBank glj3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	284288, 56181562, 33657109, 284628, 55811578
705	17832141 (1409, 1410)	Novel Protein sim. GBank glj421091[pr]S30730 - hypothetical protein o208 - Escherichia coli		UNCLASSIFIED	285008
706	20288062 (1411, 1412)	Novel Protein sim. GBank glj3024872[sp]Q55760[Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074]			284600
707	20838065 (1413, 1414)	Novel Protein sim. GBank glj3420608[gb]AAC31807.1]- (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		284603
708	20708292 (1415, 1416)	Novel Protein sim. GBank glj3649741[emb]CAA03985]- (AJ000281) mucin [Homo sapiens]			284601, 284692
709	88001439 (1417, 1418)	Novel Protein sim. GBank glj3080425[emb]CAA18744.1]- (AL022804) putative protein [Arabidopsis thaliana]	struct		18108398, 284637, 284908, 284909
710	11356683 (1419, 1420)				284369
711	17831418 (1421, 1422)				285019
712	80258184 (1423, 1424)	Novel Protein sim. GBank glj4758689[re]NP_002323.1[pl]RP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF000058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	284591
713	78263126 (1425, 1426)	Novel Protein sim. GBank glj1703266[sp]Q11056[AM12_MYCTU - PUTATIVE AMIDASE CY50.19C]		hydrolase	284905, 284607
714	27847851 (1427, 1428)	Novel Protein sim. GBank glj4502351[re]NP_001692.1[p]BAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase			284508, 284555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gl 1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	284907
716	78559072 (1431, 1432)	Novel Protein sim. GBank		dehydrogenase	284892
717	78481842 (1433, 1434)	gi 2484074 sp P55653 GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)			284636
718	94319658 (1435, 1436)	Novel Protein sim. GBank gi 3873879 emb CAA94886  - (Z71176) similar to pro-collagen domains: cDNA EST EMBL:D27978 comes from this gene: cDNA EST EMBL:D27977 comes from this gene: cDNA EST EMBL:D34199 comes from this gene: cDNA EST EMBL:D84392 comes from this gene: cDNA EST EMBL... (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]	Contains protein domain (PF000093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21908789, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388
719	17679564 (1437, 1438)	Novel Protein sim. GBank gi 2104302 emb CA08631  - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011
720	79841684 (1439, 1440)	Novel Protein sim. GBank			284908
721	15020180 (1441, 1442)	gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	284629
722	9882603 (1443, 1444)	Novel Protein sim. GBank gi 498253 (U02372) - integrase [Vibrio cholerae]			264910
723	19755589 (1445, 1446)	Novel Protein sim. GBank gi 2253054 emb CAB10705  - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	284681
724	10126494 (1447, 1448)	Novel Protein sim. GBank gi 4063013 (AF063061) - protease P1A [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	284909
725	7878679 (1449, 1450)			UNCLASSIFIED	284905, 284907
726	13086282 (1451, 1452)			UNCLASSIFIED	284636
727	13522072 (1453, 1454)				284634
728	20268471 (1455, 1456)	Novel Protein sim. GBank gi 2633910 emb CAB13411  - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			284567
729	11293753 (1457, 1458)	Novel Protein sim. GBank		UNCLASSIFIED	284490
730	18900373 (1459, 1460)	gi 2484880 sp Q45291 GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	284584
731	80058750 (1461, 1462)	Novel Protein sim. GBank gi 1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	284605
732	80258175 (1463, 1464)	Novel Protein sim. GBank gi 166396 sp P46681 AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	284591, 284594, 284595
733	20448839 (1465, 1466)	Novel Protein sim. GBank gi 3184080 emb CAA19338  - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284604
734	20435887 (1467, 1468)			ubiquitin	284604

735	11607959 (1468, 1470)	Novel Protein sim. GBank gl 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION			284594
736	10878734 (1471, 1472)	Novel Protein sim. GBank gl 400831 sp P31133 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - transport Binding-protein-dependent transport systems inner membrane component		284636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - UNCLASSIFIED Regulator of G protein signaling domain		285020
738	17895353 (1475, 1476)	Novel Protein sim. GBank gl 2508867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)			285008
739	78833670 (1477, 1478)		oxidase		284910
740	19881557 (1479, 1480)				284907, 284764, 284634, 284837
741	78827273 (1481, 1482)	Novel Protein sim. GBank gl 3261828 emb CAB10925  - (Z98260) mrp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - UNCLASSIFIED Domain of unknown function		284689, 35896286, 284510, 284808, 18108362
742	82393785 (1483, 1484)	Novel Protein sim. GBank gl 3877494 emb CAA88472.1  - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D88340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D8945...	UNCLASSIFIED		28331822, 284910, 284762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gl 127420 sp P18888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - UNCLASSIFIED C-5 cytosine-specific DNA methylase		284488, 284259, 284508, 284905, 284908, 284907, 284808, 284908, 284510, 284511, 284512, 265008, 265009, 284910, 284591, 284596, 284759, 285010, 265011, 18108351, 284763, 284288, 284768, 284768, 284693, 18108370, 284829, 18108372, 284630, 284631, 284634, 284558, 18108385, 284482, 284564, 284567
744	80230421 (1487, 1488)				18108397, 284511, 284690, 284628, 284638, 284692, 284639, 284768
745	9841983 (1489, 1490)	Novel Protein sim. GBank gl 78921 pir S04846 - UDP-N- acetyluramoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli	glycoprotein		284906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gl 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]	synthase		284600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gl 2887411 dbj BAA24848  - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - oxidase SH3 domain		66714117, 284805, 284509, 284906, 284907, 284908, 284909, 284511, 284910, 285011, 284881, 284288, 284768, 284687, 284768, 284769, 21906768, 35895917, 284691, 284693, 284628, 284634, 284635, 284639, 56182323, 83373044
748	11617923 (1495, 1496)				284690

749	20469119 (1497, 1498)	Novel Protein sim. GBank gi 1189727 sp P44848 PPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	284804 284800
750	20298427 (1498, 1500)				
751	21838169 (1501, 1502)	Novel Protein sim. GBank gi 5360088 gb AA042851.1 AF159888 - (AF159888) serine/threonine kinase PKN3 [Mycobacterium xanthus]	Contains protein domain (PF00089) - kinase Eukaryotic protein kinase domain		284805, 284559
752	82450388 (1503, 1504)	Novel Protein sim. GBank gi 1188862 sp P44428 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	284508, 284907, 284510, 285011, 284762, 284889, 35695855, 284838, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi 2851330 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED	284808, 284600, 284602, 284804, 284780, 284789, 284634
754	95083741 (1507, 1508)			UNCLASSIFIED	284508, 284808, 284907, 284908, 284909, 284759, 284802, 284784, 284789, 284628, 284629, 284630, 284632, 284634, 284635, 284837, 284838, 83373044, 18108385
755	80185449 (1509, 1510)	Novel Protein sim. GBank gi 3449276 emb CAA20420.1 - (AL031317) putative dehydrogenase (Streptomyces coelicolor)		UNCLASSIFIED	284448, 284690
756	94631686 (1511, 1512)				284769, 284689, 284638, 284639
757	78488533 (1513, 1514)	Novel Protein sim. GBank gi 4580331 emb CAB40107.1  - (AJ001206) putative glycogen debranching enzyme (Streptomyces coelicolor)		UNCLASSIFIED	284882, 284885
758	78963178 (1515, 1516)			amylase	285007, 18108387, 265007, 18108387
759	79475687 (1517, 1518)	Novel Protein sim. GBank gi 2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	284684, 284686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gi 3451312 emb CAA20448.1 - (AL031324) membrane alipase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - transport E1-E2 ATPase		28331822, 284908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 284681, 284687, 284688, 21906768, 21908768, 285020, 285021, 285022, 284635, 22279000
761	78877968 (1521, 1522)	Novel Protein sim. GBank gi 3327158 db BAA31647.1 - (AB014572) KIAA0872 protein [Homo sapiens]		UNCLASSIFIED	284768
762	80023563 (1523, 1524)	Novel Protein sim. GBank		UNCLASSIFIED	284807, 284593, 265020
763	20294813 (1525, 1526)	gi 4981268 gb AAD35822.1 AE001744 - lipopolysaccharide core biosynthesis protein KdIB [Thermotoga maritima]			284800
764	39515024 (1527, 1528)				284603



765	80025947 (1529, 1530)	Novel Protein sim. GBank gij3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	284905, 284908, 284594, 284686, 33657023
766	82417404 (1531, 1532)			UNCLASSIFIED	284603, 284762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gij541121 (pij)S40827 - hypothetical protein c300 - Escherichia coli		UNCLASSIFIED	284607
768	79418080 (1535, 1536)			UNCLASSIFIED	284592, 284585
769	80086554 (1537, 1538)	Novel Protein sim. GBank gij2982501 (emb)CAA08184 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 284559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gij283437 (pij)S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	284903, 284907, 284828, 284909, 265010, 284786, 284628, 284629, 284634, 284636, 284555
771	95329508 (1541, 1542)	Novel Protein sim. GBank gij4769004 (gb)AAD29715.1 (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	58182575, 35686288, 284259, 66714117, 284107, 68712502, 58182435, 284112, 55812038, 87188559, 284288, 21908786, 33657023, 65274620, 65274791, 18108381
772	78971382 (1543, 1544)			UNCLASSIFIED	284910
773	78945383 (1545, 1546)			UNCLASSIFIED	285020
774	78956128 (1547, 1548)	Novel Protein sim. GBank gij5531324 (emb)CAB51045.1 - (AJ008579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284909
775	20620141 (1549, 1550)			UNCLASSIFIED	284555
776	78942693 (1551, 1552)			UNCLASSIFIED	285019
777	78960378 (1553, 1554)	Novel Protein sim. GBank gij4505461 (ref)NP_003824.1 (p)NRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01008) - Hepatitis C virus non-structural protein NS4a	protease	21508754, 285020, 80170815, 284681
778	20591310 (1555, 1556)			UNCLASSIFIED	284511
779	80054024 (1557, 1558)			UNCLASSIFIED	284803
780	85288987 (1559, 1560)	Novel Protein sim. GBank gij1144520 (U34958) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	284807, 284600, 284601, 284602, 284603, 284604, 284605, 284488
781	80250049 (1561, 1562)				
782	8758529 (1563, 1564)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter (Helicobacter pylori J99)		UNCLASSIFIED	284905, 284907, 265010, 284600, 284601, 18108382, 18108374, 284558
783	18410791 (1565, 1566)				284605
784	80051187 (1567, 1568)				265020
785	58073541 (1569, 1570)	Novel Protein sim. GBank gij3451335 (AC005525) - F22162.1 [Homo sapiens]		UNCLASSIFIED	284635, 33657023, 28331828, 265017, 284585, 284586
786	20438842 (1571, 1572)	Novel Protein sim. GBank gij138748 (sp)P10805 (UGPA, ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA)	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 284604
				transport	284603
787	80258384 (1573, 1574)			UNCLASSIFIED	284593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	284908, 284602, 284803, 284769, 284638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	285007
790	86284408 (1579, 1580)	Novel Protein sim. GBank gij5708378 [dbj]BAA03089.1] - (AB026116) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 28331824, 284828, 87188559, 285018, 21908765, 21908767, 21908768, 21908769, 285020, 284692, 22279000, 284593
791	94651627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb]CAB51883.1] - (AL109883) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			284601, 284605, 284638
792	80058786 (1583, 1584)	Novel Protein sim. GBank gij393184 (L02375) - S-antigen [Plasmodium falciparum]		struct	285021, 284631, 284635, 284558
793	79838730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046] - (D26048) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox	homeobox	284693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gij105884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	284603, 284604, 284910, 284762, 284808, 284638, 284908, 284757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CAB07082] - (Z92771) bcrA [Mycobacterium tuberculosis]		carboxylase	284488, 35696052, 284905, 284907, 265010, 35698423, 284638
796	86669451 (1591, 1592)				60432228, 55811150, 284630, 284637, 284565
797	87771761 (1593, 1594)	Novel Protein sim. GBank gij2985447 [emb]CAA71519] - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 284083, 284094, 66714117, 21908787, 21908769, 265020, 265022
798	79865209 (1595, 1596)			transcript factor	284687, 284768, 284693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gij4467250 [emb]CAB37575] - (AL035568) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	284809, 284910, 284636, 284638
800	79970189 (1598, 1600)			UNCLASSIFIED	284488
801	80499389 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA18054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	284508, 284511, 285008, 285009, 284769, 284587, 284486
802	79834588 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			284805, 284693
803	20467520 (1605, 1606)			struct	284605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		kinase	284510
805	79599993 (1609, 1610)				
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683] - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	- transferase	284508, 284769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNFDCAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			284764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi3913092 sp Q48170 ARCD_CLOPE - ARGININE/ORNITHINE ANTI-PORTER		transport	284809, 284802, 21806764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016 sp P74309 ALF1_SNNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	284508, 284808, 284809, 285007, 284910, 284758, 284600, 284602, 284603, 284605, 284687, 284769, 284689, 284636, 284486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472 sp P30883 YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldolase reductase family	reductase	284389
811	80079280 (1621, 1622)			UNCLASSIFIED	284558
812	10287694 (1623, 1624)			UNCLASSIFIED	284692
813	79612280 (1625, 1626)			UNCLASSIFIED	284806
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi1146168 (J01617) - glutaminyl- RNA synthetase [Escherichia coli]		synthase	284903, 284602, 284605, 284682, 284687, 284769, 284636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi14589652 db BAA78848.11 - (AB023221) KUAA1004 protein [Homo sapiens]		UNCLASSIFIED	284488, 22278998, 22276899, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 284905, 284908, 285007, 33857402, 80433358, 80433438, 284758, 285011, 285017, 285018, 285019, 284369, 284288, 284685, 21908785, 21908787, 285020, 285021, 284692, 85274620, 33657109, 284628, 18108376, 284635, 284638, 80170394, 58182323, 284584
816	19881910 (1631, 1632)				284600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi11781144 emb CAB062541 - (Z83866) hypothetical protein Rv3089 [Mycobacterium tuberculosis]		UNCLASSIFIED	284595
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi11477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 80424269, 35696052, 55812038, 21908768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810784, 35696423, 55811576, 284636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi11001352 db BAA108381 - (D84008) ABC transporter [Synecocystis sp.]		transport	284585
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi1468814 sp P37484 YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	284600, 284602, 284604
821	76782590 (1641, 1642)				
822	80215310 (1643, 1644)			UNCLASSIFIED	284910
823	84992299 (1645, 1646)	Novel Protein sim. GBank gi3878400 emb CAA958281 - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45941); cDNA EST EMBL.D32742 comes from this gene; cDNA EST EMBL.D33817 comes from this gene; cDNA EST...		UNCLASSIFIED	284510, 284594, 284637
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi137007 emb CAA668871 - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain	struct	284509, 284687, 284691

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669  - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312  - (AL031281) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336692 sp AAD17897  - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264805, 264805, 264509, 264908, 264807, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21908768, 35895917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264583, 264586, 264488
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetylmutamyl tripeptide synthetase MurC [Heliobacillus mobilis]		UNCLASSIFIED	264758, 264634
830	20398091 (1659, 1660)	Novel Protein sim. GBank gi 1870004 emb CAB06855  - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	66714117, 264910, 264639
831	87112435 (1661, 1662)	Novel Protein sim. GBank gi 2500056 sp Q46287 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
832	19338322 (1663, 1664)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500056 sp Q46287 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428782 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]			264768, 263994, 21808767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35896052, 22279002, 264508, 264805, 264908, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35685917, 264557
837	79450450 (1673, 1674)	Novel Protein sim. GBank gi 728887 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN/APG PRECURSOR		UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi 2498533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 89.9 KD PROTEIN CYTA11.08		UNCLASSIFIED	264687
839	78641126 (1677, 1678)	Novel Protein sim. GBank gi 2498533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 89.9 KD PROTEIN CYTA11.08		UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein [finger]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264558

841	80376318 (1681, 1692)	Novel Protein sim. GBank gij139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D86733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	284784
842	80078724 (1683, 1684)	Novel Protein sim. GBank gij2114321[dbj]BAA200371 - (D86733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00356) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	284905, 284908, 285008, 285009, 18108374, 58182323, 284558
843	87002847 (1685, 1688)	Novel Protein sim. GBank gij3882325[dbj]BAA34522.11 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	284091, 28331825, 284908, 284788, 284563
844	17841439 (1687, 1688)	Novel Protein sim. GBank gij2224721[dbj]BAA208441 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	285011
845	18348844 (1689, 1690)				
846	78863441 (1691, 1692)	Novel Protein sim. GBank gij825679[pir]A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	284629 284907
847	78895348 (1693, 1694)				
848	78489355 (1695, 1696)			UNCLASSIFIED	284909
849	78756367 (1697, 1698)			UNCLASSIFIED	285020
850	78817649 (1699, 1700)	Novel Protein sim. GBank gij3183245[sp]P78061[JYCJL_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	284586 284909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gij5454130[ref]NP_008280.1[ptLN] - talin	Contains protein domain (PF01608) - JILWEQ domain		284488, 52844507, 284489, 18108388, 85274572, 58182575, 22278994, 22278995, 22278998, 35888286, 22278997, 22278998, 22278999, 20281171, 284480, 284259, 52845080, 28331822, 28331824, 66714117, 28331825, 60432289, 28331826, 28331827, 35888052, 28331828, 28146488, 28146489, 284107, 284905, 284906, 284907, 284908, 52844045, 58182435, 285008, 285007, 285008, 285009, 284910, 60432228, 60431735, 60433358, 33857402, 60433438, 284595, 284758, 284759, 21808754, 33109954, 52844288, 285010, 285011, 87189598, 285017, 285018, 285019, 284780, 284781, 284782, 284881, 18108351, 264783, 284448, 284682, 284784, 284883, 18108334, 284288, 284388, 284685, 284788, 284887, 284788, 284789, 21808785, 21808786, 21808787, 21808788, 29148627, 21808789, 28148629, 55811957, 35895917, 285020, 285021, 285022, 60170815, 52844150, 284891, 284892, 33857023, 284893, 283988, 33857109, 27486281, 27486282, 27486284, 27486285, 35895763, 60431602, 18108370, 20281089, 284629, 18108374, 18108376, 55811578, 35898423, 35895855, 284634, 284635, 284636, 284555, 60431850, 284556, 284681
852	10147366 (1703, 1704)				

853	13032587 (1705, 1708)	Novel Protein sim. GBank gl 3402836 emb CAA76082  - (Y18136) 2-enoate reductase [Moorella thermoacetica]	reductase	284838 284566
854	80052438 (1707, 1708)			
855	78641130 (1709, 1710)		UNCLASSIFIED	284682
856	11584238 (1711, 1712)		UNCLASSIFIED	284591
857	79210165 (1713, 1714)		UNCLASSIFIED	284630, 284634
858	80248910 (1715, 1716)			285008, 285009, 284601, 284602, 284603, 18108351
859	20296634 (1717, 1718)			284559
860	80041749 (1719, 1720)		UNCLASSIFIED	284489
861	65857045 (1721, 1722)		UNCLASSIFIED	33657023, 284630
862	80079487 (1723, 1724)			284600
863	80579831 (1725, 1726)	Novel Protein sim. GBank gl 2246532  (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	UNCLASSIFIED	284488, 18108398, 35696286, 284259, 18108351, 284288, 285021
864	94839904 (1727, 1728)			284259, 284112, 283974
865	80045310 (1729, 1730)	Novel Protein sim. GBank gl 5688884 emb CAB52047.1  - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	UNCLASSIFIED	284635, 284600, 284636, 284591, 284602, 284693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gl 4557876 ref NP_000341.1 pABCR - ATP binding cassette transporter	transport	284288, 284557, 284558
867	80082402 (1733, 1734)			284605
868	10075384 (1735, 1736)		UNCLASSIFIED	284909
869	80082406 (1737, 1738)			284605, 284687, 18108374
870	80248651 (1739, 1740)	Novel Protein sim. GBank gl 828860 pir S37755 - Adenylyl-transferase - Escherichia coli	transferase	284601, 284636
871	20378285 (1741, 1742)	Novel Protein sim. GBank gl 1708180 sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG	UNCLASSIFIED	284603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gl 1545959 emb CAA67763  - (X98384) paladin [Mus musculus]	UNCLASSIFIED	35696286, 22278998, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 285008, 284511, 284512, 285007, 285008, 285009, 284910, 284591, 60433358, 284596, 52846317, 87188474, 285010, 284602, 284603, 285017, 285018, 284605, 18108351, 284764, 284766, 284768, 52844229, 284769, 21906765, 285021, 284534, 284691, 52845129, 284628, 284629, 35698423, 65274791, 284631, 284632, 284635, 284636, 284558, 284637, 284638, 284639, 60432113, 22278900, 22279002, 284584
873	20189728 (1745, 1746)	Novel Protein sim. GBank gl 4156104  (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	UNCLASSIFIED	284595

874	80077682 (1747, 1748)	Novel Protein sim. GBank gi113418 sp P07818 SCRB_BACSU - SUCROSE-8- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			UNCLASSIFIED	284600
875	86608446 (1749, 1760)	Novel Protein sim. GBank gi1481000 p S37594 - mucin - human (fragment)				284258, 284448, 284288, 284657, 87168518
876	88465187 (1751, 1752)	Novel Protein sim. GBank gi13128283 (AF010498) - iron(iii) dichlorate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - ABC transporter	transport		284807, 284601, 284602, 284605, 285020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi1731074 sp P40348 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF003320) - GATA zinc finger	transcriptfactor		22278988, 284808, 284369
878	80187288 (1755, 1766)	Novel Protein sim. GBank gi11351614 sp Q09853 YAE_D_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase_associated		284369, 284555
879	94328862 (1757, 1758)	Novel Protein sim. GBank gi13875304 emb CAA98434  - (Z74030) predicted using GeneFinder; cDNA EST EMBL-C07809 comes from this gene; cDNA EST EMBL-C09023 comes from this gene; cDNA EST yk505e8.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...				56182575, 29331824, 284508, 284808, 285018, 18108351, 284448, 284883, 21908768, 21808768, 60170815, 33857023, 65274820, 33857109, 18108374, 35895855, 284583
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi1137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kingle domain	cathepsin		284508
881	11290122 (1761, 1762)	Novel Protein sim. GBank gi12632088 emb CAA75687  - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED		284508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi1155088 emb CAA84425  - (X94978) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED		284688
883	79582989 (1765, 1766)	Novel Protein sim. GBank gi12078027 emb CAB08467  - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED		284638
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi12695834 emb CAA15904  - (AL021008) sucA [Mycobacterium tuberculosis]		UNCLASSIFIED		284680
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi15689395 dbj BAA82881.1  - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED		35898052, 284608, 284600, 284603, 35895917, 35895855, 284636
886	11685138 (1771, 1772)	Novel Protein sim. GBank gi11881338 dbj BAA19385  - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]		UNCLASSIFIED		284603
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi1854065 emb CAA58337  - (X83413) U68 [Human herpesvirus 6]				284629

891	13516679 (1781, 1782)	Novel Protein sim. GBank gi4959396 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	284636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi545526 bbs 143933 - LBP- 1b-transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namatawa cells, Peptide, 541 aa]		transcription factor	22278986, 22278989, 29331828, 35696052, 284908, 284909, 285009, 285011, 284602, 285019, 284788, 21806765, 21808786, 21808789, 285020, 285021, 58526486 284688, 283987
893	78168037 (1785, 1786)	Novel Protein sim. GBank gi2829888 sp P80808 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIO)LYASE) (CSASE)		synthase	
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	284508, 284600, 284555, 284559
896	79747803 (1791, 1792)				284632
897	94991923 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284686, 29331828, 284511
898	87895109 (1795, 1796)				58182575, 60432289, 58182435, 80432229, 55811957, 22278000, 284488
899	11100463 (1797, 1798)	Novel Protein sim. GBank gi1750127 (U88480) - YncC [Bacillus subtilis]		transport	284601 284789, 284691, 284563
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi312287 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	284907, 284602, 284605, 284769, 35695917, 18108376, 284563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi335570 emb CAA200011 - (AL031124) 3-Isopropylmalate dehydratase large subunit (Streptomyces coelicolor)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	284909, 285008, 284602, 284604, 284769, 284689, 284693
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGG family of carbohydrate kinases	kinase	35696052, 284905, 284510, 284511, 284512, 284605, 284760, 18108351, 284762, 284687, 284765, 284769, 284888, 21808784, 35695917, 27486262, 35695855, 284634, 284636, 284486
903	82050208 (1805, 1806)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00481) - Arginase family	hydrolase	284604
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Arginase family	UNCLASSIFIED	284909
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]			
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi3739200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			284585, 284605
907	87913201 (1813, 1814)				
908	11754482 (1815, 1816)			UNCLASSIFIED	60432289, 284601, 284680
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi3868940 db BAA34296  - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	284636
910	18776208 (1819, 1820)	Novel Protein sim. GBank gi4589728 db BAA76883.1 - (AB003137) DnaJ homolog protein [Salix glauca]	Contains protein domain (PF00894) - DnaJ central domain (4 repeats)	UNCLASSIFIED	284602
				eph	285009



911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P33685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1  - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26895]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 17657 sp Q03604 JIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 dbj BAA83069.1  - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278998, 66714117, 264908, 264591, 21906768, 265020, 55811576, 264638 264595
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790  - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264605
917	20185985 (1833, 1834)	Novel Protein sim. GBank gi 1855699 emb CAA69032  - (Y07752) phenophorin-S [Volvox carter]		UNCLASSIFIED synthase	264259, 26331826, 264808, 265019, 264448, 265020, 264835, 83373044
918	91228785 (1835, 1836)	Novel Protein sim. GBank gi 5689898 emb CAB52005.1  - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264802, 264804, 264766, 18108370, 264563
919	80436785 (1837, 1838)				
920	79606095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858834 (1841, 1842)	Novel Protein sim. GBank gi 3650094 emb CAA21911.1  - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78882605 (1843, 1844)				
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267078 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	265019, 22279002 264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385 264510 264603
924	21431341 (1847, 1848)				
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACETHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3682325 dbj BAA34522.1  - (AB018345) KIAA0802 protein [Homo sapiens]			55811857, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070810 (1855, 1856)	Novel Protein sim. GBank gl 156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	284605
929	20830336 (1857, 1858)			UNCLASSIFIED	284603
930	5496346 (1859, 1860)	Novel Protein sim. GBank gl 4115936 gb AAD03446.1] - (AF116223) No definition line found [Arabidopsis thaliana]			284259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gl 4480609 emb CAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) -	reductase	284486
932	80420813 (1863, 1864)	Novel Protein sim. GBank gl 5459389 emb CAB50754.1] - (AL068839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	284508, 284905, 284908, 284909, 284602, 284603, 284605, 284768, 284558, 18108387, 284488
933	94326010 (1865, 1866)	Novel Protein sim. GBank gl 5688523 db EAA83045.1] - (AB028016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00827) -	UNCLASSIFIED	284508, 284686, 284688, 284693, 27486261, 18108370, 65274791, 284636, 284559, 22278002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gl 119111 sp P12978 EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			284369, 22278002
935	80063162 (1869, 1870)			UNCLASSIFIED	284604, 284605, 284693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gl 845886 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 284602, 284687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gl 1360689 pr CGHU1V - collagen alpha 1(V) chain precursor - human [Y14083] hypothetical protein [Bacillus subtilis]		synthase	263978
938	80028633 (1875, 1876)	Novel Protein sim. GBank gl 2226243 emb CAA74531.1] -		UNCLASSIFIED	284602
939	11071694 (1877, 1878)				284600
940	94144252 (1879, 1880)	Novel Protein sim. GBank gl 3560186 emb CAA20878] - (AL031526) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	284905, 284906, 284907, 284908, 284909, 284511, 284910, 284592, 33857402, 284596, 284758, 284760, 284883, 284768, 284768, 284768, 33857023, 33857109, 284628, 284629, 284630, 284635, 284636, 284555, 284637, 284556, 284638, 284639, 83373044, 18108385, 284566, 18108391
941	11389414 (1881, 1882)				284593
942	19484122 (1883, 1884)			UNCLASSIFIED	284760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gl 4033728 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	284600, 284687, 284689, 284563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gl 2494784 sp Q50729 GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	284511, 284603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gl 732353 sp P39606 YWCH_BACSU - HYPOTHETICAL 38.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	284906, 284604, 284605, 285020, 18108387
946	79248402 (1891, 1892)				265017

947	81802699 (1893, 1894)	Novel Protein sim. GBank gi 2696770 emb CAA17247  - (AL021899) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278998, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264802, 265018, 264805, 264759, 264689, 264693
948	88165538 (1895, 1898)	Novel Protein sim. GBank gi 2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgl	18108398, 58182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811388, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486285, 263972, 55811578, 264638, 60170394, 264566
949	88081788 (1897, 1898)	Novel Protein sim. GBank gi 4507885 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27488261, 21806768, 52844298, 33857349, 87188518, 56994075, 265020, 265021, 87188559, 52844150, 264637
950	78485672 (1899, 1900)	Novel Protein sim. GBank gi 1079461 ref S43865 - Cytokeratin 8, type II - potoroo (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264883, 18108381
951	20451411 (1901, 1902)	Novel Protein sim. GBank gi 5420387 emb CAB46878.1  - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	78566854 (1903, 1904)	Novel Protein sim. GBank gi 5305702 gb AAD41778.1 AF12688 - (AF126887) calpain-like protease [Mus musculus]		calhepzin	264910, 264691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gi 2495842 sp Q47142 YFHS_ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	284510
954	8893326 (1907, 1908)	Novel Protein sim. GBank gi 2360985 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	284508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gi 5454084 ref NP_006318.1 pSIP1 - SYT Interacting protein	Contains protein domain (PF00078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	rna_bind	56994075, 264509, 264805, 264908, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264801, 264760, 18108351, 264782, 264783, 264764, 264768, 264686, 264787, 264687, 264687, 264768, 264789, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 284584
956	80084224 (1911, 1912)	Novel Protein sim. GBank gi 2052129 emb CAB08155  - (Z64752) ftnJ [Mycobacterium tuberculosis]			264605
957	80058208 (1913, 1914)	Novel Protein sim. GBank gi 1709787 sp Q00451 PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264603, 18108362
958	80036448 (1915, 1916)	Novel Protein sim. GBank gi 1709787 sp Q00451 PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264808, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gi 2131050 emb CAB09280  - (Z59944) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815408 (1919, 1920)	Novel Protein sim. GBank gi 2120478 ref S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80590374 (1925, 1928)				UNCLASSIFIED	284510, 284288, 284555, 284556, 284559, 284486
964	79632019 (1927, 1928)	Novel Protein sim. GBank gl 4589622 dbj BAA78833.1  - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	284112, 284910, 284689
965	91229465 (1929, 1930)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1  - (AL243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	284488, 285017, 284448, 284634, 284558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	284906, 284592, 284586, 284604, 284768, 21906764, 284692, 284693, 284628, 284636, 284638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gl 1731207 ep Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	284760
968	79560269 (1935, 1936)	Novel Protein sim. GBank gl 268183 emb CAA75187.1 - (Y14984) putative transport protein [Methylophilus methylotrophus]			transport	284693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gl 5419878 emb CAB46422.1  - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type		dna_ma_bind	35699286, 284885, 284886, 35695917, 284692, 18108374, 284635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147820, 284828, 285006, 285007, 285008, 285009, 18108348, 33109854, 265010, 265011, 18108351, 284286, 21906767, 21906768, 18108370, 18108374, 18108377, 284630, 284635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)					284557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gl 1723119 ep P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				284604
974	80057103 (1947, 1948)				UNCLASSIFIED	284585
975	10198018 (1949, 1950)				UNCLASSIFIED	284510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gl 3881459 emb CAA92888.1  - (Z88753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...			UNCLASSIFIED	284508, 284806, 284758, 284632, 284639, 284583
977	10355349 (1953, 1954)	Novel Protein sim. GBank gl 549458 ep Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	284806
978	80025921 (1955, 1956)				UNCLASSIFIED	284600, 284602, 284603, 284604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gl 3171804 emb CAA75868.1 - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	284787, 284768, 285008, 265007, 284906
980	80025928 (1959, 1960)				UNCLASSIFIED	284600, 284602, 284605
981	80098550 (1961, 1962)	Novel Protein sim. GBank gl 3598940 (AF017388) - facitgenital dyoplasia protein 2 [Mus musculus]			UNCLASSIFIED	284692, 284555, 284556, 284557, 284559

982	80195670 (1983, 1984)	Novel Protein sim. GBank gij2950220[embjCAA71575] - (Y10545) fused-codB [Escherichia coli]		UNCLASSIFIED	284404
983	90895041 (1985, 1986)	Novel Protein sim. GBank gij476389[pirjB43402] - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56162575, 284908, 284909, 285007, 285008, 284758, 285010, 55811150, 33657023, 284634, 284557, 284558
984	20486878 (1987, 1988)	Novel Protein sim. GBank gij3451504[embjCAA07680.1] - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	284605
985	85461368 (1988, 1970)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z85438) hypothetical protein Rv3845 [Mycobacterium tuberculosis]		UNCLASSIFIED	56182435, 284600
986	87102888 (1971, 1972)			UNCLASSIFIED	284108, 284110, 265020, 60170615
987	79867231 (1973, 1974)			UNCLASSIFIED	284909
988	19858661 (1975, 1976)			UNCLASSIFIED	284600
989	88095329 (1977, 1978)	Novel Protein sim. GBank gij5725506[gbjAAD48080.1]AF08015 - (AF080152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	UNCLASSIFIED	284508, 265017, 264534, 284564
990	88057746 (1978, 1980)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z85438) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylylate and Guanylylate cyclase catalytic domain	UNCLASSIFIED	284256, 284808, 285009, 284910, 284598, 284389, 284288, 284768, 284828, 284635, 284588
991	10108140 (1981, 1982)			UNCLASSIFIED	284809
992	78845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z85438) hypothetical protein Rv3845 [Mycobacterium tuberculosis]		UNCLASSIFIED	284508, 284593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	284907
994	11080590 (1987, 1988)	Novel Protein sim. GBank gij5108572[gbjAAD39780.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]			284602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gij5108572[gbjAAD39780.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and other N-terminal domain	helicase	18108398, 65274572, 22278998, 284490, 60432049, 29331827, 29146498, 284508, 284905, 284907, 284908, 56182435, 265008, 284591, 284592, 60432228, 60431735, 33657402, 284595, 284758, 21906754, 285010, 285017, 265018, 284605, 284780, 284448, 284763, 284768, 21906785, 21908788, 21908789, 55811957, 284692, 284893, 284829, 35698423, 55811576, 35695855, 284638, 284555, 284558, 284558, 83373044, 22279002, 284583
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56328488, 87168518, 284910, 284908, 284585, 284568, 284693, 284768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2849101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35698286, 22278997, 22278999, 284508, 284905, 284908, 285010, 284600, 284602, 284605, 284688, 284769, 285021, 284585, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[spjP04929]HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			284595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2508697 sp P46480 YFCA_HAEN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	284682	
1000	20727944 (1999, 2000)			UNCLASSIFIED	284602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 db BAA20833  - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Kinase Ank repeat	UNCLASSIFIED	60432049, 284907, 284908, 284511, 284603, 284683, 284684, 284687, 284689, 28148827, 21808769, 284692, 18108385, 22279000 2850009, 284389, 285020	
1002	80186603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		struct		
1003	17833491 (2005, 2006)				285019 284635	
1004	16314887 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA56337  - (X83413) U88 [Human herpesvirus 6]				
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gi 114073 sp P07872 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	284508	
1006	37815429 (2011, 2012)					
1007	79820871 (2013, 2014)	Novel Protein sim. GBank gi 4082978 db BAA36210.1  - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	284259 284905	
1008	86094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1  - (AJ001208) putative trehalose synthase [Streptomyces coelicolor]		synthase	285007, 284602, 284605, 284760, 284638	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 AF090113  - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - Kinase PDZ domain (Also known as DHR or GLGF).	Kinase	284102, 284288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 AF016307  - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	284592	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342847 gb AA88591.1  - (U90853) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35896052, 284905, 284784, 284788, 35895917, 284628	
1012	95294458 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272  - (AL031231) guanosine pentaphosphate synthetase/ polynucleotide nucleosyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35896052, 284905, 284600, 284601, 284602, 284605, 284762, 284788, 284789, 284689	
1013	86095772 (2025, 2026)					
1014	86608828 (2027, 2028)			UNCLASSIFIED	284591, 21808768 28331824, 285019, 285020	

1015	95418878 (2028, 2030)	Novel Protein sim. GBank gl 4158895 (AF083085) - SEUL [Mus musculus]	Contains protein domain (PF000040) - Fibronectin type II domain	struct	22278994, 22278995, 56984075, 22278996, 22278998, 284259, 29331825, 29331828, 284907, 56182435, 284510, 284591, 284593, 60433356, 284594, 55812038, 284758, 21908754, 33657084, 265010, 284600, 265017, 265018, 265019, 18108351, 21906765, 21906768, 21906767, 21906768, 55811957, 265022, 33657023, 65274820, 33657182, 32833988, 18108370, 18108377, 55811576, 35686423, 284630, 22279000, 284565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gl 25088898 p 41407 ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	284688, 284693
1017	11089213 (2033, 2034)	Novel Protein sim. GBank gl 5103943 dbj BAA79259.1  - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	transport	284600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gl 4493973 emb CAB39032.1  - (AL034459) predicted using hexExon: MAL3P7.14 (PF0925w). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 28148627, 284583
1019	11703607 (2037, 2038)			UNCLASSIFIED	284686
1020	80234432 (2039, 2040)				284508, 284509, 264512, 284600, 284762, 284769, 284889, 18108370, 284638, 284638, 284486
1021	37038243 (2041, 2042)	Novel Protein sim. GBank gl 4633807 gb AAD28859.1 AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	284769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gl 1781230 emb CAB082771  - (Z83887) hypothetical protein RV3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35686052, 284508, 265008, 265009, 264769, 18108387, 284583
1023	11398341 (2045, 2046)	Novel Protein sim. GBank gl 3777485 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase associated	284593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52846842, 33657402, 33657023, 18108379, 55811576, 284631, 284556, 284557, 284559, 18108388, 284586
1025	78644200 (2049, 2050)	Novel Protein sim. GBank gl 348304 emb CAA20556  - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	284693
1026	80023948 (2051, 2052)	Novel Protein sim. GBank gl 117492 sp Q02322 UVRD_HAEIN - DNA HELICASE II		helicase	284602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gl 4767728 ref NP_004896.1 pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	285017

1028	20297828 (2055, 2056)	Novel Protein sim. GBank gl 2791409 emb CAA16003  - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	284600
1029	8465090 (2057, 2058)			UNCLASSIFIED	284595
1030	88095343 (2059, 2060)			UNCLASSIFIED	284907, 284908, 284510, 284512, 285009, 285010, 285011, 284600, 284602, 284603, 284605, 284769, 18108372, 18108374
1031	85289117 (2061, 2062)			UNCLASSIFIED	284905, 284908, 284909, 284595, 284692, 284630, 284634, 284638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gl 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	284689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gl 2882990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35886052, 284908, 284510, 18108354, 284687, 284769, 284688, 60431602, 18108385, 284486
1034	78245937 (2067, 2068)	Novel Protein sim. GBank gl 405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	284906
1035	79956355 (2069, 2070)			UNCLASSIFIED	284892
1036	85804998 (2071, 2072)				284905, 86712502, 284908, 284766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 284909, 80433438, 285019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gl 780819 (L38891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		284604, 284634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gl 2605067 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gl 2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	284082, 284083, 284094, 284693, 284689, 283987
1041	10156882 (2081, 2082)	Novel Protein sim. GBank gl 3256353 db BAA29218.1 - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	284595
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gl 2058299 emb CAA68953  - (X98309) ARI protein [Drosophila melanogaster]			284907
1043	80057138 (2085, 2086)	Novel Protein sim. GBank gl 1870167 emb CAA70125  - (Y08921) malK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	284605
1044	80025952 (2087, 2088)	Novel Protein sim. GBank gl 5688890 emb CA852053.1  - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284565, 284567
1045	52415482 (2089, 2090)			UNCLASSIFIED	285006, 284602, 285017, 29331825, 284637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		helicase	
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gl 421047 db BAA74535.1  - (AB018033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	284769
1048	78186400 (2095, 2096)	Novel Protein sim. GBank gl 3413419 emb CAA20278  - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	284687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gl 5051636 gb AAD38328.1 AF073727 EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	284805, 284634
1050	78471521 (2099, 2100)			UNCLASSIFIED	284686



1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442862 (2103, 2104)	Novel Protein sim. GBank gij13123275sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	264508, 264762, 264687, 264486
1053	94851840 (2105, 2106)	Novel Protein sim. GBank gij5441318 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			264688, 18108374, 29331824, 83373044, 21908754, 52845156, 56182435, 264689, 29331827, 27488281, 35698052, 21908765, 35698423, 21908768, 56182575, 21908769, 55811857, 87168518, 35698286, 22278897, 285020, 285011, 285021, 285022, 285007, 285016, 22278000, 22278002, 264482, 264908, 52844150, 264909, 264288, 29331822, 52845080, 264768
1054	78580225 (2107, 2108)			UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gij9052508 gb AAD38584.1 AF14560 - (AF145609) BcDNA.G-H02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	264907, 264602, 264681, 264288, 21908768, 33857108, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gij3021676 dbj BA025358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		mapolymerase	264908
1057	89867216 (2113, 2114)	Novel Protein sim. GBank gij1226281 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264682
1058	80376576 (2115, 2116)				264764
1059	94682754 (2117, 2118)	Novel Protein sim. GBank gij1170016 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA)		transcriptfactor	35698052, 35695855, 265009, 264636
1060	79461169 (2119, 2120)	Novel Protein sim. GBank gij2489087 sp Q08332 UGGQ_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146498, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gij90254 pir j28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	264634
1062	39567837 (2123, 2124)	Novel Protein sim. GBank gij3334200 sp Q49854 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gij2489886 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)			264508
1064	78881783 (2127, 2128)	Novel Protein sim. GBank gij82654 pir jA0088 - 10K zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij2120988 prij S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	284800, 284802, 284889
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gij2808382 pjp18042 DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	285009
1067	10132178 (2133, 2134)				284909
1068	82062037 (2135, 2136)	Novel Protein sim. GBank gij4007668 emb CAA22355 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldol/keto reductase family	reductase	284888, 18108362, 284558, 284800, 284760
1069	83002854 (2137, 2138)	Novel Protein sim. GBank gij4589484 dbj BAA76770.1 - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	284804
1070	82101892 (2139, 2140)	Novel Protein sim. GBank gij120304 pjp15932 FLOK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	284804, 284760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	284802
1072	82356540 (2143, 2144)			UNCLASSIFIED	284887, 284888, 21906784, 35888052, 35895917, 35895855, 284800, 284801, 284802, 285009, 284805, 284508, 284905, 284880, 284906, 284782, 284828, 284768
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij477532 prij A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	284809
1074	80105882 (2147, 2148)	Novel Protein sim. GBank gij3893109 emb CAA76940 - (Y17920) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	284808
1075	81850283 (2149, 2150)			UNCLASSIFIED	58994075, 22278998, 284594, 284757, 284586, 285018, 285019, 284881, 284389, 284888, 285020, 18108384, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij1176203 pjp48442 YHGM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)		ATPase-associated	284769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487 pjp44472 TUD4_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	284905
1078	20288874 (2155, 2156)			UNCLASSIFIED	284800
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij3413828 emb CAA20286 - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 284769, 284634, 284636
1080	11787188 (2159, 2160)			UNCLASSIFIED	284684
1081	84747080 (2161, 2162)				83373044, 285019, 22278002, 284482, 18108351, 284882, 284908, 284893, 284487
1082	81490656 (2163, 2164)			UNCLASSIFIED	284758, 284768, 284789, 21906787, 284511, 284910, 284634, 284635, 284905, 284636, 284908, 284837, 284907, 284908, 284764, 284638, 20281099, 284766, 284595

1083	87446717 (2185, 2186)	Novel Protein sim. GBank gij1722945[sp]Q10523Y01N_MYCTU - HYPOTHETICAL 44.9 KD PROTEIN CY427 23		UNCLASSIFIED	60424178, 264905, 264908, 264510, 60432229, 264759, 87188474, 264605, 264768, 264688, 18108364, 18108376, 35895855, 264638 264768
1084	37789308 (2167, 2168)	Novel Protein sim. GBank gij16384[sp]P32057WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475388 (2169, 2170)	Novel Protein sim. GBank gij1899180 (U80204) - heat shock protein 80 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	60432229, 264687
1086	79608289 (2171, 2172)	Novel Protein sim. GBank gij1172858[sp]P46176[RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	264488
1087	79603978 (2173, 2174)	Novel Protein sim. GBank gij160188[lemb]CAA154311 - (AL006583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gij2883155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80218800 (2177, 2178)	Novel Protein sim. GBank gij4981768[sp]AAD38280.1(AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264882, 264768, 264688, 21908784, 35895917, 265020, 32633986, 18108370, 35895855
1090	11038925 (2179, 2180)	Novel Protein sim. GBank gij4007680[lemb]CAA22388 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gij2485562[sp]P77239[YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252288 (2183, 2184)	Novel Protein sim. GBank gij286009[lemb]CAA17998.1 - (AL022121) ntlh [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264586 264768, 35895917, 35895855, 264600, 264602, 264603, 264605, 18108351 264686
1093	80486304 (2185, 2186)	Novel Protein sim. GBank gij1001642[dj]BAA103731 - (B84002) dGTP triphosphohydrolase [Synechocystis sp.]		UNCLASSIFIED	
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gij456557[lemb]CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264908, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264766, 264768, 264636, 264558, 18108367, 60432113, 264482, 264486
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gij115001[sp]P16206[BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]		synthase	264800, 264602, 264603, 264604, 264605, 35895917, 264692, 264631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gij115001[sp]P16206[BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]		UNCLASSIFIED	265018 264687
1097	79239560 (2193, 2194)	Novel Protein sim. GBank gij114135[sp]P08205[ARGA_ECOLI - AMINO-ACID ACETYL TRANSFERASE (N-ACETYL)GLUTAMATE SYNTHASE) (AGS)]		synthase	
1098	79186424 (2195, 2196)				

1099	39523638 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (MIG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	284603
1100	65736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp O84420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	284259, 284638
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	284769
1102	79777814 (2203, 2204)			UNCLASSIFIED	284810, 284809
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		struct	284757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	29331822, 21908754, 284555, 284558, 284558, 22278002
1105	80255121 (2209, 2210)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284566
1106	79314110 (2211, 2212)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284555, 284389
1107	80470019 (2213, 2214)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284908, 284769
1108	80440818 (2215, 2216)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		transport	284807, 284510, 284511, 284600, 284602, 284605, 284768, 284769
1109	80064815 (2217, 2218)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		helicase	284602, 284605, 284638
1110	80503554 (2219, 2220)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)			284908, 284593, 285010, 284601, 284603, 284604, 284605, 284682, 284769, 284693, 284638
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)			18108370, 284557
1112	95010088 (2223, 2224)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)			284908
1113	82458352 (2225, 2226)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284600, 284602, 284604, 284605, 284762, 284769, 284585
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		dehydrogenase	284636
1115	11765583 (2229, 2230)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284686
1116	79841152 (2231, 2232)	Novel Protein sim. GBank gi 117435 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)		UNCLASSIFIED	284908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gij3255965[emb]CAA84089] - (Z70200) U5 snRNP-specific 200KD protein (Homo sapiens)	Contains protein domain (PF00270) - DEAD/DEAH box helicase	18108382, 264488, 263994, 264489, 18108398, 58182575, 22278995, 22278998, 35898286, 59994075, 22278997, 22278998, 22278999, 264259, 29331822, 58182181, 29331824, 68714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35898032, 33856970, 26146488, 264508, 264805, 264509, 264808, 264907, 264908, 66712502, 264909, 52844045, 58182435, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21908754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264804, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264784, 264683, 264288, 264389, 264894, 264685, 264786, 264787, 264886, 264887, 264788, 264789, 264888, 18108358, 264689, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 29148784, 35895917, 265020, 285021, 265022, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35895763, 264691
1118	79563328 (2235, 2236)		UNCLASSIFIED	264691
1119	79942463 (2237, 2238)		UNCLASSIFIED	264807
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (AJ243459) proleophosphoglycan [Leishmania major]	collagen	29331827, 265018, 265019, 264681, 265021, 60170815, 18108367
1121	79471718 (2241, 2242)	Novel Protein sim. GBank gij1644450 (U87864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	264683, 264832, 18108388
1122	78458246 (2243, 2244)		UNCLASSIFIED	
1123	78637119 (2245, 2246)	Novel Protein sim. GBank gij98800[pr]S17768 - 3- dehydroquininate synthase (EC 4.8.1.3) - Mycobacterium tuberculosis	UNCLASSIFIED synthase	264639, 264583 264693, 27486265
1124	78811596 (2247, 2248)		UNCLASSIFIED	264909
1125	78757861 (2249, 2250)	Novel Protein sim. GBank	UNCLASSIFIED	264910
1126	78758914 (2251, 2252)	gij138154[sp]P03643VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)	epn	264805, 264809, 264910
1127	11800830 (2253, 2254)		UNCLASSIFIED	264682
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gij5002704[emb]CAB44358.1] - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank glj5689485[jb]BAA83026.1] - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	285011, 284788
1130	79420151 (2259, 2260)	Novel Protein sim. GBank glj4981328[jb]AAD35881.1]AE00174 - (AE00174) bloY protein [Thermotoga maritima]		UNCLASSIFIED	284593
1131	80055391 (2261, 2262)	Novel Protein sim. GBank glj1841552 (U89338) - unknown [Homo sapiens]		UNCLASSIFIED	35686286, 22278998, 28331828, 284603, 284605, 284559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank glj1841552 (U89338) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 284908, 285009, 284600, 284602, 284604, 284605, 284760, 32833988, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	285018
1134	80235376 (2267, 2268)			UNCLASSIFIED	284512, 284534
1135	80028393 (2269, 2270)	Novel Protein sim. GBank glj4539171[jmb]CAB39700.1] - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	284508, 284600, 284602, 284603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank glj4982454[jb]AAD36931.1]AE00182 - (AE00182) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	284908, 284908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank glj497274[jb]AAD34786.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22278998, 22278999, 35686052, 284907, 285009, 80433358, 284598, 285010, 284448, 284682, 284767, 284689, 285020, 284692, 55811578, 35695855, 284631, 284632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank glj731607[jp]P38739[YHC8 YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR			284908
1139	79833561 (2277, 2278)	Novel Protein sim. GBank glj3650031 (AC003398) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	284693
1140	39480358 (2279, 2280)			UNCLASSIFIED	284593
1141	79838019 (2281, 2282)			UNCLASSIFIED	285019, 284693
1142	18635948 (2283, 2284)			UNCLASSIFIED	284631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank glj382800[jmb]CAA05880] - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain		56182575, 284908, 284600, 284632, 87168518
1144	80088988 (2287, 2288)			UNCLASSIFIED	284635, 284638, 284907, 284593, 284908, 284586, 284909
1145	14610262 (2289, 2290)			UNCLASSIFIED	284112
1146	82062092 (2291, 2292)			UNCLASSIFIED	284769, 284689, 35696286, 284760, 284905, 284486, 284559
1147	80071761 (2293, 2294)				284557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank glj2499003[jp]P76422[THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)]	kinase		284591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank glj2886734[jmb]CAA17213.1] - (AL021897) hypothetical protein Rv1087c [Mycobacterium tuberculosis]			284591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase-associated	264488, 35696286, 264907, 264808, 264809, 264810, 264593, 264598, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264584, 264566, 264567, 264595
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655(gbIAAD16978) - (AF108181) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275(embjCAB07311.1) - (Z92825) predicted using GeneFinder; Similarity to Yeast low affinity glucose transporter HXT4 (PS:32487); cDNA EST EMBL: C12955 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thl...		glycoprotein	264488, 22278988, 264805, 264628, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315(dbjBAA74938.1) - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557, 265008
1154	83002985 (2307, 2308)	Novel Protein sim. GBank gij37617(ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLCATING P. TYPE ATPASE)	Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264890, 264636, 264603
1155	78411098 (2309, 2310)	Novel Protein sim. GBank gij418480(espjP32139)VIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264908, 264907, 264758, 264766, 264789, 264689, 264638, 264568
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij2486481(espIQ50724)Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	264908, 264762, 264687, 264769, 264689, 18108374, 35695855
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij1136408(dbjBAA11490) - (D78989) similar to pig tubulin-tyrosine ligase. [Homo sapiens]		UNCLASSIFIED	264687, 26331822, 26331824, 68714117, 26331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563, 264389, 264693
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij4503375(refjNP_001376.1)DPYS - dihydropyrimidinase		UNCLASSIFIED	
1159	78188451 (2317, 2318)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	264488, 35696286, 22278989, 264259, 68714117, 60432289, 35698052, 264905, 58182435, 265006, 60433436, 264759, 21808754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35698423, 35695855, 264558, 18108385, 60432113
1160	91229883 (2319, 2320)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		transport	
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1162	78635357 (2323, 2324)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1163	78563186 (2325, 2326)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1164	78650828 (2327, 2328)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1165	80491888 (2329, 2330)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1166	88098456 (2331, 2332)	Novel Protein sim. GBank gij14589478(dbjBAA78768.1) - (AB023136) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	

1167	79903862 (2333, 2334)	Novel Protein sim. GBank gl 2580433 dbj BAA23138  - (D76414) ppGpp hydrolase [Staphylococcus aureus]		Kinase	284488
1168	88094678 (2335, 2336)			UNCLASSIFIED	284259, 28331827, 56182435, 60433438, 285019, 33857023, 35695855, 284586
1169	11805403 (2337, 2338)			UNCLASSIFIED	284881
1170	21832244 (2339, 2340)			UNCLASSIFIED	284602
1171	20434662 (2341, 2342)	Novel Protein sim. GBank gl 27272814 (AF028249) - precollagen D [Mytilus edulis]		UNCLASSIFIED	284556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gl 4757646 ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35696052, 284634, 284488
1173	60235713 (2345, 2346)	Novel Protein sim. GBank gl 2584053 dbj BAA22848  - (AB007832) Bm trachealless [Bombyx mori]			284508, 284906, 284907, 284909, 284591, 284632, 284638, 284639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank gl 2811027 emb CAA175201 - (AL021858) mmsA [Mycobacterium tuberculosis]		dehydrogenase	284600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gl 1183333 sp P23334 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	284601
1176	80252645 (2351, 2352)	Novel Protein sim. GBank gl 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00568) - AIR synthase related protein	synthase	284508, 284805, 284593, 284602, 284605
1177	80084647 (2353, 2354)	Novel Protein sim. GBank gl 119791 sp P28643 FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00108) - short chain dehydrogenase	reductase	284605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gl 5031697 ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase, associated	65274572, 18108398, 22278998, 22278999, 28331828, 284508, 284908, 284828, 33857402, 33109954, 284769, 21808765, 21808788, 21808788, 55811857, 33657023, 284628, 55811576, 35698423, 284636, 284556, 58182323, 60432113, 22279000, 22279002
1179	80055576 (2357, 2358)	Novel Protein sim. GBank gl 2880090 emb CAA17888.1  - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	transport	284603
1180	11794448 (2359, 2360)	Novel Protein sim. GBank gl 2559814 emb CAA04787  - (AJ001483) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	284638
1181	17848362 (2361, 2362)			UNCLASSIFIED	285017
1182	81494264 (2363, 2364)	Novel Protein sim. GBank gl 5420387 emb CAB46679.1  - (AJ243438) proteophosphoglycan [Leishmania major]			285007, 285009, 284584, 284909, 284693
1183	76574044 (2365, 2366)	Novel Protein sim. GBank gl 4091877 (AF061331) - alpha galactosidase precursor [Saccharomyces cerevisiae]			284689, 35698423, 284638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gl 2128478 pir S1839 - chitinase (EC 3.2.1.14) precursor - beetle		UNCLASSIFIED	284602
1185	79491185 (2369, 2370)			glycoprotein	283987



1188	20224012 (2371, 2372)			UNCLASSIFIED	264559
1187	78248834 (2373, 2374)			UNCLASSIFIED	29331825, 265017, 18108351
1186	78831387 (2375, 2376)	Novel Protein sim. GBank gl 2896039 (AF054525) - hypothetical protein [Synecococcus PCC7002]		UNCLASSIFIED	264905, 264906
1189	79609367 (2377, 2378)				
1190	78930589 (2379, 2380)			UNCLASSIFIED	264892
1191	80310105 (2381, 2382)			UNCLASSIFIED	265018
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMR1 family related peptide family	UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486
1193	11103584 (2385, 2386)				264636
1194	7883947 (2387, 2388)	Novel Protein sim. GBank gl 8540851emb CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	263978
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gl 1780277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	265007, 265008
1196	13000888 (2391, 2392)			UNCLASSIFIED	264605
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gl 2487360 sp Q50715 IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain		264689
1198	85280101 (2395, 2396)				264594
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gl 1708325 sp P54673 P3K1_DICDI - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)			264603
1200	9848880 (2399, 2400)				264259, 264757, 33109934, 21806768
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gl 2498877 sp P70845 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)	UNCLASSIFIED	calhepsin	264910
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gl 606342 (U18987) - ORF_0822; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]	ribosomalprot		264766, 264769
1203	82125373 (2405, 2406)				264600, 264558
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gl 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SEC SUBUNIT	UNCLASSIFIED		264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264829, 264908, 264909, 264786
1205	80053981 (2409, 2410)				264905, 264769, 264636
1206	80241985 (2411, 2412)			UNCLASSIFIED	264586
1207	79841192 (2413, 2414)			UNCLASSIFIED	264556, 264557, 264558
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gl 2645560 (AF027954) - Bcl-2 related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 264909, 265021, 18108370, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689

1208	79185742 (2417, 2418)	Novel Protein sim. GBank gi 1175033 sp P44388 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	284887, 284688
1210	56426884 (2419, 2420)			UNCLASSIFIED	284907, 284693
1211	94665855 (2421, 2422)	Novel Protein sim. GBank gi 421095 pir J30388 - hypothetical protein o248 - Escherichia coli		transferase	284591, 284592, 284595
1212	79167829 (2423, 2424)	Novel Protein sim. GBank gi 3880525 emb CAB07859  - (293785) predicted using Genefinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		284689, 283967
1213	78858633 (2425, 2426)	Novel Protein sim. GBank gi 228292 pir J1505375A - vir gene [Bordetella pertussis]		kinase	284909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi 5728285 gb AA048398.1 AF12816 - (AF128162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	284908
1215	80050108 (2428, 2430)	Novel Protein sim. GBank gi 2326739 emb CAB10953  - (289289) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 284801, 284602, 284603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi 417328 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYL-PYRUVYL TRANSFERASE) (EPT)		transferase	284604
1217	95011344 (2433, 2434)			UNCLASSIFIED	284805, 284907, 284908, 284591, 284786, 284891, 284693, 284828, 284630, 284636, 284564
1218	11083680 (2435, 2436)	Novel Protein sim. GBank gi 1805460 dbj BAA08022  - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	284801
1219	91218252 (2437, 2438)				56181688, 28331822, 60432289, 284601, 284892, 284829
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi 4240315 dbj BAA74936.1  - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52844507, 284905, 284909, 265008, 265019, 265020, 52844150, 33657023, 284693, 33657182, 35695763, 284834, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi 2143886 pir J152523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	284788, 285020, 284906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi 730805 sp P36663 SPHR_SYN7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	284601
1223	11615847 (2445, 2446)				284593
1224	80432845 (2447, 2448)	Novel Protein sim. GBank gi 1172827 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE [GAMMA-GLUTAMYL KINASE] (GK)	Contains protein domain (PF01472) - PUA domain	kinase	284593, 284600, 284601, 284603, 284605, 284788, 18108376, 284635, 18108387

1225	80434427 (2448, 2450)	Novel Protein sim. GBank gij2105050jemb CAB08838  - (Z95438) hypothetical protein RV3844c [Mycobacterium tuberculosis]			polymerase	284768 284905, 284512, 284689
1226	80237518 (2451, 2452)					
1227	78422138 (2453, 2454)	Novel Protein sim. GBank gij1708788 sp P8133 FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)			UNCLASSIFIED	284908, 284637, 284639
1228	78208027 (2455, 2456)	Novel Protein sim. GBank gij1653801 dbj BAA18811  - (D90817) acriflavine resistance protein [Synecococcus sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family			284605, 284634
1229	84329135 (2457, 2458)				UNCLASSIFIED	87188474, 265011, 87188559, 284681, 284689, 284693, 65274620, 18108374, 284909, 284605, 18108388
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230 sp P28598 CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family			
1231	79843141 (2461, 2462)				UNCLASSIFIED	284908
1232	78953104 (2463, 2464)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			transport	284909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij118298 sp P20730 CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)			UNCLASSIFIED	265017, 284564
1234	78242158 (2467, 2468)	Novel Protein sim. GBank gij728671 sp P40280 H2A_MAIZE - HISTONE H2A	Contains protein domain (PF00125) - histone Core histone H2A/H2B/H3/H4			265008, 265010, 18108381
1235	78914423 (2469, 2470)					284834, 284762
1236	81927147 (2471, 2472)	Novel Protein sim. GBank gij3875133 emb CAA94750  - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL:...			UNCLASSIFIED	265018, 35811150, 284565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij3885470 (AF081443) - G protein-coupled receptor LGR4 [Rattus norvegicus]				284758, 284601, 284766, 284687, 18108372, 284555, 284559
1238	87411577 (2475, 2476)					
1239	82187449 (2477, 2478)	Novel Protein sim. GBank gij4007990 gb AAC95339  - (AF084383) DOK protein [Mus musculus]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat			284259, 28331822, 29331824, 35696052, 284508, 284908, 52844045, 52848317, 284288, 284769, 284693, 284632, 284634, 284558, 87188518, 284563
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192 sp P45420 YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR			oncogene	284509, 284511, 284759, 284760, 284764, 284557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383 sp P18904 GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase		UNCLASSIFIED	284601, 284604, 284638
1242	78775890 (2483, 2484)					284908, 284907, 284908, 284834

1243	78779458 (2485, 2486)	Novel Protein sim. GBank glij3355671embjCAA189711 - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank glij2970848 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank glij4586338jdbjBAA76357.11 - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank glij3581849jembjCAA208051 - (AL031541) putative phenylalanine synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank glij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank glij1352403jpp09487f16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 26331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264780, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank glij2791407jembjCAA160011 - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]	transport		264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2498, 2500)	Novel Protein sim. GBank glij112785jpp051003MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264883, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank glij5670178jppAAD46616.11AF18131 - (AF181317) NRAMP manganese transport protein MntA [Salmonella typhimurium]	glycoprotein		264800, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank glij103160jppjS22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906787, 55811857, 264892, 264556, 264639
1255	79169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank glij2985353jembjCAA04608.11 - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	80432288, 264600, 264605, 264764, 264687, 264769, 264688, 27486285, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank glij3193308 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80166012 (2517, 2518)			UNCLASSIFIED	264806, 264448, 264908
1260	80084808 (2519, 2520)			UNCLASSIFIED	264834, 264639

1261	87412602 (2521, 2522)	Novel Protein sim. GBank gl 568851 dbj GAA03039.1  - (AB028010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264908, 264768, 264769, 264889, 264693, 264639, 18108384, 264563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gl 95100 pir S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gl 3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264602
1264	80033396 (2527, 2528)				264634
1265	80253578 (2529, 2530)				264563
1266	78914604 (2531, 2532)			UNCLASSIFIED	264768, 264838, 264639, 264587
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gl 1085002 pir S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21908754, 284369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gl 4888445 emb CAB43370.1  - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278895, 56994075, 60424269, 29331827, 264108, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87188559, 264600, 265018, 265019, 264369, 264688, 21908787, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22278002, 264488
1269	78821948 (2537, 2538)	Novel Protein sim. GBank gl 3334781 emb CAA19939  - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264908, 264687, 264893
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gl 2851634 sp Q50591 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	78840499 (2541, 2542)			ATPase associated	35696052, 264908
1272	78462878 (2543, 2544)				264586, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gl 1655665 emb CAB03731  - (Z81389) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)				
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gl 123726 sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	UNCLASSIFIED	264905, 264908, 264909, 264769
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gl 2128476 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602
1277	20438185 (2553, 2554)				264369
1278	11088385 (2555, 2556)	Novel Protein sim. GBank gl 1175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264558
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gl 1929513 (U84318) - ATP synthase subunit beta [Moorella thermoacetica]		UNCLASSIFIED	264603
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gl 4938504 emb CAB43882.1  - (AL078465) putative protein [Arabidopsis thaliana]		synthase	264605
				struct	283976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gl 136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	28331825, 28331828, 284766, 83373044
1282	87537895 (2863, 2864)	Novel Protein sim. GBank gl 3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20468305 (2565, 2566)	Novel Protein sim. GBank gl 3261721 (emb CAB07057) - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20638325 (2567, 2568)	Novel Protein sim. GBank gl 3929022 (AF057696) - LspB [Haemophilus ducreyi]			284604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gl 417154 (sp P33126) HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - eph Hsp90 protein		264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gl 2078004 (emb CAB08451) - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 284602, 264766, 264687, 284769, 264689, 18108370, 264636, 18108385, 284583
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gl 5353510 (gb AAD42161.1) (AF088891) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35966052, 284107, 284508, 284509, 284905, 284906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 284910, 285009, 33657402, 284595, 264758, 285011, 265019, 264760, 18108351, 264681, 264764, 284288, 264685, 284766, 264687, 264768, 264769, 285020, 265021, 284534, 264692, 18108370, 264628, 18108374, 35696423, 284555, 284556, 284557, 264558, 18108385, 264564, 284566, 284567, 284488, 18108391, 284637
1289	11813647 (2577, 2578)	Novel Protein sim. GBank gl 1169885 (sp P46023) GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	284583
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gl 2072674 (emb CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain		265007, 265008, 264769
1291	80470286 (2581, 2582)				
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gl 1835755 (U86338) - zinc finger protein Phg-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	284092, 284259, 29331822, 29331824, 264508, 284908, 264909, 264512, 265008, 285009, 284591, 265019, 264369, 264288, 284686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 284563
1293	80067538 (2585, 2586)	Novel Protein sim. GBank gl 2129173 (p F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	265008, 55812038, 264369, 264556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gl 5441778 (emb CAB46803.1) - (AL086811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindap		284802, 284605, 264760, 18108351, 264689, 33857023, 264559
1295	11686895 (2589, 2590)		dehydrogenase		264689

1296	11887904 (2591, 2592)	Novel Protein sim. GBank gl 4982191 gb AAD36886.1 AE00180 - (AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01357) - 5'3' exonuclease	UNCLASSIFIED	264591, 264639
1297	79839300 (2593, 2594)	Novel Protein sim. GBank gl 1843770 (U97181) - F53F10.1 gene product [Caenorhabditis elegans]		polymerase	264693
1298	94238508 (2595, 2596)	Novel Protein sim. GBank gl 1843770 (U97181) - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 265017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]			
1300	80084867 (2599, 2600)	Novel Protein sim. GBank gl 4082973 dbj BA36204.1  - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264488, 264908, 264909, 22278002, 264566
1301	17939614 (2601, 2602)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]		UNCLASSIFIED	264906
1302	95418198 (2603, 2604)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]			
1303	9684121 (2605, 2606)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]			85656542, 265020
1304	78377188 (2607, 2608)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]			264908
1305	18905899 (2609, 2610)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31685 2 [Homo sapiens]		UNCLASSIFIED	264508
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gl 3242273 emb CAB07017  - (Z92669) hypothetical protein Rv0238c [Mycobacterium tuberculosis]		UNCLASSIFIED	264566
1307	82201028 (2613, 2614)	Novel Protein sim. GBank gl 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]			264636
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gl 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - reductase	UNCLASSIFIED	264907, 264592, 264764
1309	78283011 (2617, 2618)	Novel Protein sim. GBank gl 955181 pir S16288 - ferric enterobactin transport protein fepC - Escherichia coli	Envelope glycoprotein GP120	transport	264555
1310	20466318 (2619, 2620)	Novel Protein sim. GBank gl 5459220 emb CAB48893.1  - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			264906, 18108354
1311	87813142 (2621, 2622)	Novel Protein sim. GBank gl 5459220 emb CAB48893.1  - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264605
1312	88081720 (2623, 2624)	Novel Protein sim. GBank gl 4453118 gb AAD21084  - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00086) - dna_ma_bind Zinc finger, C2H2 type		35696288, 29331827, 264908, 265008, 264764, 264766, 264688, 21908787, 21908769, 35695917, 264691, 264693, 22278895, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21908768, 265020, 265021, 33657023, 22278002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gl 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - ribosomalprot Ribosomal protein S16		22278896, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21908787, 29146827, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1314	58926053 (2627, 2628)	Novel Protein sim. GBank gl 2589223 (AF026565) - ring (finger protein [Mus musculus])			264693
1315	84357182 (2629, 2630)	Novel Protein sim. GBank gl 2589223 (AF026565) - ring (finger protein [Mus musculus])	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691

1318	85561608 (2631, 2632)	Novel Protein sim. GBank gl 5689407 dbj BAA82987.1  - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181866, 20281171, 29331822, 29331824, 60424289, 29331825, 35696052, 52644045, 264591, 60432229, 265018, 265019, 55311150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87188518, 60432113, 22279002, 264584
1317	86055187 (2633, 2634)	Novel Protein sim. GBank gl 4938757 gb AAD30541.1 AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264606, 264909, 264369, 264684
1316	95322893 (2635, 2636)	Novel Protein sim. GBank gl 4680204 gb AAD27587.1 AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	84236546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108388, 264628, 264629, 18108377, 264639
1320	86603587 (2639, 2640)	Novel Protein sim. GBank gl 4240183 dbj BAA74870.1  - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gl 4888505 emb CAB43377.1  - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gl 5282591 emb CAB45736.1  - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264893, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gl 5459516 dbj BAA82407.1  - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87188474, 18108351, 264288, 21906766, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gl 5031717 ref NP_005704.1 pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278986, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108378, 264631, 264632, 264634, 264636, 264638, 264593, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gl 3294501 U64857  - similar to the DPTU/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85688542, 264760, 264768, 264769, 264691, 35698423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gl 1397275 U61947  - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635



1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 278932 sp F39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21908754, 285010, 285011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21908787, 21908788, 28148629, 265020, 264690, 264691, 264692, 264693, 263967, 33657109, 33657182, 27486282, 33657349, 18108370, 18108374, 55810764, 35695855, 264634, 56182323, 83373044, 87188518, 60432113, 22279000, 22279002, 264563, 264567, 264488, 22278997, 29331828, 264595, 18108351, 264766, 22278002, 264482, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	
1329	87755278 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26968.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2658, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56526488
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 db BAA76815.1  - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21908765, 55811957, 265020, 33657023, 33657109, 263973, 55811578, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 db BAA82407.1  - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	83274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 58182435, 264510, 21908754, 87188559, 265018, 265019, 264448, 264288, 264369, 264686, 21908765, 21908766, 21908767, 21908768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	98098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 db BAA83047.1  - (AB029016) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526488 264905
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662538 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	
1335	87644788 (2669, 2670)	Novel Protein sim. GBank gi 4240285 db BAA74921.1  - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21908754, 87168559, 265017, 264288, 21908765, 21908767, 21908768, 21908769, 265020, 33657109, 27486284, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi465445 sp P33485 VNUA_PVK_A - PROBABLE NUCLEAR ANTIGEN				264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi4589471 dbj BAA83019.1  - (AB028990) KIAA1067 protein [Homo sapiens]	UNCLASSIFIED			5618575, 56994075, 22278998, 22278999, 284092, 284259, 60432289, 29331826, 284908, 284908, 284909, 264112, 265008, 285008, 60433358, 55812038, 33857084, 265011, 265017, 265018, 265019, 264682, 284448, 264683, 284369, 264688, 264689, 21808766, 21808769, 285020, 284691, 27488281, 20281089, 18108379, 55811576, 35895855, 56182323, 60432113, 22279002, 284587
1338	80368114 (2675, 2676)		UNCLASSIFIED			29331822, 265010, 264288, 264689, 18108370, 35895855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED			35895852, 264809, 264688, 264556, 264558
1340	88316311 (2679, 2680)					
1341	88101485 (2681, 2682)					284681, 284685, 284686, 284682
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi5019584 emb CAB44507.1  - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Im7	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		284629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2		Contains protein domain (PF00560) - Leucine Rich Repeat		264910, 284686, 264534
1344	20562559 (2687, 2688)					263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi2144101 pir I55210 - tricarboxylate carrier - rat (fragment)	glycoprotein			264809, 60170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi3681052 emb CAA18523  - (AL023843) predicted using GeneFinder: similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk356c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278998, 284907, 264681, 284685, 264689, 285020, 264693, 22279000, 22279002, 284566
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379 ref NP_003858.1 pHG38 - orphan G protein- coupled receptor HG38	glycoprotein	Contains protein domain (PF00560) - Leucine Rich Repeat		284808, 264908, 284909, 265008, 264910, 265011, 265017, 264764, 264768, 264767, 284769, 284631, 284634, 264638, 264567, 284488
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3399720 dbj BAA32100  - (AB010998) peptidylarginine deiminase type IV [Rattus norvegicus]	UNCLASSIFIED			284488, 264489, 264508, 264509, 264510, 284511, 284512, 284591, 284592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 284557, 264558, 22279002, 284488

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gl 214410 pr j 55210 - l-tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52846842, 35695266, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264581, 60433438, 264757, 21908754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21908765, 21908768, 21908767, 21908768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22278900, 22278902, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52846842, 264259, 29331825, 264908, 264511, 264804, 264288, 21908769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22278902, 264486
1351	87381327 (2701, 2702)	Novel Protein sim. GBank gl 4887239 gb AAD32246.1  - (AF084564) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gl 2144101 pr j 55210 - l-tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	35698286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264810, 264758, 264598, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52844229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264829, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264584, 264586
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gl 4889108 gb AAD27763.1 AF07703 - (AF077030) hypothesized 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278998, 23331826, 264906, 265008, 33657402, 21908754, 265011, 87186559, 264684, 264388, 264769, 264689, 21908765, 21908768, 52844150, 33657023, 264692, 264693, 18108374, 83373044, 87186518, 22278900
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gl 1489199 db BAA094871 - (O50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bld	22278996, 22278997, 264259, 66714117, 264511, 21908754, 265010, 264769, 264689, 21908765, 21908768, 21908769, 264532, 27486282, 264829, 264836, 264558, 264638, 264639, 264482, 264484

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1367	87721210 (2733, 2734)	Novel Protein sim. GBank gl 4884088 emb CAB43240.1  - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264486, 52646942, 52846365, 22278995, 56994075, 35696286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265008, 60170831, 33657402, 55812038, 21908754, 265011, 67168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264389, 264686, 264767, 264688, 21908765, 21908766, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gl 484561 sp P35289 RB15_RAT - RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87188559, 264600, 264601, 264760, 264764, 264765, 264788, 52844229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52844332, 264558, 264639, 83373044, 264563, 264566, 264486, 264567, 265008, 60432228, 60433358, 33657084, 21908764, 21908768, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gl 2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gl 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264769, 21908767, 35695917, 18108362, 35696423, 264632, 264635, 264638, 264555, 264638, 264556, 264639, 18108385, 65274727, 264404, 264563, 264568, 264486
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gl 5032203 ref NP_005714.1 TSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657162, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gll840708[dbj BAA09334] - (D50885) trans-aldolase [Trypanosoma cruzi]		collagen	263976	264769, 21908765, 21908767, 22278989, 264691, 264910, 55812036, 265010, 264681, 264684
1373	80469421 (2745, 2746)			UNCLASSIFIED		264684
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gll111878[pir JC1241] - beta-interferon-induced protein - rat		interferon		264510, 265007, 264512, 265008, 60432229, 264689, 85274781, 264555, 264556, 264557, 83373044, 60432113
1375	94238942 (2749, 2750)	Novel Protein sim. GBank gll5949179[gb AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat			52644507, 52645156, 52646842, 52646365, 56182575, 56181886, 22278988, 56994075, 35698286, 22278987, 22278988, 22278989, 264259, 29331822, 52645080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35698052, 33658970, 264905, 264909, 264908, 264907, 264908, 29331830, 265009, 33657402, 60433356, 52646317, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 85274620, 52645129, 33657109, 27488261, 33657349, 27488265, 35695783, 18108378, 55810784, 35698423, 35695855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264563, 264564, 264568, 264587, 264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35698032, 264508, 264509, 264905, 264906, 264928, 264908, 264629, 18108372, 264909, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526486, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264486, 264768
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gll138350[sp P28988 VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		22279002, 264563, 264564, 264568, 264587, 264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35698032, 264508, 264509, 264905, 264906, 264928, 264908, 264629, 18108372, 264909, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526486, 265010, 265011, 264600, 264563, 264762, 264564, 264565, 264764, 264486, 264768
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gll1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		2331824, 264581, 265019, 264686, 264768, 55811957, 264693, 22278002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[db][BAA36283] - (AB001772) PEM-5 [Clona savigny]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 28148827, 55811957, 264691, 18108366, 33657109, 18108368, 264635, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb]/AAD30662.1 - (AF088834) germ cell specific Y-box binding protein [Homo sapiens]		nucL_rept	264510, 264512, 265009, 264288, 264564
1381	88178656 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb]/AAD28508.1[AF12538 - (AF125384) L82A [Drosophila melanogaster]		UNCLASSIFIED	87168559, 265017, 264628, 22279002
1382	84847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433396, 85858542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264908, 264909, 264511, 264512, 264910, 284760, 18108351, 284766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		Inf	60432289, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264568
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb]/CAA10600 - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895164[gb]/AAD32753.1[AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]		glycoprotein	65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1388	91256016 (2777, 2778)	Novel Protein sim. GBank gij5699397[dj]BAA82977.1) - (AB028948) KIAA1025 protein (Homo sapiens)	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278899, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29148499, 264908, 68712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21908765, 21908766, 21908767, 21908768, 265020, 265021, 264692, 33657023, 33657348, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564
1389	94111916 (2779, 2780)	Novel Protein sim. GBank gij3702295 (AC005783) - R33063_1 [Homo sapiens]	peptidase		52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264908, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21908765, 21908769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486281, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gij1346910[sp]P28650[P]UA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278894, 22278895, 35696288, 56994075, 22278897, 22278898, 22278899, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656870, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52648317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906784, 21906787, 35695917, 265020, 265021, 33657109, 52645129, 27486281, 27486282, 27486285, 33657348, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264568, 18108381
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845[dj]BAA21534) - (DB8461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381



1386	95363253 (2781, 2782)	Novel Protein sim. GBank gi 2135604 pir  54810 - pHLEIF1 - human			22278997, 22278998, 264259, 29331825, 60432289, 29331828, 29148498, 29148499, 284907, 284908, 29331830, 284909, 265006, 285007, 265008, 265009, 60433356, 265010, 284602, 265017, 285018, 285019, 18108354, 52944229, 18108358, 21908767, 29148627, 21908768, 21908769, 29148629, 28148784, 285021, 285022, 18108368, 18108374, 58182323, 18108385, 284563, 284567, 35898286, 284907, 66712502, 284510, 35895917, 284692, 264693, 35898423
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB4680.1  - (AJ243460) proteophosphoglycan [Leishmania major]			284259, 29331822, 29331824, 29331825, 29331827, 35698052, 33656970, 87168474, 285018, 265019, 284682, 284768, 21908767, 265020, 33857023, 27486261, 55811576, 264632, 284639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi 2498887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III chicken		UNCLASSIFIED	284768, 18108370, 264555, 264557
1400	95418064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pir  S27839 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	58182575, 22278994, 22278997, 284259, 29331822, 29331825, 29331826, 29331827, 29331828, 284908, 56182435, 264112, 265009, 265011, 265017, 285018, 265019, 284760, 264762, 264765, 264288, 264685, 284687, 56181582, 264769, 21908768, 21908767, 55811957, 264691, 264692, 264828, 264629, 55811578, 264634, 264555, 264637, 284557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3255185 emb CAA15485  - (AL008835) dJ510H18.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 284909, 264758, 284768, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nel homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain		264905, 264907, 264908, 284909, 284112, 284693, 33857109, 284634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1  - (AL080158) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21908765, 21908769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	85274572, 22278998, 29331822, 29331828, 66712502, 285008, 60433436, 265017, 284693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gij1854065[emb]CA58337] - (X83413) U88 [Human herpesvirus 8]			264488, 56994075, 35696288, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33857402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33857023, 33857109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264488, 264567, 264907, 264605
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij1624076[gb]AAC86425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X), similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedium bursaria Chlorella virus 1]	collagen		
1407	84129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696288, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 26146498, 264107, 264908, 265008, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264886, 21908785, 21908789, 264692, 33857109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95381477 (2815, 2816)	Novel Protein sim. GBank gij2564653 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264768, 264887, 264689, 21908787, 265021, 264690, 264691, 33857023, 264692, 264693, 33857109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567, 264693
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[db]BAA23714] - (AB007902) H-0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2463780[sp]Q80994[ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)]	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265008, 265010, 264601, 264886, 264769, 21908787, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gij3123155jip91343jym3m, CAEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME 1	Contains protein domain (PF00400) - Kinase receptor WD domain, G-beta repeat	22278995, 22278997, 22278998, 28331822, 60432289, 28331828, 284907, 285017, 285018, 284682, 21906768, 21906768, 21906769, 285020, 284690, 284691, 33657023, 33657109, 27486284, 284628, 283972, 284634, 284558, 18108385 284757
1412	84380919 (2823, 2824)			
1413	95418558 (2825, 2826)	Novel Protein sim. GBank gij3879121jemb[CAA94370] - (270310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL: T01823 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED homodimer 56994075, 28331822, 35686052, 28331828, 28331830, 284909, 52644045, 284510, 52644286, 85658542, 87168474, 285017, 285018, 284681, 284687, 21906768, 35695917, 285020, 52644150, 284692, 283987, 27486264, 35695763, 284639, 18108387, 284566 284682, 284683, 285022, 284636
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED 52646365, 58182575, 22278994, 22278995, 56994075, 22278998, 22278997, 22278998, 22278999, 284259, 28331822, 28331824, 28331825, 28331826, 28331827, 28331828, 29146498, 66712502, 28331830, 52644045, 284113, 284511, 33657402, 284757, 21906754, 55811388, 265017, 285018, 265019, 284761, 284683, 284369, 284288, 284688, 284689, 21906768, 21906767, 29146827, 21906769, 55811857, 265020, 285021, 284690, 33657023, 65274620, 52645129, 27486262, 27486284, 60431528, 284629, 35695855, 58182323, 284559, 60432113, 284404, 22278902, 284482
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein [Arabidopsis thaliana]		

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gij5106597gb/AAD39749.1 AF123052 MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278998, 35686286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29145498, 284905, 264907, 284908, 284828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21908754, 87168474, 265010, 265011, 87188559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264882, 264883, 264766, 52644229, 264886, 264889, 21908765, 21908766, 21906767, 29148827, 21908768, 55811957, 29148829, 265020, 52644150, 18108391, 33657023, 18108362, 18108368, 264828, 18108370, 264829, 18108374, 18108378, 55811576, 65274791, 264834, 264638, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000 264107, 264448
1417	87826683 (2833, 2834)	Novel Protein sim. GBank gij4958935 gbjBAA78095.1  - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	
1418	87594276 (2835, 2836)		UNCLASSIFIED	264258, 264808, 265010, 52644229, 21906784, 21906768, 264690, 264639, 18108388
1419	87757188 (2837, 2838)	Novel Protein sim. GBank gij2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264288
1420	87286628 (2838, 2840)	Novel Protein sim. GBank gij5174421 ref NP_008023.1 pCPNE - copine VI (neuronal) (Z69635) Similarity to Yeast uridine kinase	ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gij3876090 emb CAA93439.1  - (SW URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE177 comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	kinase	18108358, 18108398, 18108399, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27488261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	65178777 (2843, 2844)	Novel Protein sim. GBank gi 4505939 ref NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		mapolymerase	56994075, 35698286, 87168559, 55611957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264768, 264887, 21808765, 21908766, 21908767, 21908768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22278002, 264583
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi 1007989 ref S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi 2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US11 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35698286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21908754, 265018, 264288, 21908765, 21908766, 21908767, 21908769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi 5616074 gb AAD45616.1 AF08194 - (AF081943) prolactin- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264883, 264288, 18108354, 21908765, 21908768, 29148629, 33657023, 18108374, 35698555, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi 138350 sp P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	55181686, 264259, 264807, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 85274791, 22279002, 264568
1429	87886889 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi 1181619 gb BAA11565  - (D82384) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264881, 21906765, 21906767, 85274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1  - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	67463004 (2863, 2864)	Novel Protein sim. GBank gi 414787 (L18866) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi 2460318 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264239, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264882, 264891

1435	94708213 (2868, 2870)	Novel Protein sim. GBank gi 3970850 dbj BAA34789.1  - (AB015330) HRIHFB2007 [Homo sapiens]			Transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33856970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906787, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108378, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22278000, 22279002, 264563, 264482, 264585, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515  - (X56044) protein H19C [Mus musculus]			UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 24968877 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN CDBF5.2 IN CHROMOSOME III			UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264892, 264893
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1905908 (AD000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]		Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264906, 264909, 264757, 264600, 264801, 264605, 264788, 264789, 264690, 35696423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi 3876289 emb CAA94892  - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]		Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33856970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 18108354, 264288, 18108355, 264757, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22278000, 264486
1440	87423843 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714  - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			UNCLASSIFIED	264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gij4403956[embjCAB11123.2] - (Z88551) predicted using hexExon; MAL3P8.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein ZK287.5 (TR:....	Contains protein domain (PF00846) - helicase F-box domain.	18108392, 284488, 283994, 284489, 58182575, 22278994, 22278995, 56994075, 35698286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35698052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85858942, 87188474, 265010, 87168559, 264800, 264802, 265017, 264604, 285018, 264605, 265019, 284760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21908765, 21805766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 284628, 18108370, 284629, 18108374, 55811578, 35696423, 65274791, 35695855, 284631, 264634, 284635, 284636, 284637, 284638, 56182323, 284558, 60170394, 264639, 284559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264488, 264906, 285007, 264693, 264558
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gij5103027[dbj]BAA78765.1] - (AB023419) mSox7 [Mus musculus]	transcription factor	
1443	87108935 (2885, 2886)	Novel Protein sim. GBank gij488728[gb]AAD32244.1[AF15075] - (AF15075) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447[embjCAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...	UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94980470 (2889, 2890)	Novel Protein sim. GBank gij285988[embjCAA11022] - (A1222968) L-periaxin [Mus musculus]	UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gij5081610[gb]AAD39494.1[AF13544] - (AF13544) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01646) - FF domain	264369, 18108396, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 285018, 264288, 21906766, 21906767, 264692, 264634, 264566
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gij3880411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	29331827, 264509, 264909, 285008, 264595, 18108357, 18108385, 264566, 264486

1449	87860859 (2897, 2898)				UNCLASSIFIED	56714117, 264906, 264908, 264591, 264601, 264764, 264632
1450	87456698 (2899, 2900)	Novel Protein sim. GBank gl 1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35686286, 35696032, 265008, 265009, 60170831, 33109954, 264683, 264689, 35698423, 35698555, 56328488
1451	87767970 (2901, 2902)	Novel Protein sim. GBank gl 4160304(emb CAA10600) - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692899 (2903, 2904)	Novel Protein sim. GBank gl 2632909(dbl BAA24608.1) - (CB9340) diploidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gl 728831(sp P39188)ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III			kinase	264510, 264768
1454	11204688 (2907, 2908)					
1455	87787888 (2909, 2910)				UNCLASSIFIED	264556
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gl 726230(sp P41004)CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3			transport	29331822, 66714117, 29331825, 264805, 29331830, 265008, 265009, 265011, 265019, 18108351, 21906768, 33657109, 18108376, 264632, 56182323, 87168518
1457	80076800 (2913, 2914)					22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906785, 21906786, 21906767, 21906769, 29148629, 18108370, 22278000
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gl 2246532 (U93872) - ORF 73. contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			UNCLASSIFIED	264107, 264566
1459	95360820 (2917, 2918)	Novel Protein sim. GBank gl 5524667(gb AAD4333.1)AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 265017, 265018, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1460	95354602 (2919, 2920)			Contains protein domain (PF00168) - C2 domain	kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264566
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gl 1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]			UNCLASSIFIED	29331822, 264591, 55811857, 264691, 264693, 65274820
1462	87732018 (2923, 2924)			Contains protein domain (PF00202) - gaba		22278997, 29331822, 35696032, 265009, 264768, 265017, 265018, 265019, 264760, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27488281, 264555, 83373044
1463	80080605 (2925, 2926)	Novel Protein sim. GBank gl 1770466(emb CAA66912) - (X98259) M-phase phosphoprotein 8 [Homo sapiens]		Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization MOffiler) domain	UNCLASSIFIED	264555, 264556
					struct	60432049, 264259, 29146499, 264905, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108385, 18108388



1464	87620482 (2927, 2928)	Novel Protein sim. GBank gl 3874447 emb CAB02772  - (Z81039) predicted using GeneFinder; cDNA EST EMBL:TO1209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21908754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21906765, 21906766, 21908767, 21906769, 35695917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264595
1465	87425192 (2928, 2930)	Novel Protein sim. GBank gl 4589598 db BAA7682.1  - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264259, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264596, 55812038, 55811366, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87608227 (2931, 2932)	Novel Protein sim. GBank gl 2248532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gl 507241 ref NP_003137.1 SSRP - structure specific recognition protein 1		struct	22278998, 264758, 265018, 265019, 21906789, 265020, 33657109, 22279002
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gl 4507241 ref NP_003137.1 SSRP - structure specific recognition protein 1		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108388, 18108374, 18108381, 18108382, 18108384, 18108388
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gl 1906566 (U81788) - kinesin-73 [Drosophila melanogaster]		UNCLASSIFIED	18108394, 18108398, 56182375, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264368, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87188518, 60432113, 264404, 22279002, 264482, 264587, 264487
1470	94890482 (2939, 2940)	Novel Protein sim. GBank gl 5648170 gb AAD43131.2 AF15909 - (AF159092) syld708613 protein [Homo sapiens]		transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gl 3876146 emb CAB01750  - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:TO1651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins		

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF132986 - (AF132988) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	284905, 18108351, 21906765, 284486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - MHC Nucleosome assembly protein (NAP)		18108384, 22278995, 56394075, 22278999, 29331822, 29331824, 68714117, 29331825, 29331826, 35696052, 284908, 284807, 56182435, 265007, 284758, 285018, 285019, 284760, 284784, 264288, 264685, 284686, 284788, 21908769, 55811957, 285021, 284691, 284693, 284629, 55811578, 284634, 284636, 56182323, 22279002, 284566, 284486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2484890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		284486, 35695917, 35696286, 264692, 33657023, 284693, 33657109, 35696052, 284508, 284905, 284908, 284907, 284629, 284908, 284909, 35696423, 35695855, 284511, 284910, 264632, 284634, 284635, 284636, 284637, 284558, 264557, 264639, 284758, 60432113, 284804, 284605, 284565, 284586, 284764, 264488, 264885, 264766, 264681, 264682, 264288, 284568
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - UNCLASSIFIED Fibronectin type III domain		
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004684.1 pANGP - angiotensinogen 3	Contains protein domain (PF00147) - glycoprotein Fibrinogen beta and gamma chains, C-terminal globular domain		60424179, 56181886, 29331824, 60424269, 29331826, 35696052, 284508, 284905, 284906, 284907, 284908, 284909, 284512, 265007, 285008, 285009, 284910, 33657402, 284595, 284596, 55812038, 285011, 284601, 284762, 18108351, 264288, 264369, 264685, 284766, 284689, 55811957, 264691, 284692, 284693, 18108370, 60431528, 18108374, 35696423, 284634, 284635, 284636, 60431850, 284555, 284638, 284557, 264639, 18108382, 18108388, 60432113, 22279002, 284259, 284107, 284905, 265008, 265010, 285011, 284682, 284288, 265020, 265021, 263974
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2488308 sp Q60870 DPI_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (T82 PROTEIN HOMOLOG) (GP108)		UNCLASSIFIED	
1478	11754412 (2955, 2956)				284686

1479	91840140 (2857, 2858)	Novel Protein sim. GBank gi 5489741 gb AAD43978.1 AF15286 - (AF152861) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 86714117, 264906, 264907, 56182435, 285006, 80170831, 33657402, 264758, 33108954, 21908754, 265017, 265018, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486281, 27486282, 33657349, 18108370, 60431528, 263978, 55811576, 284556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2859, 2860)	Novel Protein sim. GBank gi 3550456 emb CAA06328.1  - (AJ005073) A1ix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35698266, 56994075, 22278998, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 28146499, 264103, 264105, 264108, 264807, 52644045, 264112, 265007, 265008, 265009, 60433356, 60433438, 264588, 33108954, 33657084, 52644256, 87168474, 265010, 87168539, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2861, 2862)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14678 - (AF146793) PFT27 [Mus musculus]		MHC	265008, 265007, 265010, 18108374
1482	85320442 (2863, 2864)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Vmi inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264808, 264910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Plasum salivum]	Contains protein domain (PF00036) - struct EF hand		264259, 29331822, 52645080, 29331825, 29331826, 33655970, 29331830, 265007, 55812038, 33108954, 285017, 264288, 21908768, 21908769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 gb t180090 - (S83384) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Parliai, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29146827, 33657023, 27486282, 18108374, 35698423, 83373044, 60432113
1485	80184441 (2869, 2870)	Novel Protein sim. GBank gi 5360129 gb AAD2883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - struct Kinesin motor domain		264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi 4589516 dbj BAA76780.1  - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	Kinase	56182575, 22278999, 264806, 264907, 21908754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566, 21908754, 264486
1487	88452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB4443.1  - (A1132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	
1488	87732028 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAD47378.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	fgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265008, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264782, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q62786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35896423, 35895855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87380127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35895855, 264635, 60170394, 56526486, 22278002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 285671 L11275 - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III (Saccharomyces cerevisiae)		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805383 (2983, 2984)	Novel Protein sim. GBank gi 1656005 U71205 - nt [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2885, 2886)	Novel Protein sim. GBank gi 5689515 dbj BAAB3041.1  - (AB029012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 52846365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52844045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264882, 264885, 264886, 52844229, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108384, 18108385, 33657109, 33657182, 27488261, 27488262, 27488264, 33657349, 27488265, 35695763, 18108370, 264829, 18108374, 52844332, 56182323, 87188518, 22279002, 264564, 264566, 264567
1494	87605265 (2887, 2888)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - Kinase KRAB box	264907, 265009, 264789, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2889, 2890)	Novel Protein sim. GBank gi 4568568 dbj BAA76816.1  - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - Transcription factor KRAB box	22278997, 264259, 264906, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2891, 2892)	Novel Protein sim. GBank gi 5420387 emb CA846678.1  - (AJ243458) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2893, 2894)	Novel Protein sim. GBank gi 3874825 emb CAA92591 - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE). cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33258 comes from this gene....	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	264910, 264758, 265011, 264784, 264288, 264690, 264634, 264635, 56526486
1498	90634838 (2895, 2896)	Novel Protein sim. GBank gi 728835 sp P39193 ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	oncogene	264488, 65274572, 29331822, 265017, 265018, 21905765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2897, 2898)	Novel Protein sim. GBank gi 2570198 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]	glucosylase	263978, 264568
1500	80498388 (2899, 3000)	Novel Protein sim. GBank gi 2078483 (U43200) - anifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	22278999, 264769, 18108379
1501	85795287 (3001, 3002)		UNCLASSIFIED	264569
1502	80206141 (3003, 3004)			264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gi 3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to C07537 (PID:gi1171889) [Homo sapiens]	transferase Glycosyl transferases	29331822, 265007, 264369

1504	78640051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gll475375jemb CAB41970.1  - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35686052, 264509, 284908, 264907, 284908, 284909, 264511, 264810, 55812038, 264759, 264763, 264764, 284689, 35685917, 265022, 33657109, 18108374, 284631, 264635, 264638, 264568
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gll1304201db BAA08170  - (D29786) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264082, 60432049, 264259, 52845080, 29331822, 29331827, 264106, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21908754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264389, 264887, 264889, 21908765, 29148627, 21906788, 21906789, 29148628, 52644150, 33657023, 18108376, 65274791, 58182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gll5689513db BAA83040.1  - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11818758 (3015, 3016)	Novel Protein sim. GBank			264593
1509	87318451 (3017, 3018)	gll5031975ire NP_005875.1 pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331828, 264591, 33109954, 264563
1510	95362843 (3019, 3020)	Novel Protein sim. GBank		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gll113161 sp P28614 ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gll4598353 gb AAD23014.1 AC006558 - (AC006558) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108386, 56994075, 60432289, 265008, 60433356, 60433438, 21908754, 87168474, 87168559, 265018, 264782, 264783, 264887, 21906785, 21906789, 27486282, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87438228 (3025, 3026)	Novel Protein sim. GBank gll1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264908, 264907, 284908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3026)	Novel Protein sim. GBank gl14559353[gb]A023014.1(A006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 5274572, 22278994, 35898288, 5694075, 284259, 52845080, 29331822, 29331825, 35898052, 28331830, 52644045, 56182435, 285008, 60433358, 60433436, 55812038, 21908754, 52848317, 52844296, 87168474, 87168559, 264448, 52844229, 21906765, 21906766, 21906767, 21906768, 35895917, 265020, 52844150, 33657023, 52845129, 33657108, 33657182, 27486261, 27486262, 27486264, 27486265, 35895763, 18108376, 35896423, 35895855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3028, 3030)	Novel Protein sim. GBank gl3879501[emb]CAA87795] - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33985 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin	UNCLASSIFIED	
1516	86073538 (3031, 3032)	Novel Protein sim. GBank gl488015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 56182323, 22278002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gl3415134 (AF082024) - Phyb1 [Plimpinella brachycarpa]		UNCLASSIFIED	264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gl728838[sp]P39185[ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII (AL080188) hypothetical protein [Homo sapiens]	im7		68714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264766, 264768, 18108374, 264636, 264638, 264486 264569, 264489, 60432049, 265009, 33857402, 264598, 21906754, 265018, 264369, 21908765, 21906768, 21906769, 264691, 65274620, 33657182, 27486281, 18108374, 264557, 264639, 87168518, 22278002
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gl2662161[db]BAA23712] - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108382, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970698 (3041, 3042)	Novel Protein sim. GBank gl15052351[gb]A038518.1(A038518) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleoside transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108384, 35898423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)	Novel Protein sim. GBank gl3776587 (AC005388) - Strong similarity to F21B7.33 gl2809264 from A. thaliana BAC gb AC002560. EST gb n65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED		29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gl3776587 (AC005388) - Strong similarity to F21B7.33 gl2809264 from A. thaliana BAC gb AC002560. EST gb n65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED		55274572, 21906768, 264693
1524	80203723 (3047, 3048)	Novel Protein sim. GBank		UNCLASSIFIED	264112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gl14759040[ref]NP_004283.1(pRIN1) - ras inhibitor		UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21908785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262612 (3053, 3054)	Novel Protein sim. GBank gi 2792498 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264288, 21908766, 21908769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21908765, 21908766, 21908767, 21908768, 21908769, 265022, 264683, 83373044, 18108385
1529	94120783 (3057, 3058)	Novel Protein sim. GBank gi 4408663 gb AAD20053  - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 80433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264786, 18108357, 264788, 52644229, 21908765, 21908766, 21908767, 21908768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 80432113, 22279002, 264583, 264584, 264486, 264567
1530	95012785 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043842) - malrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264568, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gi 1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811388, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264568



1532	85718224 (3063, 3064)	Novel Protein sim. GBank gl 3874716 emb CAA81265  - (Z68484) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264889
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gl 1490324 emb CAB01543  - (Z78141) unknown [Mus musculus]			struct	26331824, 28146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263987, 20281149, 18108374, 263981, 264568
1534	95343841 (3067, 3068)	Novel Protein sim. GBank gl 81286 pir S22687 - extensin - Volvox carlari (fragment)			UNCLASSIFIED	264905, 264907, 264766, 264637
1535	90938732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 28331822, 60432289, 29331827, 28146499, 265008, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21808768, 29148829, 265021, 265022, 18108377, 58182323, 60432113, 22279000, 22278002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gl 108024 pir B32891 - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor		264886, 18108357, 18108394, 21906767, 21908768, 29148829, 35696286, 265020, 265021, 52844150, 264693, 68714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35895855, 265009, 264634, 264636, 264638, 18108385, 58526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	96354556 (3073, 3074)	Novel Protein sim. GBank gl 3876332 emb CAB02086  - (Z79764) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk428f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 58182575, 60432049, 264259, 29331828, 265008, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gl 403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gl 321841 emb CAA19575.1  - endonuclease ga mna subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P38707, YAR008W, IRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:289, E(0.6e-2...		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 284258, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87188559, 285017, 265018, 265019, 18108351, 284288, 52844228, 18108359, 21906764, 21906767, 21906788, 35695917, 285020, 265021, 52844150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 284558, 56182323, 60170394, 83373044, 87188518, 60432113, 22278000, 22279002, 264568
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gl 5052634 gb AAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gl 5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 284259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 284512, 284910, 284592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811937, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 284632, 284634, 264635, 264639, 18108385, 284583, 284584, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gl 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 55274572, 29331822, 264508, 265007, 265008, 285009, 265011, 264882, 18108354, 18108355, 52844150, 18108368, 264636, 18108381, 18108382, 264106, 33109954, 265019, 264883, 35695917, 264690, 264692, 33657109
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gl 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gl 3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nuc. recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264883, 33657109, 35696423, 264631, 87188518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gl 1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP-P22062) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79478589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86959584 (3093, 3094)	Novel Protein sim. GBank gl 2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	55811386, 265010, 264600, 265017, 265019, 264288, 264768, 285020, 265022, 55811578, 18108380, 264563

1548	94233065 (3095, 3098)	Novel Protein sim. GBank glij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank glij5689519[dbj BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]	eph	60424178, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264908, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21906765, 21906788, 21906789, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank glij544463[sp P53530]GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - tm7 7 transmembrane receptor (rhodopsin family)	65274572, 60432289, 265008, 264910, 265011, 265017, 265018, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank glij4758568[ref NP_004798.1]pHS6S - heparan-sulfate 6-sulfotransferase	UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264881, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)		UNCLASSIFIED	264259, 28331828, 66712502, 264764, 264288, 264688, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank glij4589570[dbj BAA76807.1] - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - dehydrogenase Gamma-lonins family	56182575, 35696286, 29148499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233068 (3107, 3108)	Novel Protein sim. GBank glij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - transferase Gonadotropin-releasing hormones	35696286, 22278997, 264259, 28331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264881, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gl 2257485 db BAA21392  - (AB004534) p 015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331828, 35696052, 264508, 264905, 264908, 264907, 264908, 52644045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87186559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21908765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56528486
1556	91228268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011
1557	87840809 (3113, 3114)	Novel Protein sim. GBank gl 3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; z C3HC4.hmm, score: 34.09; most similar to drosophila goliath protein (SV: Q06003) [Caenorhabditis elegans])	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432289, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264584, 264486
1558	84840376 (3115, 3116)	Novel Protein sim. GBank gl 5360105 gb AAD42871.1 AF15510 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21908754, 265017, 265018, 264448, 21908787, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87186518, 22279000, 22279002
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gl 12908 sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264107, 264110, 21908754, 33109954, 87186559, 264760, 264763, 21908784, 21908785, 21908789, 265021, 264680, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gl 3880146 emb CAA92704  - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263987
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87786371 (3127, 3128)	Novel Protein sim. GBank gl 168287 sp P45953 ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	18108394, 35696286, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21908765, 21908788, 265021, 80170815, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22279002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gij129728jip[P05307(PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264585, 284567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445[embjCAA20328] - (AL031266) VM108R.1 [Caenorhabditis elegans]		inf	22278996, 22278999, 264259, 29331822, 29331824, 80432289, 29331827, 66712502, 264808, 265008, 18108351, 52644229, 21908765, 21908767, 21908768, 21908769, 33657109, 264555, 264639, 264482, 56182575, 21908769, 264692
1567	84989008 (3133, 3134)	Novel Protein sim. GBank gij4929699[gbjAAD34110.1]AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gij4827063[refjNP_005072.1]pZNF1 - zinc finger protein 142 (clone pHZ-49)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21908767, 21908768, 264691, 264693, 22279000, 22279002
1569	80936668 (3137, 3138)	Novel Protein sim. GBank gij5689451[dbjBAA83009.1] - (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265018, 264784, 21908765, 21908769, 55811957, 60170815, 52844150, 264692, 33657023, 33657109, 18108377, 264583, 264567
1570	86843981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731[refjNP_001061.1]pTUBG - tubulin, gamma polypeptide	Contains protein domain (PF00091) - TubulinFtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21908765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384, 35696052, 264905, 264906, 264908, 264910, 264758, 264768, 35695917, 264637
1572	81201864 (3143, 3144)			UNCLASSIFIED	
1573	80207068 (3145, 3146)			UNCLASSIFIED	263972

1574	84216142 (3147, 3148)	Novel Protein sim. GBank g j4758334 ref NP_004258.1 pFADS - delta-8 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264389, 264288, 264685, 264766, 264686, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 264690, 264691, 264693, 20281089, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264568
1575	95340019 (3149, 3150)	Novel Protein sim. GBank g j3881810 emb CAA94856  - (Z70783) similar to EF-hand calcium binding protein; cDNA (EST EMBL: C08700 comes from this gene [Caenorhabditis elegans])	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432288, 29331828, 264909, 265006, 265008, 265009, 285010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811857, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	85314019 (3151, 3152)	Novel Protein sim. GBank g j2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]	UNCLASSIFIED	UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264636, 83373044, 264486
1577	87813800 (3153, 3154)	Novel Protein sim. GBank g j2489130 ep P70315 WASP - MOUSE - WISKOTT - ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)	UNCLASSIFIED	UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank g j2978255 db BAA25190  - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35698288, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank g j4324682 gb AAD16986  - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	85087431 (3161, 3162)	Novel Protein sim. GBank g j2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906784, 55811957, 35695917, 264692, 55811578, 264637, 55182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gl 5420387 emb CAB46878.1  - (AJ243459) proleophosphoglycan [Leishmania major]		phosphatase	264259, 60432288, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gl 5578958 emb CAB51351.1  - (AL050308) dJ47587.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gl 5531815 gb AAD44482.1  - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432288, 29331827, 29331828, 35696052, 29146488, 68712502, 29331830, 52644045, 56182435, 284510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811388, 52644296, 87188474, 87188559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811578, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87188518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gl 4240132 dbj BAA74846.1  - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264805, 285008, 265007, 265008, 60433356, 33109954, 87188474, 265011, 265017, 264604, 264369, 264288, 264885, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108386, 264482, 264564
1586	88087081 (3171, 3172)	Novel Protein sim. GBank gl 3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			285017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gl 3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264807, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802538 (3175, 3176)	Novel Protein sim. GBank gl 1077573 pir J552680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170815, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gl 2137756 pir J48746 - senaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264450, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	95318825 (3178, 3180)			UNCLASSIFIED	264489, 22278998, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 80433356, 21906754, 265017, 265018, 265019, 264448, 264785, 264288, 52844229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27488265, 35695763, 86528488, 60432113, 22278000, 22279002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator		MHC	264259, 264905, 29331830, 284595, 265017, 264448, 264288, 264690, 264629, 87168518
1592	87802533 (3183, 3184)			UNCLASSIFIED	65274572, 60432048, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35688423, 22279000, 264595, 264567
1593	84991661 (3185, 3186)			UNCLASSIFIED	264488, 29331827, 264905, 264906, 264807, 264908, 264909, 264910, 284592, 264593, 264757, 264802, 264604, 264780, 264681, 264288, 264768, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 284563, 264564, 284568
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060  - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	29331826, 264908, 55811857
1595	78819425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments Integral membrane proteins	UNCLASSIFIED	
1596	78933928 (3191, 3192)			UNCLASSIFIED	28148498, 264758, 263967
1597	86871857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	cyto450	284092, 29331824, 264508, 264682, 264389, 264688, 264630, 264563
1598	87882939 (3195, 3196)				264259, 264634
1599	87849828 (3197, 3198)	Novel Protein sim. GBank gi 4508797 ref NP_000324.1 pSCAT - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52845080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023248 (3201, 3202)				264635
1602	86928987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	29148499, 264112, 264762, 18108351, 28148827, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken		collagen	264480, 29331824, 264907, 264908, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264389, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4788831 gb AAD29633.1 AF116827 - (AF116827) unknown [Homo sapiens]	ATPase associated	ATPase associated	263977



1605	91221129 (3209, 3210)			struct	264905, 264509, 264906, 264907, 264908, 264909, 264604, 264768, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gl 4505313 ref NP_003794.1 pMYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct	22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518, 264689
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gl 5174473 ref NP_003888.1 pPPI - Intracisternal A particle-promoted polypeptide		transcript/factor	
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gl 2224829 db BAA20802  - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264909, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gl 4884073 emb CAB43213.1  - (AL048934) hypothetical protein [Homo sapiens]			52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 264508, 264509, 264807, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21908754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21908768, 21908769, 59811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486291, 27486262, 35695763, 264628, 18108370, 18108376, 35698423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	65468200 (3219, 3220)	Novel Protein sim. GBank gl 263920 p S27639 - lensin - chicken		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gl 107284 p J35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase	35696288, 21906765, 264691, 35698473
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gl 3874846 emb CAA94337  - (Z70307) Similarly to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL-C09951 comes from this gene; cDNA EST EMBL-C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264508, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi 4680873 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - ERF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21908787, 21908788, 21906789, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264568 22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1615	86121809 (3228, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1  - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3878260 emb CAB01696  - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07849 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35698286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 35696970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644228, 21906764, 264689, 21908785, 21906786, 21906789, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486282, 33657349, 27486265, 35695783, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264768, 264769, 264689, 264693, 18108374, 264635, 264636, 264638
1617	86090742 (3233, 3234)	Novel Protein sim. GBank gi 468053 sp P34879 YO41_CAEL - HYPOTHETICAL 88.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264768, 264769, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1  - (AB020676) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264688, 21908788, 265021, 60170815, 33657023, 65274820, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486 264684
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	56182323, 56526486 264684

1621	87078708 (3241, 3242)				UNCLASSIFIED	264910	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29148499, 284905, 264808, 284909, 284928, 52644045, 284592, 60433356, 21906754, 284602, 285017, 284369, 21906768, 55811957, 265021, 60170615, 264635, 284557, 60170394, 83373044, 18108385, 22279000, 22279002, 284568
1622	94741738 (3243, 3244)	Novel Protein sim. GBank gij3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain		UNCLASSIFIED		18108398, 264259, 284909, 56182435, 87168474, 284448, 21908768, 35695917, 264691, 87168518, 264583
1623	87778108 (3245, 3246)	Novel Protein sim. GBank gij731086[ipP40389]UV22_SCHPO - UV-INDUCED PROTEIN UV122			UNCLASSIFIED		66714117, 29331825, 284909, 265008, 264758
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gij387566[emb]CAB05478] - (Z83104) cDNA EST EMBL.T00015 comes from this gene; cDNA EST EMBL.D33685 comes from this gene; cDNA EST EMBL.D36540 comes from this gene; cDNA EST yk24018.3 comes from this gene; cDNA EST yk38768.3 comes from this gene; cDNA ES...					
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gij458622[dbj]BAA76833.1] - (AB023208) KIAA0989 protein [Homo sapiens]			Kinase		264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 284106, 284508, 33657084, 265017, 265018, 18108351, 284683, 284369, 264288, 21906765, 21908766, 21908767, 21906769, 35695917, 265021, 264691, 65274820, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gij587907[gbj]AAD6844.1[AF160904] BcDNA.HL05938 [Drosophila melanogaster]					52844507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 284906, 66712502, 284909, 285008, 285009, 60432229, 60433356, 60433438, 21908754, 52846317, 52644296, 285011, 87168559, 284804, 265018, 284448, 284369, 264288, 264768, 52844229, 284689, 21906785, 21908768, 35695917, 265021, 285022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486285, 35695763, 263972, 52844332, 80170394, 87168518, 60432113, 264587
1627	83368773 (3253, 3254)				UNCLASSIFIED		284288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gij3686087 (AC004667) - hypothetical protein [Arabidopsis thaliana]			eph		284288, 284686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gij4240175jdbj[BAA74866.1] - (AB020850) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87756454 (3261, 3262)	Novel Protein sim. GBank gij1915892jembj[CAA69995] - (Y06740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811857, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264908, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264583, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gij2558501jdbj[BAA22866] - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264768, 264691, 264692, 29148489, 264509, 264905, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				264488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1634	85892817 (3267, 3268)	Novel Protein sim. GBank gij4887229jgbjAAD3244.1 AF150755 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	struct	265007, 264637, 22279002
1635	94232800 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52844045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21908785, 21908788, 265021, 264690, 264482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gij4557811jre NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED - kinase	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gij3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			264558
1638	87101854 (3275, 3276)				21908785, 21908787, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264908, 18108370, 264628, 265007, 33657402, 21908784, 264602, 264604, 264764, 264683, 264586, 264288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gij5420389jembj[CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265008, 265008, 264757, 264758, 55811366, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21908767, 55811957, 264691, 33657023, 65274620, 18108370, 55810784, 55811576, 264558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3278, 3280)	Novel Protein sim. GBank gll2842469[emb]CAA18847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35686286, 60432049, 60432289, 29331827, 35698052, 52644045, 56182435, 284510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21908785, 21908786, 21908788, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35698423, 65274781, 35695855, 264632, 264555, 58182323, 22279000
1641	87825160 (3281, 3282)			UNCLASSIFIED	28148489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gll1575333 (U80416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278899, 28147620, 29331828, 29331828, 33658970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564, 29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22278002, 264482
1643	94131768 (3285, 3286)				264505, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1644	88085125 (3287, 3288)			UNCLASSIFIED	264885, 264893
1645	95013858 (3289, 3290)	Novel Protein sim. GBank gll1076802[pir]S49915 - extensin like protein - maize		UNCLASSIFIED	22278894, 56994075, 35686286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gll5002573[emb]CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264359, 21808768, 60170615, 264639, 22278000
1648	87842098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264886, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1648	95347628 (3297, 3298)	Novel Protein sim. GBank gij654085[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52844045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 284602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52844229, 264689, 21906765, 21906768, 21906767, 21906768, 55811937, 35695917, 265021, 265022, 52844150, 264692, 33657023, 33657109, 20281149, 18108370, 284628, 18108374, 18108376, 35696423, 35696555, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 284404, 60432113, 22278000, 22279002, 264482, 264565, 264566, 264487
1650	87418538 (3298, 3300)	Novel Protein sim. GBank gij3647335[emb]CAA21059] - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			265011, 284602, 21906767, 18108374, 18108377, 18108385
1651	81639773 (3301, 3302)	Novel Protein sim. GBank gij4884278[emb]CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52643156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906768, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695955, 264556, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564
1652	86596622 (3303, 3304)	Novel Protein sim. GBank gij1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	struct	22278997, 29148498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1653	84256983 (3305, 3306)	Novel Protein sim. GBank gij3776054[emb]CAA06273] - (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432269, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274791, 18108384, 60432113, 264567
1654	79756471 (3307, 3308)			UNCLASSIFIED	33657109, 264565

1655	86889346 (3309, 3310)	Novel Protein sim. GBank gij355717[embjCAA73486] - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35686286, 22278998, 22278999, 29331824, 29331825, 29331826, 33856970, 264908, 5264045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526488, 50432113
1656	76962287 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbjBAA16847] - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557845[refJNP_001524.1]pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526488, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[embjCAA67060] - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal protkaryotic L21 protein	UNCLASSIFIED	22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265005, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264389, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148628, 265021, 265022, 18108382, 263969, 263971, 18108374, 35698423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij538218[pirlJ538038] - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87188518, 22278996, 265020, 22278999, 87188559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264835, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2487012[spjQ10010]YSV4_CAEEL - HYPOTHETICAL 26.8 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264688, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264893, 33657109, 264628, 35698423, 35695855, 264634, 264835, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264488, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284488, 22278988, 284259, 29331824, 29331828, 29331827, 29331828, 284509, 86712502, 29331830, 284908, 52844045, 265007, 284512, 60433358, 60433438, 55812038, 21906754, 285018, 284448, 264766, 284768, 284769, 21906788, 21906769, 285020, 33657023, 33657109, 65274791, 87168518, 284482, 284563, 284584, 284565, 284567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730302 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 284106, 285008, 285007, 285008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108365
1663	94217148 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CA843275.1  - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52845156, 58182575, 22278994, 22278995, 35698286, 22278998, 56994075, 22278997, 22278998, 22278999, 284259, 29331822, 29331828, 29331827, 29331828, 33656970, 29331830, 284908, 56182435, 284511, 60433358, 33657402, 33109954, 87168474, 87168559, 285017, 285018, 284605, 18108351, 284764, 284288, 284766, 284768, 21906765, 21906766, 21906767, 21906768, 21906769, 285021, 285022, 284691, 33657023, 284693, 283967, 33657109, 284630, 52844332, 83373044, 87168518, 60432113, 22279000
1664	94234078 (3327, 3328)	Novel Protein sim. GBank gi 3043692 dbj BAA25510  - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	284488, 283994, 35698288, 29331824, 35698052, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 285009, 284910, 60170831, 284591, 284592, 284595, 87168474, 285011, 284600, 284601, 284604, 284605, 284760, 284762, 18108351, 284681, 284682, 284763, 284683, 284784, 284288, 284684, 284768, 284687, 284768, 284769, 21906764, 21906765, 21906767, 35695917, 285021, 284534, 80170815, 284690, 284691, 284692, 33657109, 33657182, 284628, 18108370, 284629, 35698423, 35695855, 284634, 284635, 284555, 284636, 284637, 284638, 284639, 264558, 83373044, 87168518, 284553, 284568, 284488



1665	91226952 (3329, 3330)	Novel Protein sim. GBank gji1083506 pirij S50085 - eloadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	284488, 29331826, 29331828, 284509, 284906, 284907, 284909, 284510, 284511, 284910, 284592, 284593, 284595, 284758, 284598, 284600, 284760, 284762, 284764, 284766, 284768, 284629, 284630, 284634, 284638, 83373044, 284584, 284586, 284587, 284488
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gji3913431 spj042843 DDX8 - SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	56994075, 22278999, 284259, 29331824, 29331826, 29331827, 29140498, 285009, 33108954, 87188559, 285019, 284288, 284688, 21808767, 21908769, 284691, 33857182, 18108370, 18108374, 18108385, 22278002
1667	91226855 (3333, 3334)	Novel Protein sim. GBank gji5889535 dbj BAA83051.1  - (AB029022) KIAA1089 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	284259, 29331822, 29331826, 284905, 284906, 284908, 284510, 285009, 284595, 284758, 285011, 87188559, 285017, 285018, 285019, 284448, 284768, 284688, 21908765, 21908767, 21908769, 285020, 285021, 60170815, 284890, 284692, 284693, 18108368, 18108370, 283972, 55810764, 284555, 83373044, 60432113, 22278000, 22278002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gji2078894 gbj AAB53983.1  - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	kinase	86714117, 284508, 284509, 284906, 284907, 284908, 284511, 284910, 284784, 284687, 284688, 33857109, 35698423, 35695855, 284832
1669	91227848 (3337, 3338)	Novel Protein sim. GBank gji3875371 emb CAA85414.1  - (Z38948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D84658 comes from this gene; cDNA EST EMBL:D66829 comes fr...	UNCLASSIFIED	29331825, 33108954, 284369, 284767, 284689, 33857109, 83373044
1670	87628009 (3339, 3340)		UNCLASSIFIED	284259, 29331824, 28331827, 60433438, 265022, 284638
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gji462451 spjP34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35698286, 22278997, 29331825, 284909, 21908754, 265017, 285018, 285019, 284682, 284683, 284768, 284688, 21908766, 21908767, 21908768, 21908769, 284691, 284555, 284558, 22279000, 284566, 284906, 284909, 284632, 18108381
1672	86281834 (3343, 3344)	Novel Protein sim. GBank gji1814270 (U74586) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]	deaminase	

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gl 2076894 gb AA53883.1  - (AF002187) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	Kinase	264488, 264569, 18108394, 56994075, 22278998, 284259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33857023, 264692, 264693, 33857109, 264628, 264629, 18108374, 35698423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264568, 264567, 264489
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gl 5262467 emb CAB45683.1  - (AL080062) hypothetical protein [Homo sapiens]		kinase	60433358, 87188559, 264448, 264288, 264688, 264691
1675	87608468 (3349, 3350)	Novel Protein sim. GBank gl 3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 68712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35698423, 35695855, 264637, 264639, 18108385, 264564
1676	85358086 (3351, 3352)	Novel Protein sim. GBank gl 4184065 gb AA053271  - (AF111081) latrophilin 3 splice variant bbar [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21908765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gl 3327046 db BAA31591  - (AB014516) KIAA0816 protein [Homo sapiens]		UNCLASSIFIED	264808
1678	86868828 (3355, 3356)	Novel Protein sim. GBank gl 550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carboxymethyl-phosphate synthase (CPase)	UNCLASSIFIED	29331824, 264102
1679	91214108 (3357, 3358)	Novel Protein sim. GBank gl 550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]		carboxylase	264488, 18108392, 18108394, 52648842, 18108397, 18108398, 35696288, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21908765, 29146627, 28148629, 264690, 18108361, 18108362, 18108384, 18108385, 18108386, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	81005372 (3359, 3360)	Novel Protein sim. GBank gl 2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	63274572, 22278994, 22278999, 68714117, 29331827, 56182435, 21908754, 265018, 264238, 21908769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gl 5689537 db BAA83052.1  - (AB028023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278998, 29331822, 264908, 264593, 264804, 265019, 264683, 55811957, 264690, 33857023, 35698423, 83373044, 264583
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - UNCLASSIFIED START domain	263994, 35696286, 35696052, 264508, 284509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264389, 264766, 264768, 35695917, 264692, 33657109, 35698423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 284488
1684	80083408 (3367, 3368)		UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.6; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00825) - Guanylate kinase	60424178, 52846842, 22278994, 35698286, 22278998, 264259, 52845080, 29331824, 29331826, 265007, 33657084, 265018, 284681, 264446, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27488262, 284635, 52844332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1  - (AB005287) thrombospondin 1 [Bos taurus]	UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 284512, 265009, 264910, 264758, 285010, 285011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 284630, 284631, 284634, 284635, 264637, 264638, 284639, 284585, 264486, 264587, 35695917, 284806, 264907, 264908, 264510, 265006, 265007, 264910, 264558, 18108381, 18108383, 265011
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680879 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]	UNCLASSIFIED	264905, 264910, 264760, 264629, 264555 264559, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274781, 83373044, 264089 264369, 21908766, 264682, 264639, 87188518
1688	82158442 (3375, 3376)		UNCLASSIFIED	264768, 33657109, 29331827, 29148629, 264510, 264108, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264768, 263974
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1  - (AB020659) KIAA0852 protein [Homo sapiens]	UNCLASSIFIED	264106
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00029) - Cadherin domain	264369, 21908766, 264682, 264639, 87188518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]		264768, 33657109, 29331827, 29148629, 264510, 264108, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264768, 263974
1692	88106709 (3383, 3384)			264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	26331826, 264508, 264905, 264807, 264595, 265010, 265011, 21908768, 33657023, 284629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_008225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	inapolymerase	35696286, 22278998, 22278998, 22278998, 22278998, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29148499, 264905, 284908, 52644045, 284511, 285008, 265007, 285009, 264592, 60433356, 21908754, 265010, 265011, 18108351, 264763, 264682, 284448, 284883, 284288, 284788, 264689, 21908768, 60170815, 264691, 284692, 264693, 18108370, 18108374, 283978, 35696423, 35695855, 264558, 18108381, 18108385, 87168518, 264482, 264488, 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680878 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1698	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22980 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21908766, 18108370
1697	85740883 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10382) - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33857402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21908769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002
1699	87424783 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir IS41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED nuc_recpt	35696286, 264635 29331824, 52644045, 265008, 265009, 263989, 263971
1701	86570488 (3401, 3402)	Novel Protein sim. GBank gi 3877439 emb CAA86852 - (Z72510) similarity to yeast UTR3 protein [Swiss Prot accession number P21374]; cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		UNCLASSIFIED MHC	22278995, 22278997, 264092, 29148498, 29148499, 264107, 264508, 264907, 284110, 284112, 265009, 60170831, 21908754, 265011, 265017, 264782, 18108351, 264288, 21908765, 35695917, 265021, 60170615, 263987, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56529486, 87168518, 60432113
1702	87785092 (3403, 3404)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1703	78568651 (3405, 3406)	Novel Protein sim. GBank gi 1263289 (U47856) - fibron-4 [Araneus diadematus]		UNCLASSIFIED	264368
1704	86622878 (3407, 3408)	Novel Protein sim. GBank gi 4518621 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]		UNCLASSIFIED	264569, 35696288, 284907, 265010, 264687, 264768, 284692, 264693, 264636, 264568, 22278996, 22278998, 264259, 264509, 265018, 264764, 284685, 284686, 21908768, 21908769, 265022, 264691, 264558, 22279000
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			
1706	87790987 (3411, 3412)				

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gl 4321684 gb AAD15797  - (AF055470) ZNF258 [Homo sapiens]	UNCLASSIFIED	18108398, 22278997, 264259, 29147820, 29331826, 29146498, 284905, 264906, 265008, 264593, 264595, 264758, 264598, 265018, 284760, 18108351, 284764, 264766, 264889, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gl 5174591 ref NP_005947.1 pMTHF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - synthase Formate-tetrahydrofolate ligase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 285009, 60170831, 33857402, 33109954, 87168559, 265019, 18108351, 264448, 21908765, 21908767, 21908768, 29148627, 29148628, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563, 264107, 55811957, 263974, 263976, 263977, 263981
1709	80222583 (3417, 3418)		UNCLASSIFIED	263981
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gl 5031735 ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase	UNCLASSIFIED	264556
1711	91013729 (3421, 3422)		sulfotransferase	85274572, 29331824, 29331826, 264768, 60431528, 35698423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gl 5454168 ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	56984075, 264093, 264259, 29331822, 264089, 29331824, 29331827, 264107, 284110, 264511, 264592, 265011, 265018, 264883, 264886, 264889, 265020, 33657023, 263967, 33657109, 263974, 35698423, 35698555, 264630, 264636, 264558, 264569, 22278985, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1713	84143453 (3425, 3426)	Novel Protein sim. GBank gl 160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	22278997, 264757, 21906765, 265020, 265021, 264892, 56528486
1714	87420048 (3427, 3428)		UNCLASSIFIED	264509, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 285011, 264786, 264788, 264769, 264891, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gl 5689537 dbj BAA83052.1  - (AB028023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264886, 285020, 264693, 55811576, 264558, 60432113, 22279002
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gl 4589469 dbj BAA78761.1  - (AB012808) mBOCT [Mus musculus]	transport	

1717	87583223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749  - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264688, 18108357, 35695917, 264690, 264692, 264683, 264628, 264629, 35698423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108398, 18108391
1718	87032828 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14999 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264686, 264689, 21906765, 265021, 264691, 33657023, 264683, 18108370, 35695855, 264632, 264634, 264636, 18108398, 22279002
1719	94315258 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35698286, 22278997, 60432049, 58182181, 68714117, 60432289, 29331828, 35696052, 29331828, 264906, 29331830, 58182435, 264592, 60431735, 60433438, 5812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35698423, 55811576, 35695855, 264631, 58182323, 264559, 264564, 264486
1720	84853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pir J S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	58182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264768, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87188518
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1  - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278994, 22278999, 29331822, 265008, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108365, 264486
1722	84134549 (3443, 3444)	Novel Protein sim. GBank gi 5688375 dbj BAA02968.1  - (AB030844) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - kinase Tudor domain		5694075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044

1723	95358181 (3445, 3448)	Novel Protein sim. GBank gij4428982[gjAAD20633] - (AF126082) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264768, 21906767, 21908768, 56182579, 55811857, 22278997, 22278998, 265020, 264258, 264692, 33857023, 29331822, 29331824, 29331825, 60432289, 33857182, 33856970, 33857349, 28146489, 264508, 264907, 18108370, 264628, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432228, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33108954, 33857084, 87188518, 87188474, 285010, 265011, 87188559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264586, 264764, 264288, 264587, 264488, 264389, 264788
1724	87713808 (3447, 3448)	Novel Protein sim. GBank gij2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	UNCLASSIFIED	2648905, 18108359, 264693, 264628, 264631, 264638, 264555, 264558, 264558, 264559, 35698286, 264259, 29331822, 35698052, 264508, 264509, 264905, 264905, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264768, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264638, 264638, 87188518, 264586
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF000023) - homeobox Ank repeat	homeobox	28146498, 264683, 264689
1726	85754255 (3451, 3452)	Novel Protein sim. GBank gij4689348[gjAAD27861.1]AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264805, 265011, 264689, 21906768
1727	85286362 (3453, 3454)			UNCLASSIFIED	

1728	95348515 (3455, 3456)	Novel Protein sim. GBank gl 4406549 gb AAD20027  - (AF131738) Unknown [Homo sapiens]		UNCLASSIFIED	60424170, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264368, 264685, 264766, 264687, 264769, 21906764, 264688, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)			UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gl 831600 pir IS47094 - hypothetical protein - rabbit		UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gl 4240231 dbj BAA74894.1  - (AB020878) KIAA0871 protein [Homo sapiens]		struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264638, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gl 1575756 U70674  - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PTD).	- synthase	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264636, 264556
1734	87785261 (3467, 3468)				264693



1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi4836807 gb AAD30566.1 AF14678 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278986, 80432048, 264259, 29331822, 264908, 265008, 265007, 265008, 265009, 264591, 33857402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21908765, 21908768, 21908769, 29148829, 29148784, 265021, 265022, 52844150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1738	95362884 (3471, 3472)	Novel Protein sim. GBank gi4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433358, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431650, 264637, 60170394, 264558, 264639, 264564 29331822, 29331830, 264591, 265011, 265018, 265019, 22279002 264908, 264909, 265008, 264910, 264566
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi2143607 pi S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	kinase
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi222594 emb CAA68714  - (Y08480) Mdes protein [Mus musculus]	UNCLASSIFIED	UNCLASSIFIED
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED
1740	83592839 (3479, 3480)	Novel Protein sim. GBank gi4809 emb CAA44309  - (X62452) YCR601 [Saccharomyces cerevisiae]	traffic	264604, 21906764, 18108384, 264629, 35695855, 264638
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi4883888 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi4505193 ref NP_003687.1 pMLD  - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	264688, 21908769, 265020, 33657109 264908, 264910, 264758, 265011, 264631, 264638, 264568
1743	86966475 (3485, 3486)			265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi726832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	22278998, 264508, 264907
1745	20280075 (3489, 3490)		UNCLASSIFIED	264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi731756 sp P38873 YHY8_YEAST - HYPOTHETICAL 175.8 KO PROTEIN IN GND1-K11 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi1658503 (U75467) - Alu [Drosophila melanogaster]	transcript factor	52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264388, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 284482

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00584) - DnaJ central domain (4 repeats)	eph	264489, 5618257, 29331824, 56182435, 284112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811578, 264635, 284555, 264556, 264557, 264559
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AAD45948.1 AF151968 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	264106
1750	84321684 (3499, 3500)	Novel Protein sim. GBank gi 4996894 gb AAC28444.2  - (AF065184) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 dbj BAA21841 - (AB010054) outer arm dynein light chain 2 [Anthodidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase_associated	33657402, 264288, 52644150, 263974, 83373044
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3919482 sp P74346 YG29_SYNY3 - HYPOTHETICAL 39.0 KO PROTEIN SLR1829	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	deaminase	264510, 264593, 264682, 21906765, 18108370
1753	84235159 (3505, 3506)	Novel Protein sim. GBank gi 2832636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906768, 264692, 264693, 65274820, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39881 YE44_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CANT INTERGENIC REGION		transport	264488, 35696286, 264509, 264908, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264804, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567, 264688
1755	78470282 (3509, 3510)	Novel Protein sim. GBank gi 1178422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	82962614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708  - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87188518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CA846856.1  - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21908768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612871 (3515, 3516)	Novel Protein sim. GBank gij3881040jembj[CAAI184031 - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33658970, 284508, 285008, 285007, 265009, 284591, 33657402, 33109954, 87168474, 264600, 265017, 285018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 284632, 52844332, 22278002, 264563
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gij5262748jembj[CAB45688.1] - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432048, 35696052, 264905, 284908, 264907, 264908, 284909, 285006, 285009, 264910, 60432229, 284592, 284595, 55812038, 284758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811857, 35695917, 284690, 284692, 264628, 264629, 55811576, 35696423, 264832, 264834, 264636, 264557, 264639, 60432113, 284565, 284486
1761	87409588 (3521, 3522)	Novel Protein sim. GBank gij127749jisp10569jMYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 284685, 264686
1762	95318887 (3523, 3524)	Novel Protein sim. GBank gij3169159 (AC004770) - BC289730_2 [Homo sapiens]	Contains protein domain (PF00173) - desaturase Heme-binding domain in cytochrome b5 and oxidoreductases		22278999, 264259, 264905, 264907, 60170831, 285010, 265011, 285017, 264448, 21806765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gij4809028jgbjAAD30062.1] - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181888, 29331825, 35696052, 264905, 284908, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35698423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gij1360689jpirj[CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - collagen Fibrillar collagen C-terminal domain		22278998, 264259, 35696052, 29331828, 56182435, 285008, 265017, 265018, 264448, 284288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gij486806jpirj[S35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)]		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 284104, 264508, 284905, 264807, 264511, 265007, 265008, 264910, 285009, 21906754, 265010, 265017, 284603, 265018, 265019, 18108351, 284682, 284448, 264369, 264288, 264766, 18108356, 21806768, 21906767, 29148627, 29148628, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 249087 sp Q09332 JUGG, DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	5264156, 87168559, 60170615, 33657023, 284683, 33857109, 27486261, 264555, 83373044
1767	87755968 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1  - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	85411314 (3539, 3540)	Novel Protein sim. GBank gi 116204 sp P00736 C1R, HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	complement	264488, 264768, 264769, 56182575, 55811957, 264890, 264891, 35696052, 264905, 264509, 264906, 264907, 264828, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264694, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914181 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAc TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AA034351.1 AF12136 - (AF121360) DNZDHHG/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264784, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278998, 35696286, 22278999, 264259, 29331824, 60424289, 28331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52844045, 264511, 265008, 265007, 265008, 60170831, 60433438, 264758, 55811388, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52844150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264584, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495698 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906787, 21906788, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gl 1469199 dbj BAA094871 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278987, 29331822, 29331828, 60432289, 29331828, 35696052, 29331830, 68712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 284448, 264288, 264689, 21906765, 21906768, 21906767, 21906768, 265020, 265021, 265022, 264691, 33857023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56326486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1  - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gl 3218938 sp P87115 YDK9 SCHPO - HYPOTHETICAL 118.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1		nuc1_recp	56994075, 29331828, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94651624 (3555, 3556)	Novel Protein sim. GBank gl 3875648 emb CAA91454.1  - (Z68561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9.		UNCLASSIFIED	29331828, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1  - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265009, 265007, 265008, 18108386, 65274727, 264482, 264369, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gl 729225 sp P4123 CTXN_RAT  - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264563
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gl 2257543 dbj BAA21436  - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gi 1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 284259, 35698052, 284508, 284905, 284906, 284907, 68712502, 284908, 284909, 285007, 285008, 285009, 284910, 284591, 284594, 284757, 284758, 284759, 285010, 285011, 284601, 284602, 284604, 284605, 18108351, 284762, 284763, 284784, 284368, 284766, 284687, 284788, 284688, 21908768, 35695917, 284690, 284691, 284692, 284693, 284628, 18108374, 35698423, 284631, 284632, 284635, 284637, 284638, 284639, 18108385, 22279000, 22279002, 284565, 284568, 284488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi 4589552[db][BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	55274572, 284259, 29331822, 29331824, 29331825, 29331827, 29331828, 284905, 284906, 284908, 66712502, 56182435, 284511, 285007, 60433356, 55811150, 284683, 284369, 284687, 52844229, 21908767, 52844150, 33857023, 65274620, 33857182, 65274791, 35695855, 284555, 65274727, 22279002
1786	85298485 (3571, 3572)	Novel Protein sim. GBank gi 117788[sp][P28770]CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)	UNCLASSIFIED	284908, 35698423, 284636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 3877175[emb][CAA90338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D88896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284905, 284908, 284909, 284595, 284784, 284786, 284692, 60431528, 284629, 284636, 284564, 284566
1788	91228779 (3575, 3576)		UNCLASSIFIED	284488, 83373044
1789	88084529 (3577, 3578)	Novel Protein sim. GBank gi 2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	284488, 29331828, 284909, 18108351, 284288, 285021, 284555, 284638
1790	82489734 (3579, 3580)			35698052, 284905, 284906, 284907, 284908, 284909, 285008, 284910, 284758, 265011, 265019, 284784, 284786, 284769, 284628, 284635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gll2114321[ob]BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33857023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264588, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87782680 (3583, 3584)	Novel Protein sim. GBank gll4337106[gb]AAD18082] - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33857402, 87188559, 264369, 33857023, 35695855, 20281071, 264559, 18108387, 87188518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gll5578331[gb]AAD45504.1[AF14573] - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - ATPase associated Glycosyl hydrolase family 47	ATPase associated	95274572, 22278995, 22278998, 22278997, 22278999, 264093, 264259, 29331824, 86714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265018, 264681, 264682, 264288, 52644228, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170815, 52644150, 33857023, 33857109, 18108370, 18108374, 85274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gll4814604[emb]CAB43877.1] - (AL050389) hypothetical protein [Homo sapiens]	Contains protein domain (PF01788) - Putative snRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87188474, 265011, 285017, 18108351, 264783, 264448, 264683, 264369, 21906765, 21906766, 21906767, 21906769, 29148784, 35695917, 60170815, 33857023, 264629, 18108374, 18108378, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264564
1795	78747858 (3589, 3590)			UNCLASSIFIED	264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1798	86568488 (3591, 3592)	Novel Protein sim. GBank gll585084[sp]Q07803[EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)]		glycoprotein	264488, 264907, 264909, 264594, 264595, 264768, 264687, 21906765, 21906767, 264628, 264630, 264559

1787	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278998, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1788	91221276 (3595, 3596)	Novel Protein sim. GBank gl 2832806[dbj BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 80433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264446, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264488
1789	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541[dbj BAA83054.1] - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank		UNCLASSIFIED	264691, 264558, 264556
1801	95060723 (3601, 3602)	gl 4680879[gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920[sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696288, 66714117, 264508, 264509, 58182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264488
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gl 4680879[gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264789, 264689, 21906769, 35696288, 35695917, 264259, 264691, 264692, 264693, 20281098, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 68712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264596, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264583, 264764, 264586, 264288, 264486, 264567, 264765, 264766



1804	87770203 (3607, 3608)	Novel Protein sim. GBank gl 3878914 emb CAA8538.1  - (Z74043) predicted using GeneFinder: cDNA EST EMBL: C13850 comes from this gene; cDNA EST EMBL: C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21908754, 264766, 21908765, 21908768, 35895917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gl 5453644 ref NP_006461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35898423, 264638, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1  - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35898423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gl 488407 emb CAB43235.1  - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35896286, 86714117, 35896052, 86712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35895917, 33657109, 35895763, 55810764, 18108379, 35896423, 35895855, 56182323, 264563, 264584, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gl 1918927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29146629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gl 1352944 sp P47179 YJBP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35896052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264688, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264587
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gl 2134984 pir j137275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase	Contains protein domain (PF00023) - Ank repeat	264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	76245772 (3623, 3624)				29331822, 29331824, 265018, 18108351, 21908769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi 5031636 gb AAD38326.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 284259, 29331824, 66714117, 29331828, 35696052, 284509, 284905, 284908, 264907, 284908, 66712502, 284909, 265007, 284910, 284591, 284593, 55812038, 265011, 285018, 264780, 264682, 284764, 284683, 284369, 284788, 284788, 284769, 21908768, 21908768, 284691, 284693, 18108374, 35695855, 284634, 284635, 284637, 284639, 284559, 22279000, 22279002, 284568
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643808 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	284486, 35698286, 22278998, 284092, 284094, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 284105, 284107, 52644045, 56182435, 285009, 60432229, 60433356, 87188474, 87188459, 284369, 284288, 21908765, 35895917, 265021, 265022, 33657023, 33857109, 18108374, 35698423, 284638, 56528486, 264482
1815	85298473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		struct	22278998, 284508, 284509, 284907, 284908, 284910, 265011, 284780, 284786, 284834, 284636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1178823 sp P41846 Y096_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 284509, 284907, 284908, 284909, 285009, 284591, 265011, 265017, 284687, 284688, 285022, 284691, 18108362, 18108368, 18108370, 18108374, 18108378, 284635, 284557, 284564, 284567, 284488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27488282, 18108370, 18108374, 60170394, 56182323, 22279002
1817	86095288 (3633, 3634)	Novel Protein sim. GBank gi 376637 emb CAA21429  - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	284488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27488282, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 387912 emb CAA84370  - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL.T01923 comes from this gene; cDNA EST EMBL.D32335 comes from this gene; cDNA EST EMBL.D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcript factor	35866286, 60433356, 284758, 284369, 284686, 21906769, 284693, 284632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HM/GIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 284259, 29331826, 284908, 285007, 285008, 285009, 60432229, 265017, 265018, 265019, 284448, 284288, 21908768, 21908769, 265020, 18108381, 18108384, 22279000, 22279002, 284567

1820	87769455 (3839, 3840)				284905, 284807, 284594
1821	80431510 (3841, 3842)				284807, 284788, 283978
1822	91221523 (3843, 3844)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1  - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 284259, 29331824, 29331825, 29331826, 35888052, 29331828, 284908, 29331830, 60170831, 284591, 284593, 60433356, 284598, 285017, 285018, 18108351, 284783, 284683, 21906765, 21906787, 21906788, 21906789, 35895917, 265020, 265021, 33857023, 18108384, 18108370, 35895855, 22279000, 22279002, 284488, 284259, 284511, 284288, 264768, 264693, 35896423, 284634, 18108385, 284486
1823	85522330 (3845, 3846)			UNCLASSIFIED	284807, 284908, 284909, 284511, 284631, 284634, 284635, 284637, 284638, 284639, 284758, 284588
1824	88612025 (3847, 3848)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	60432049, 284910, 284487
1825	87430125 (3849, 3850)	Novel Protein sim. GBank gi 3036803 emb CAA18493  - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi 4680885 gb AAD27732.1 AF13295 - (AF132957) CGI-23 protein [Homo sapiens]	ATPase associated		52844507, 52845156, 52846842, 22278994, 22278996, 56994075, 284259, 60432049, 52845080, 35888052, 66712502, 52844045, 285008, 285009, 60432229, 60433356, 60433438, 52846317, 52844298, 285011, 87188558, 284448, 284288, 284369, 284688, 52644229, 284689, 21906765, 21906788, 265020, 60170815, 52844150, 33657023, 27488262, 27488264, 27486265, 35895763, 35896423, 35895855, 83373044, 87168518, 284404, 22279002
1827	81647212 (3653, 3654)				284758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank g k4503571 ref NP_001419.1 ENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - onco-gene Enol-ase	264488, 52646842, 56182576, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52844045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33108954, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 285021, 60170615, 33657023, 33657349, 263972, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264555, 264484, 264557 264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1829	80197720 (3657, 3658)			
1830	94312842 (3659, 3660)	Novel Protein sim. GBank g 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease 52645156, 22278994, 22278995, 35696286, 22278998, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644298, 87168559, 265019, 21906765, 21906766, 21906787, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695783, 263974, 35696423, 35695855, 52844332
1831	94138063 (3661, 3662)		UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265018, 265022, 264693, 65274791 264602
1832	94521863 (3663, 3664)	Novel Protein sim. GBank g 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk48e8.5; coded for by C. elegans cDNA yk48d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk48e8....		

1833	85314184 (3665, 3668)	Novel Protein sim. GBank gi 5174413 ref NP_006028.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35698052, 29146498, 264508, 264509, 264908, 264907, 68712502, 264908, 52844045, 264909, 264512, 265008, 264591, 264593, 60433358, 21908754, 33857084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 29148829, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27468284, 33657349, 85274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)			264259, 264807, 264689, 22279000, 22279002
1835	84135718 (3669, 3670)		UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21908768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759288 ref NP_004268.1 UCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	29331825, 264908, 265019, 264764, 264686, 21908765, 264635
1837	84234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	84324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 pir JAS6154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain	29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAC09118.1  - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264601, 21908765, 21906766, 265021, 33657109, 264556
1840	87391708 (3678, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MOV10_MOUSE - PROTEIN MOV-10	UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572484 gb AA023834.1 AF12365 - (AF12365) FEZ1 [Homo asplena]		56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	90982645 (3683, 3684)	Novel Protein sim. GBank gll1326268 (U58728) - C54H2.1 gene product (Caenorhabditis elegans)		UNCLASSIFIED	85274572, 29331822, 29331824, 29331825, 68714117, 29331826, 29331827, 264907, 264908, 52644045, 58182435, 264510, 265006, 285007, 285009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108384, 33857109, 18108368, 264628, 55810764, 58182323, 18108384, 264593, 264584
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 58182435, 264769, 29331826, 29331828, 264511, 265006, 285007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264587, 264595, 264766
1844	87444784 (3687, 3688)	Novel Protein sim. GBank gll2496887/spiQ09232/yQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gll1175484/spiQ09819/YACS_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 68712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52644150, 33657109, 264555, 264566, 264557, 58182323, 18108382, 83373044, 18108385, 264584
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gll3881080/embjCAA217391 - (AL032857) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL-D35398 comes from this gene; cDNA EST yk331h8.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk487g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gll5059323/gbJAAAD38667.1JAF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gll5701854/embjCAB52181.1 - (AJ245417) Gsb protein [Homo sapiens]		lm7	29331825, 29331826, 29331827, 265017, 264683, 264288, 264766, 264768, 21906767, 21906788, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gll4503665/repNP_001988.1JpFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase-associated	58182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gll4589582/gbJBAAY76813.1 - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gll220637/gbJBAAO1477 - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35896052, 264910, 60433438, 264688, 35895917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174829 ref NP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35686286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52844045, 265007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21908765, 21908767, 21908769, 265021, 265022, 52844150, 264893, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22278002, 264563 264887, 264768, 52644507, 264769, 21908765, 21908767, 21908768, 22278995, 56994075, 22278999, 52844150, 264259, 264892, 29331822, 29331824, 52845128, 29331827, 33656970, 33657349, 35695763, 264508, 264806, 264628, 264907, 264629, 264909, 35698423, 35695855, 264510, 265008, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52846317, 52844288, 87188518, 87188559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264587, 264288, 264369, 264768 264582
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072864 (U83569) - putative p150 [Homo sapiens]	nuclease		
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CA839994.1  - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif		18108392, 52846385, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21908754, 87188474, 265011, 87188559, 264681, 264288, 264768, 18108359, 21908764, 21908768, 29148627, 265020, 265021, 265022, 52844150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264638, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA06945  - (AJ008278) acetylglucosaminyltransferase-like protein (Mus musculus)		UNCLASSIFIED	56994075, 264259, 29331826, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120  - (AF094508) dentin phosphoryn [Homo sapiens]	ATPase-associated		22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 80170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi 4881903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	264757	
1859	84407484 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAA74837.1  - (AB020721) KIAA0914 protein [Homo sapiens]		22278998, 28331824, 285007, 33109954, 285019, 284369, 21908768, 29148784, 27486261, 52644332, 22279002 285019	
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi 40095522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir j 84503 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrile synthase	264887, 284259, 28331822, 28331824, 29331825, 285007, 285009, 284591, 33109954, 285010, 285019, 284369, 284288, 284886, 284691, 284693, 27486264, 18108370, 18108374, 263977, 55811576, 58182323, 284639, 22279000, 22279002, 264482	
1862	87372823 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35698286, 264259, 87188474, 284369, 21908768, 284558, 284563	
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CAA09299  - (AJ010842) Dof protein [Drosophila melanogaster]	UNCLASSIFIED	284601, 284766, 29148627, 29148629, 264692, 284629, 284635	
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 4322263 gb AAD15985  - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	22278998, 284259, 284807, 285018, 18108370, 284634, 284635, 284555, 284556, 284638, 18108387	
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2495727 sp Q93073 Y258_HUMAN - HYPOTHETICAL PROTEIN KIAA0256		22278998, 284490, 28331822, 66714117, 68712502, 285006, 285007, 285008, 285009, 284591, 60433438, 285010, 285019, 284760, 284448, 284768, 29148627, 29148629, 285020, 285022, 18108385, 60432113	
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi 5282617 emb CAB45748.1  - (AL080157) hypothetical protein [Homo sapiens]	kinase	18108374, 284769, 18108377, 21908765, 21908766, 35696423, 58182575, 21908769, 29148629, 35696288, 35695917, 285021, 284510, 284511, 284512, 284534, 284535, 60170831, 52844150, 284555, 284691, 284259, 284556, 284692, 284557, 33657023, 80433358, 28331822, 284559, 284595, 28331824, 18108385, 21908754, 33657182, 29331827, 35696052, 33656970, 87168518, 285017, 60431602, 22279000, 284508, 284509, 18108351, 284907, 284682, 284567, 18108372, 284765, 284486 284094	
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078098) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED		



1868	87357459 (3735, 3738)	Novel Protein sim. GBank gij3881525[embj CAA93884] - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D32524 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357110.5 comes from this gene [Caenorhabditis elegans]		nuclease	264488, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33857402, 87188474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 27486284, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264566, 264567
1869	86877292 (3737, 3738)	Novel Protein sim. GBank gij4826772[ref NP_004981.1 ]pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) Leucine Rich Repeat	glycoprotein	294508, 264509, 264906, 264808, 264909, 264810, 264591, 264800, 18108351, 264883, 264766, 264768, 35895855, 264834, 264556, 264639, 18108385, 264563, 264488
1870	95348488 (3739, 3740)	Novel Protein sim. GBank gij1869859[embj CA806722] - (Z88089) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35895817, 80170815, 264692, 18108368, 35895763, 35696423, 65274791, 264638, 264639, 58528486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264583, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351138 (3747, 3748)		Contains protein domain (PF00283) - Bacterial muT protein	UNCLASSIFIED	264488, 35685917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33857402, 264558, 18108385, 264600, 264604, 264764, 264567, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gij4589520[dbj BAA76782.1] - (AB023155) KIAA0838 protein [Homo sapiens]		UNCLASSIFIED	35896286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gij263810[bsj 22920 - collagen alpha chain [Riftia pachyptila=lube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gij3883358[gb AAC83924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264906, 264907

1878	95351058 (3755, 3756)	Novel Protein sim. GBank gl 4510345 gb AAD21434.1  - (AC008921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264589, 264488, 35696286, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264508, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33857402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264881, 264882, 264764, 264389, 264288, 264768, 264887, 264788, 264789, 21908766, 35695917, 265021, 60170815, 33857023, 264892, 264893, 33657109, 27486265, 264628, 18108370, 264829, 18108374, 35698423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264584, 264566, 264486, 264567
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gl 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264908, 255007, 264565, 264586
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gl 1550785 emb CAA69283  - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214948 (3761, 3762)	Novel Protein sim. GBank gl 93144 p I B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264887, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gl 2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gl 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4929843 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 58181688, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 68714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 284511, 265007, 284512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87188559, 264780, 55811150, 264761, 264882, 264763, 264883, 264764, 264288, 264369, 264768, 264886, 264768, 264769, 28148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810784, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22278002, 264583, 264584, 264565, 264566, 264488, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	58182575, 264259, 264905, 264909, 265008, 264598, 264768, 265020, 264628, 60431528, 264634, 58528488, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2834158 gb AAC02577.1  - (AF045841) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264810, 265018, 264766, 21906768, 29148828, 264690, 264693, 264628, 264555, 264488
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 PCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264908, 265007, 264681, 264768, 29148827, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87822804 (3775, 3778)	Novel Protein sim. GBank gi 3318931 emb CAB10841  - (Z98046) dJ1408.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir IA56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21805765, 21906768, 21908769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22278000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240185 db BAA74876.1  - (AB020680) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108388, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21908765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	284686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264809, 18108378, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gl 568953 cbj BAA83051.1  - (AB029022) KIAA1089 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533828 (3785, 3786)			lamilin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 86714117, 29331828, 264906, 265008, 265009, 264592, 265016, 264681, 264448, 264683, 18108354, 264369, 264884, 264885, 264766, 264687, 264689, 21908768, 265020, 265022, 60170815, 52644150, 264690, 264691, 264692, 33857023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631881 (3789, 3790)	Novel Protein sim. GBank gl 5262574 emb CAB45729.1  - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264805, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	18108379, 264634, 56182323, 56526486
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gl 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		cadherin	264907, 265008, 264692, 264686, 21906768, 264629, 264631, 264634, 264555
1898	87817637 (3795, 3796)	Novel Protein sim. GBank gl 127560 sp P23246 MV10_MOUSE - PROTEIN MOV-10			264259
1899	86673087 (3797, 3798)	Novel Protein sim. GBank gl 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21908765, 21906766, 21908768, 21906769, 60170615, 55810764, 22279000
1900	87841858 (3799, 3800)	Novel Protein sim. GBank gl 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21908765, 21908769
				UNCLASSIFIED	264683

1801	95196847 (3801, 3802)	Novel Protein sim. GBank gi 565859 sp P38378 S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52845156, 18108398, 5264385, 52846842, 18108397, 56182575, 22278994, 22278995, 56994075, 35896286, 22278997, 22278998, 284490, 60432049, 284259, 28331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35698032, 33656970, 29148498, 284908, 264907, 29331830, 284908, 52844045, 284909, 284112, 285006, 284512, 285008, 284910, 285009, 60170831, 60432228, 60433356, 33657402, 60433438, 55812038, 284758, 33109954, 21908754, 33657084, 52844296, 87168474, 265010, 285011, 87168559, 265017, 265018, 265019, 18108351, 264448, 284288, 264688, 52844228, 21908765, 21806768, 21908767, 21908769, 55811957, 35695917, 265020, 265021, 52844150, 18108362, 33657023, 264693, 263887, 33657109, 33657182, 27488284, 33657349, 35895763, 18108370, 18108378, 55811576, 35698423, 35695855, 60431850, 264638, 263981, 52844332, 60170384, 83373044, 18108385, 87168518, 80432113, 284584
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gi 4426613 gb AAD20451  (AF098788) SLM-1 [Mus musculus]		dna_ma_bind	264107, 263978
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gi 3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 28331825, 29331827, 264508, 264907, 285008, 60170831, 60433358, 60433438, 284759, 21908754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811578, 264555, 264556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gi 135291 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264806, 264907, 264908, 265007, 284910, 284886, 284788, 264887, 264769, 264693, 264628, 18108374, 284634, 264638, 264637, 264585
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gi 3043714 gb BAA25521  (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00283) - Bacterial muT protein		264488, 264768, 264769, 264889, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29148499, 264508, 264509, 264905, 264906, 264907, 66712502, 284908, 264909, 35898423, 35695855, 264510, 264511, 284512, 284910, 264634, 264635, 264637, 264638, 33657402, 284758, 85858542, 284602, 264760, 264781, 264482, 264563, 284762, 264483, 284784, 264586, 264288, 264769
1908	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank g 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21908754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21908765, 21908768, 21908768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313841 (3815, 3816)	Novel Protein sim. GBank g 3986770 (AF109806) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29148499, 264905, 264908, 264907, 264908, 66712502, 264908, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264598, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264805, 55811150, 264681, 264448, 264268, 264686, 264688, 264789, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264486 264259, 264508, 264805, 264806, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank g 2224653 db JBAA20813  - (A8002354) KIAA0358 [Homo sapiens]		UNCLASSIFIED	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486
1910	94216821 (3818, 3820)	Novel Protein sim. GBank g 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	

1911	81725345 (3821, 3822)	Novel Protein sim. GBank gi 4808339 gb AAD30184.1 AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33658970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264389, 21908765, 21908768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA63003.1  - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00099) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 26331824, 56182181, 29331825, 66714117, 35696052, 264805, 264806, 264807, 264908, 52844045, 58182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264881, 264369, 264684, 264288, 264686, 264768, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 85274791, 264637, 56182323, 83373044, 56526486, 22278002, 264583, 264588
1913	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 22278999, 29331826, 29331827, 265008, 55812038, 265010, 265017, 265018, 265018, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21908765, 21908768, 21908768, 21908769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1  - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA62891.1  - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565 264683, 264639
1916	78640761 (3831, 3832)				

1917	97821680 (3833, 3834)	Novel Protein sim. GBank gl 568938 dbj BAA82979.1 - (AB028950) KIAA1027 protein [Homo sapiens]		struct	264769, 264889, 21906765, 21906769, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264805, 264906, 264628, 264907, 264608, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264568, 264784, 264766
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gl 5281617 gb AAD41524.1 AF154831 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35696266, 35695917, 22278998, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52645129, 35696052, 29331828, 27486262, 27486264, 35695763, 264508, 264905, 264509, 264908, 264628, 264907, 18108370, 264908, 264829, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644298, 56526468, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264584, 18108351, 264762, 264682, 264585, 264448, 264784, 264586, 264486, 264587, 264369, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gl 3878584 emb CAB01237 - (Z77887) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 28331822, 265007, 60170831, 60432226, 60433438, 264448, 264682, 264288, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002, 264510, 264511, 264512, 264566
1920	91229853 (3839, 3840)	Novel Protein sim. GBank gl 1808231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gl 4580897 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693



1922	87641663 (3843, 3844)	Novel Protein sim. GBank gi1138595 sp P02845 VT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV1); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264584, 18108351
1923	84323589 (3845, 3846)	Novel Protein sim. GBank gi1191110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278895, 264094, 264259, 35886052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265008, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264881, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181552, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33857109, 18108370, 264628, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264584, 264565, 264566, 264567, 26531826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338825 (3847, 3848)	Novel Protein sim. GBank gi13877655 emb CAA86657  - (Z72511) possible zinc finger protein; cDNA EST EMBL:IM89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1....	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi4881803 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278895, 22278896, 22278897, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	86084739 (3851, 3852)	Novel Protein sim. GBank gi12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		struct	264905, 264906, 264907, 264910, 264593, 265018, 264780, 264764, 264288, 264692, 264693, 263976, 264631, 264634, 264637, 264593
1927	85654657 (3853, 3854)	Novel Protein sim. GBank gi13043632 db BAA25480  - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87786054 (3855, 3856)	Novel Protein sim. GBank gi11665761 db BAA13377  - (B87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Extracellular link domain	Inf	264488, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi15001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Diosostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52993 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35888286, 29331828, 284905, 284907, 284908, 284909, 284511, 284910, 284758, 284801, 285017, 285019, 284805, 284780, 284784, 284766, 284688, 284769, 285022, 35898423, 284638, 60432113
1931	87787278 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284906, 284908, 60432229, 284758, 284764, 284288, 285020, 284892, 284634, 284637, 284884, 284891, 284635
1932	15030972 (3863, 3864)			UNCLASSIFIED	284595
1933	11813688 (3865, 3866)			struct	56182375, 56182435, 284510, 284757, 284758, 55812038, 55811388, 285018, 55811150, 21906765, 284681, 284631, 284635, 284637
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gi 115749 db BAA38494  - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		UNCLASSIFIED	284886, 285011, 284511, 284905, 18108351, 284584, 284681, 284259, 18108370, 284566, 284764, 284369, 284595
1935	87752511 (3869, 3870)			UNCLASSIFIED	60432289, 285007, 285010, 285011, 285019, 33657109, 18108374
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gi 482704 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1937	84847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	8558542, 21906767, 35689517, 60170815, 284683, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	284488, 29146498, 284905, 284559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500858 db BAA03210  - (D14188) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 285017, 21906765, 21906766, 21908788, 55811957, 27486284, 35686423, 80432113, 284564
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132  - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	284488, 29331822, 284448, 284683, 284288, 285020, 33657023, 284831
1941	94147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 284259, 29331824, 29331827, 284805, 285008, 33657084, 285017, 285018, 284288, 284687, 21906765, 21908786, 21908787, 285020, 52644150, 27486284, 83373044, 18108387, 60432113, 22278002, 284585
1942	87641870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	284488, 18108388, 29331825, 27486281, 284509, 18108370, 18108374, 284482
1943	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3128952 sp O15736 TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35686052, 284511, 285008, 284592, 60432229, 285017, 285018, 285019, 284684, 284692, 33657109, 65274791, 284636

1944	94232858 (3887, 3888)	Novel Protein sim. GBank gl 1786570 gb BAA13432  - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52845080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432228, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 285017, 285018, 285019, 18108351, 264369, 264686, 264768, 21908765, 21908768, 21908787, 21908769, 35695917, 265020, 265021, 60170815, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264553
1945	87641872 (3888, 3890)	Novel Protein sim. GBank gl 4927204 gb AAD33048.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264488, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gl 2498104 sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21908767, 52844150, 264693, 27488284, 264637, 87168518, 264563
1947	86438882 (3893, 3894)	Novel Protein sim. GBank gl 3914801 sp Q54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		mapolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264784, 264288, 264766, 264688, 21908768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]		struct	264909, 60170831, 264591, 264594, 235010, 265011, 284784, 284369, 264689, 264631, 264638
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gl 3876766 emb CAA93466.1  - (Z88637) predicted using GeneFinder: Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264369, 264768, 264698, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gl 2626753 gb BAA23424 - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52845080, 29331824, 29331825, 29331827, 55812038, 52846317, 285018, 265019, 264369, 21908765, 21908767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gl 4929833 gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00106) - reductase short chain dehydrogenase	reductase	264591, 264593, 284594, 264595, 264555, 264556, 264557, 264558, 264559

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gij1188715sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	Complement	264259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gij4240271 dbj BAA74914.1 - (AB020898) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263394, 18108394, 35688286, 22278998, 29331822, 68714117, 29331828, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264910, 265009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264786, 264789, 35895917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264638, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264584, 264586, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 58182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264768, 21906765, 21906768, 21906767, 55811857, 265020, 265021, 52645129, 33657109, 27488264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gij1665821 dbj BAA134071 - (D87469) Similar to D melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21908769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264583, 264584

1957	94328510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA78856.1  - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52846842, 56182575, 22278997, 22278998, 22278999, 29331824, 88714117, 29331827, 29148498, 284593, 33857402, 33109954, 87168474, 285018, 284448, 284389, 284288, 284788, 21908766, 21908767, 21908768, 21908769, 285020, 265021, 284692, 85274620, 27486264, 33657349, 27486265, 35695855, 22279002, 284482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1  - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 284092, 284094, 284259, 80432049, 29331824, 58182181, 88714117, 284107, 264109, 284909, 284511, 60170831, 60432229, 21906754, 285010, 21906769, 35695917, 285022, 65274620, 263987, 283978, 35696423, 284631, 284632, 284634, 284635, 18108385, 22279000, 22279002, 284593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860  - (Z88056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3918, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515  - (D84159) 3-7 gene product [Homo sapiens]		struc1	284905, 284806, 284907, 284908, 284908, 285006, 265007, 284910, 284595, 265017, 284604, 285018, 18108351, 284764, 284369, 284768, 284788, 21908765, 18108368, 284628, 18108379, 284635, 284636, 284637, 284638, 284488, 284635
1961	16292607 (3921, 3922)				
1962	91008385 (3923, 3924)				
1963	80936017 (3925, 3926)	Novel Protein sim. GBank gi 3721853 dbj BAA33581  - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		UNCLASSIFIED	65274572, 284592, 284593, 285019, 284691, 85274572, 18108398, 35698286, 28331825, 60432289, 29331827, 284828, 285006, 285009, 80433386, 60433438, 21906754, 285020, 265021, 33657023, 33657109, 27486265, 35695855, 284555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1  - (AL080169) hypothetical protein [Homo sapiens]		cadherin	284488, 284092, 284259, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 285007, 285009, 284910, 284592, 284593, 284594, 284595, 284758, 284600, 284803, 284604, 284805, 284760, 284762, 284448, 284764, 284288, 284685, 284768, 284768, 284769, 21908768, 284691, 284692, 284693, 18108370, 284628, 284629, 18108374, 284630, 284631, 284634, 284636, 284637, 284638, 18108382, 83373044, 18108385, 264483, 284584, 284565, 284566, 284486, 284567, 284488, 284510, 284760, 284768, 284486
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294  - (AB001773) PEM-6 [Clona savignyi]	Contains protein domain (PF01428) - ANI-like Zinc finger	ubiquitin	

1966	84192058 (3931, 3932)	Novel Protein sim. GBank glj4929707[gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264885, 264886, 265022, 264891, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264488, 264587
1967	87396123 (3933, 3934)	Novel Protein sim. GBank glj2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 58526486
1968	88095841 (3935, 3936)	Novel Protein sim. GBank glj2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264905, 264509, 264908, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264584, 264585, 264586, 264587
1969	84328529 (3937, 3938)	Novel Protein sim. GBank glj2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1970	80596049 (3939, 3940)	Novel Protein sim. GBank glj4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1971	94843914 (3941, 3942)	Novel Protein sim. GBank glj134208[sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264486, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21908765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264836, 264637, 264638, 264639, 18108385, 60432113, 22278900, 264583, 264584, 264585, 264586, 264486
1972	87645444 (3943, 3944)	Novel Protein sim. GBank glj4519623[db BAA75671.1  - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278998, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644286, 265018, 265019, 264761, 264889, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264556, 60432113
1973	86395533 (3945, 3946)			UNCLASSIFIED	29331828, 264692, 35696423, 264631, 264595, 264596, 264557, 264558, 264559
1974	80396629 (3947, 3948)	Novel Protein sim. GBank glj3309543 (AF036382) - ML1 [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	04316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 58182435, 265008, 284757, 55812038, 285010, 265017, 284369, 55811957, 65274791, 35895855, 58182323, 60432113
1976	95358814 (3851, 3952)			UNCLASSIFIED	284259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852684 (3953, 3954)	Novel Protein sim. GBank gl 2499520 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264808, 264596, 265021, 264566
1978	87447845 (3955, 3956)	Novel Protein sim. GBank gl 103421 pir A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcription factor	60170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gl 2244815 emb CAB10238.1 - (Z97338) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	28331828, 29146498, 264905, 284907, 265007, 265009, 265010, 265018, 264686, 18108359, 21908788, 35695917, 265020, 60170815, 264693, 18108368, 18108370, 284631, 284635, 284556, 264558, 18108384, 22279000, 264585
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gl 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked		ubiquitin	264489
1981	87608874 (3961, 3962)	Novel Protein sim. GBank gl 4406693 pb AAD20060 - (AF131848) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 284259, 29331825, 29331828, 29146498, 29146499, 284107, 264908, 264910, 284595, 21906754, 265010, 265017, 265018, 265019, 264448, 284288, 21908787, 33657023, 27486284, 18108370, 18108374, 18108376, 284630, 284831, 264635, 18108385, 87168518, 22279000, 264482, 264584
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gl 5689523 db BAA83045.1 - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 28331825, 35696052, 33656970, 264809, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098688 (3965, 3966)	Novel Protein sim. GBank gl 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcription factor	22278996, 35696286, 284259, 29331822, 20281099, 29331824, 60432289, 29331827, 284509, 264905, 264906, 264907, 86712502, 284908, 52844045, 264909, 284510, 264512, 284910, 265009, 264591, 264592, 60433356, 60433438, 284758, 265010, 264600, 264603, 284604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21908765, 55811957, 35695917, 284690, 264692, 264693, 284628, 264629, 263978, 18108379, 35698423, 35695855, 20281071, 264632, 284634, 264635, 264555, 264636, 284637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1884	85760989 (3967, 3968)	Novel Protein sim. GBank gij2896695[mbjCAA17174.1] - (AL021897) <i>fadD14</i> [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811857, 56984075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33857182, 29148499, 264628, 18108370, 264908, 264628, 55811576, 35695855, 265008, 265007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1885	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131[gbjAAD47379.1] (AF12049) - (AF120499) <i>DEM1</i> protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108365, 264584
1886	80200507 (3971, 3972)	Novel Protein sim. GBank gij4868443[gbjAAD31319.1] (AF14457) - (AF144573) <i>Mx-interacting protein kinase PKM</i> [Mesocricetus auratus]	Contains protein domain (PF000069) - Eukaryotic protein kinase domain	UNCLASSIFIED	264488, 264629
1887	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gbjAAD31319.1] (AF14457) - (AF144573) <i>Mx-interacting protein kinase PKM</i> [Mesocricetus auratus]		UNCLASSIFIED	22278999, 29331830, 265007, 265018, 21906768, 33657023, 264692, 264693, 18108377, 264635, 60170384, 22279002
1888	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264688, 264768, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1889	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein <i>spc87</i> homolog <i>GCP2</i> [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1890	85699888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dj]BAA83074.1] - (AB024728) $\alpha$ -1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1891	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dj]BAA74922.1] - (AB020706) <i>KIAA0899</i> protein [Homo sapiens]	Contains protein domain (PF01802) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35698288, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264768, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264488
1892	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF000096) - struct Zinc finger, C2H2 type	struct	29331827, 264906, 264907, 264909, 265007, 264603, 264768, 264686, 264768, 21906768, 264628, 264635, 264636, 18108385, 56526486, 264586, 264587
1893	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG28 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35698423



1984	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - mapolymerase SET domain	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 284907, 284908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 284684, 284369, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 85274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56528486, 22278900, 22278902, 264564
1995	65414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit	UNCLASSIFIED	264488, 18108396, 22278994, 56994075, 22278996, 35896286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331828, 29331827, 35896052, 29146499, 284905, 284907, 66712502, 56182435, 265008, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 284288, 284766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906768, 21906767, 29148627, 21906768, 21903769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35896423, 55811576, 65274791, 35895855, 284631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567, 264564
1998	80254185 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020  - (X88028) extensin-like protein [Vigna unguiculata]	UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein; phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - phosphatase Ank repeat	264808, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 db BAA76039.1  - (AB023212) KIAA0995 protein [Homo sapiens]	UNCLASSIFIED	264113, 264685, 264555, 264567

1899	94324803 (3997, 3998)	Novel Protein sim. GBank gi 5225312 gb AAD0846.1 AF07244 - (AF072441) catchneurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 285008, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264882, 264369, 264685, 264686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108379, 35695855, 264834, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3998, 4000)	Novel Protein sim. GBank gi 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C104.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21908754, 52644296, 265017, 265018, 265019, 264761, 264389, 264286, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 85274620, 52645129, 27486261, 27486262, 27486284, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi 107560 pir J338637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21908768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi 728433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264810, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074448 (4005, 4006)	Novel Protein sim. GBank gi 86388 pir J27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1  - (AL049998) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 284259, 32645080, 28331824, 29331826, 29331827, 35895052, 29331828, 33656870, 29331830, 284908, 284592, 60433356, 33657402, 52846317, 21906754, 33657084, 52644298, 87168474, 87168559, 285017, 285018, 285019, 284763, 284883, 284288, 52844228, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52845129, 33657109, 33657182, 27486281, 27486282, 33657349, 27486265, 35895763, 18108374, 18108376, 18108377, 35896423, 35895855, 284631, 52844332, 284558, 18108385, 56826486, 87168518, 60432113, 284483, 284488, 284906
2005	87400884 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795  - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33388 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this gene...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613  - (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 284259, 56182181, 60424269, 68714117, 35696052, 284908, 68712502, 284909, 284510, 60433356, 85658542, 285010, 285018, 285019, 284682, 284448, 284288, 284768, 28148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810784, 55811576, 35695855, 87168518, 60432113, 284583, 284482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712  - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	284488, 263894, 35696052, 284508, 284905, 284906, 284907, 284908, 284909, 265007, 284910, 284592, 264595, 284758, 285011, 284760, 284762, 284764, 284766, 284685, 284767, 284768, 284769, 55811957, 35895917, 265020, 284691, 284693, 284628, 284629, 65274791, 35695855, 284631, 284632, 284634, 284635, 284637, 284638, 284839, 284586
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550763 emb CAA69257  - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	284909, 284768, 35695855

2008	85740240 (4017, 4018)	Novel Protein sim. GBank gll3882305[db][BAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264681, 264683, 21806768, 264691, 33857182, 33857348, 264631, 87168518, 264404, 22279002, 264583
2010	95422458 (4019, 4020)	Novel Protein sim. GBank gll5262628[emb][CAB45763.1] - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	eph	52844507, 52845156, 52846365, 52846842, 18108397, 65274572, 22278994, 56994075, 35898286, 22278996, 22278997, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432228, 60433356, 21908754, 52846317, 33109954, 52844298, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52844229, 264689, 21908765, 21908766, 21908767, 21808768, 35895917, 265020, 52844150, 264691, 264692, 33857023, 263967, 52845128, 35895763, 18108376, 35896423, 65274791, 35895855, 264631, 264634, 60431850, 264637, 264638, 52844332, 60170394, 18108385, 87168518, 22279002, 264584, 264585, 264586, 264587, 56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35896052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264389, 264288, 264685, 264766, 264687, 21908765, 21908767, 21908768, 21908769, 265020, 265022, 264691, 33857023, 65274620, 33857109, 264629, 264557, 264559, 89373044, 87168518, 60432113, 22279002, 264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21908764, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gll3347853 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	18108398, 264908, 285007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692, 264488, 29331826, 264907, 264638, 264555, 264639, 264558
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gll1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	89373044, 87168518, 60432113, 22279002, 264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21908764, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gll4507985[ref][NP_003427.1]pZNF1 - zinc finger protein 135 (clone pHz-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	18108398, 264908, 285007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692, 264488, 29331826, 264907, 264638, 264555, 264639, 264558
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gll127720[epi]P20938[MYPO_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	

2015	88094822 (4029, 4030)	Novel Protein sim. GBank gl 81286 pir  S22697 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	56182575, 35696286, 284259, 35696052, 284508, 284908, 284907, 284510, 284512, 87108474, 285010, 284681, 284288, 284689, 284628, 35698423, 35698555, 284639, 284563, 284564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gl 285046 pir  S28413 - t-complex protein Tcp-10 - mouse	sinud		284102, 284508, 284110, 265009, 33109954, 21908768, 265021, 33657109, 27488262, 263972, 18108374, 263976, 284555, 284564
2017	79464293 (4033, 4034)			UNCLASSIFIED	284685, 284636
2018	78637087 (4035, 4036)	Novel Protein sim. GBank gl 124735 sp P18175 INVO_PIG - INVOLUCRIN			284683
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gl 2143910 pir  S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat	phosphatase		284107, 284110, 264112, 265017, 263976
2020	94874476 (4039, 4040)	Novel Protein sim. GBank gl 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saiida]		UNCLASSIFIED	264259, 264508, 284591, 265018, 284682, 264288, 284688, 22278002
2021	88718818 (4041, 4042)	Novel Protein sim. GBank gl 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 284593, 33109954, 21908754, 21908768, 33657023, 33657109, 27486261, 87108518
2022	85285665 (4043, 4044)	Novel Protein sim. GBank gl 4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			284757, 284767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gl 5410230 gb AAD42892.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2		18108394, 22278999, 264259, 264905, 264906, 284908, 284595, 284762, 284769, 264634, 264638, 87108518, 60432113, 22279000, 284482, 284585
2024	87898443 (4047, 4048)				60433438, 265017, 284688, 284692, 284693, 284636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gl 4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 284906, 284909, 55812038, 265017, 265021, 265022, 60170815, 284558
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gl 165569 emb CAA60032  - (Y07752) pterophorin-S [Volvox carterii]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 284112, 60170831, 87108559, 284288, 284688, 284689, 21908768, 33657109, 18108370, 284638, 18108385, 60432113, 22279000, 22278002, 284564, 284566, 284587
2027	80249001 (4053, 4054)			UNCLASSIFIED	263976, 284634, 284488

2028	84699884 (4055, 4056)	Novel Protein sim. GBank g11330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - ubiquitin-HECT-domain (ubiquitin-transferase).	32644507, 52645156, 52646842, 56182575, 56994075, 35696266, 22278997, 22278998, 22278999, 80432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264908, 264907, 264908, 29331830, 52644045, 56182435, 265008, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644429, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 58526486, 22278000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank g13599940 (AF017368) - facicentital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED
2030	91213734 (4059, 4060)	Novel Protein sim. GBank g15630080 [gb]AAD45825.1 (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor
2031	80245281 (4061, 4062)			18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 80432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2032	91232607 (4063, 4064)	Novel Protein sim. GBank g15689491 [dbj]BAA83029.1 - (AB028000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase
2033	95000808 (4065, 4066)	Novel Protein sim. GBank g12494828 [sp]OP4686 [CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACII)] (STY)		synthase
2034	91232528 (4067, 4068)	Novel Protein sim. GBank g14826984 [ref]NP_005147.1 [PROD1 - UNKNOWN]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind

2035	83553451 (4099, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324633 (4073, 4074)	Novel Protein sim. GBank gll2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331828, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264584, 5612038, 33109954, 21808754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21908767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264583
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gll3880825 (embjCAB07858) - (Z63785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL:U01682 comes from this gene; cDNA EST EMBL:IM75823 comes from this gene; cDNA EST EMBL:D27559 comes from this gene...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264583, 264584, 264586
2039	95514628 (4077, 4078)	Novel Protein sim. GBank gll2224653 (dbj BAA20813) - (AB002354) KIAA0358 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35698423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gll2500825 (sp P70700 RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21908766, 265021, 265022, 264692, 33657109, 264628, 264628, 35698423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 4406590 gb AAD20040  - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 284509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 284595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21908765, 35695917, 264535, 52644150, 264691, 264692, 18108385, 27486281, 27486262, 27486285, 18108374, 35696423, 65274791, 35695855, 264555, 284558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 284563, 284564, 284566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF145632) BcDNA.GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52648385, 56994075, 22278897, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 28146498, 284509, 264908, 52644045, 56182435, 265006, 33657402, 21908754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906766, 21908767, 21908768, 21908769, 265020, 285021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27488261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 284558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 284567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2248532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		stfuc1	264093, 29331827, 264905, 66712502, 264592, 264689, 21908765, 21908769, 265020, 264692, 264566
2045	79835532 (4089, 4090)	Novel Protein sim. GBank gi 4406698 gb AAD20062  - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22278002
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 4101720 (AF008466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29148498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gi 4598658 db BAA78850.1  - (AB023223) KIAA1008 protein [Homo sapiens]		UNCLASSIFIED	264909
2048	84606378 (4095, 4096)			UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 284910, 264603, 264763, 21908767, 21908768, 264629, 264634, 264637, 22278002, 264564, 264565, 284566, 264567



2050	79833835 (4089, 4100)			UNCLASSIFIED	284693
2051	87780188 (4101, 4102)			UNCLASSIFIED	284488, 284259, 284509, 284808, 284907, 284789, 18108374, 35698423, 284583, 284586, 284488
2052	88096383 (4103, 4104)	Novel Protein sim. GBank gij4529889[gblAAD21812.1] - (AF134728) G8A [Homo sapiens]	Contains protein domain (PF00356) - SET domain	kinase	284488, 283994, 35698052, 284508, 284905, 284509, 284906, 284907, 284908, 284908, 284113, 284511, 285008, 284910, 60170831, 284592, 284758, 285010, 285011, 284605, 284760, 284682, 284764, 284389, 284766, 284686, 284788, 284789, 52844228, 284689, 35695917, 33857023, 33857109, 284828, 18108374, 35698423, 55811578, 35695855, 284830, 284631, 284832, 284634, 284635, 284838, 284556, 284638, 284639, 18108385, 58528486, 60432113, 284563, 284584, 284586, 284488, 284587, 284488, 283994, 35698052, 284508, 284905, 284909, 284906, 284907, 284908, 284909, 284113, 284511, 285009, 284810, 60170831, 284592, 284758, 285010, 285011, 284805, 284760, 284682, 284764, 284389, 284766, 284688, 284768, 284789, 52844228, 284689, 35695917, 33857023, 33857109, 284828, 18108374, 35698423, 55811578, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284556, 284638, 284639, 18108385, 58528486, 60432113, 284563, 284584, 284586, 284488, 284587
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gij2895449[emb]CAA75113] - [Y14848] midline 1 protein [Mus musculus]		UNCLASSIFIED	22278998, 22278997, 284259, 29331822, 284102, 284508, 35695917, 283972, 284482, 60424178, 284084, 284259, 28331825
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gij3876326[emb]CAB02080] - (Z78754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain		60424289, 284908, 60432229, 60433356, 87188559, 285019, 284760, 284288, 284686, 21908789, 33857023, 284893, 55810764, 55811578, 284635, 56182323, 60432113
2055	88258449 (4109, 4110)	Novel Protein sim. GBank gij5353748[gblAAD42226.1]AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED	284488, 29331826, 60432289, 29331828, 60433356, 285019, 284883, 284884, 285021, 33857109, 18108374, 284637, 18108385, 87188518, 60432113, 22278000, 284584

2056	86177396 (4111, 4112)	Novel Protein sim. GBank g K826960 ref NP_005042.1 pQARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	synthase	284488, 52845156, 56182575, 22278994, 35898286, 58894075, 22278998, 22278998, 22278999, 60432049, 284259, 29331824, 60432289, 29331827, 29331828, 33656970, 284104, 284808, 284808, 285006, 285008, 60170831, 264591, 60432229, 60433438, 18108348, 21908754, 33857084, 52844286, 87168474, 265010, 87168559, 265017, 265018, 284760, 18108351, 284881, 284882, 284448, 264883, 284389, 284288, 264685, 284687, 254888, 264689, 21908785, 21908766, 21908787, 21908769, 55811957, 35895917, 265022, 33657023, 18108362, 33857109, 18108388, 33857182, 27486281, 27486284, 27486285, 33657349, 264828, 18108370, 284829, 18108374, 18108377, 18108378, 35898423, 55811578, 20281152, 264838, 264852, 18108385, 18108388, 87198518, 284482, 284595, 284598, 284567 52846842, 52846365, 56182575, 35898288, 22278998, 22278997, 22278998, 264093, 52845080, 35898052, 29331828, 33656970, 285008, 52846317, 55811386, 52844286, 52844229, 21908788, 35895917, 265021, 60170815, 52844150, 33657109, 33657182, 27486261, 27486282, 35895763, 35898423, 35895955, 52844332
2057	87877805 (4113, 4114)	Novel Protein sim. GBank g J728850 p P08840 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	285007, 285008, 284591 29331825, 264682, 264686, 264691, 264693, 22278002
2058	86276998 (4115, 4116)	Novel Protein sim. GBank g J119714 p P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	
2059	79866684 (4117, 4118)	Novel Protein sim. GBank g J281122 U87318 - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 284910, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2486947 sp Q09289 YQ09_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF000069) - Eukaryotic protein kinase domain	kinase	22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 68712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265008, 264910, 264591, 33657402, 21906754, 65658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906785, 21906787, 21906788, 21906789, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264558, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56526488, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264628, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264782, 264565, 264764, 264487, 264788
2063	87801272 (4125, 4126)	Novel Protein sim. GBank gi 4569562 db BAA78803.1  - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278998, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811578, 18108384, 22279002, 264482, 264563, 264584, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 db BAA13413.1  - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264781, 18108351, 264682, 264369, 264286, 52644229, 21906785, 21906787, 21906788, 35695817, 33657109, 18108368, 18108374, 35698423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264488
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331828, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85656542, 265018, 55811150, 264681, 264766, 264692, 60431828, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264764, 264286, 56182323, 264567
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	

2067	95303892 (4133, 4134)				35688288, 22278997, 22278998, 60432049, 284259, 60432289, 60433438, 284682, 284448, 284369, 284288, 18108355, 21908765, 21908768, 265022, 33657109, 35688423, 35688555, 284558, 284404, 284583, 284488
2068	84344754 (4135, 4136)			UNCLASSIFIED	284687
2069	94318177 (4137, 4138)	Novel Protein sim. GBank gl 3152882 (AF084604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcript factor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35688052, 29331828, 33656870, 284509, 284905, 56182435, 265009, 60433356, 87188559, 265017, 285018, 264604, 265019, 284448, 284764, 284766, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 33657109, 263976, 284555, 284557, 56182323, 83373044, 87188518, 60432113, 22278000, 22278002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gl 5712131(gb)AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	356885917, 264805, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gl 3551531(dbj) BAA33016] - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265008, 265007, 265008, 265009, 284594, 265010, 265011, 18108351, 18108354, 18108364, 18108385, 18108368, 284634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35688288, 22278997, 22278998, 22278999, 284480, 60432049, 284259, 29331822, 29331824, 29331826, 35688052, 265008, 33657402, 21908794, 285011, 265018, 18108351, 284682, 284389, 21908765, 21908766, 21908767, 21908768, 21908789, 356885917, 265020, 265021, 284680, 284692, 35688423, 264555, 264556, 284598, 22278000
2073	27825684 (4145, 4146)	Novel Protein sim. GBank gl 1504026(dbj) BAA13212] - (D86976) similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	284559
2074	94324787 (4147, 4148)	Novel Protein sim. GBank gl 4240317(dbj) BAA74837.1] - (AB020721) KIAA0914 protein [Homo sapiens]			28331822, 284809, 264511, 265009, 284594, 284595, 265010, 265011, 265017, 265018, 265019, 284448, 284683, 265020, 265021, 18108370, 284632, 83373044, 284587

2075	94314886 (4149, 4150)	Novel Protein sim. GBank glj5138930[gbjAA040382.1] - (AF093860) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278998, 35696286, 22278998, 264259, 29331822, 29331825, 29331827, 35886052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264780, 264448, 264288, 264766, 264767, 264688, 21908768, 21908767, 21908769, 265021, 265022, 60170615, 33657023, 27486282, 27486285, 35698423, 35695855, 264631, 264634, 264639, 87188518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331828, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11389877 (4153, 4154)			UNCLASSIFIED	
2078	87539384 (4155, 4156)	Novel Protein sim. GBank glj4220390[gbjBAA74578] - (D87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 58526488
2079	88095916 (4157, 4158)	Novel Protein sim. GBank glj4240255[gbjBAA74908.1] - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281089, 264809, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264583, 264564, 264448, 264684, 264587, 264685
2080	94138689 (4159, 4160)	Novel Protein sim. GBank glj2408021[embjCAB18219.1] - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank glj5524734[gbjAAD4360.1]AF18635 - (AF186350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21908767, 21908768, 264693, 18108385, 22279000, 22279002
2082	87628628 (4163, 4164)	Novel Protein sim. GBank glj3880558[embjCAA94234] - (Z70271) predicted using GeneFinder: similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	
2083	94141000 (4165, 4166)	Novel Protein sim. GBank glj2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Cryptotagus cuticulus]	Contains protein domain (PF00183) - Mitochondrial carrier proteins	transport	56182575, 22278998, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264583, 21908764, 265018, 265019, 264448, 264288, 264685, 21908769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264583
2084	95199288 (4167, 4168)	Novel Protein sim. GBank glj728638[gbjP39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	84989476 (4169, 4170)	Novel Protein sim. GBank gij1655699[emb]CAA69032] - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264783, 264369, 264688, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gij3875032[emb]CAA8936] - (Z49125) similarity to Trichostromyolus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 comes...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35695423, 35695655, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gij3880930[emb]CAA16334, 1]- (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		UNCLASSIFIED	264488, 22276994, 35696286, 22276996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264389, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35696423, 35695855, 83373044, 87168518, 22278000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gij4756118[ref]NP_004623.1 pDAP3 - Death associated protein 3	cadherin		18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22276994, 22276995, 35696286, 22276998, 56984075, 22276997, 22276998, 22276999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33696970, 29146488, 29146489, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264908, 264907, 264808, 68712502, 264828, 52644045, 264809, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170631, 264592, 264593, 60433356, 33697402, 60433438, 264595, 55812038, 264758, 21908754, 33657084, 55811388, 52644296, 265010, 265011, 87169559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108356, 56181582, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148628, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690

2080	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 26331826, 35686052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 265022, 60170815, 33857023, 35696423, 35695955, 264652, 18108387, 22279000, 263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21908765, 21908768, 21908769, 265022, 264628, 264583, 264587, 22278997, 22278999, 66712502, 87168559, 264683, 265021, 264488
2081	95309161 (4181, 4182)	Novel Protein sim. GBank glj4580987[gb]AAD24571.1[AF12108] cAMP Inducible 2 protein [Mus musculus]	UNCLASSIFIED		264905, 264908, 264907, 264908, 264510, 265008, 265007, 265009, 264910, 264596, 21908754, 87168474, 265011, 264603, 265018, 265019, 264760, 264768, 264769, 21908767, 21908768, 21908769, 265021, 264680, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264554
2082	88223605 (4183, 4184)		homeobox		35696286, 265017, 265018, 265019, 18108388
2083	87406073 (4185, 4186)	Novel Protein sim. GBank glj2352427 (AF004181) - peroxisomal Ca-dependent solute carrier [Cryptotagus curticulus]	Contains protein domain (PF000153) - Mitochondrial carrier proteins	transport	265008, 87168559, 18108351, 21908769, 29148784, 265020, 33857023, 27466262, 18108374, 18108388
2084	91230929 (4187, 4188)	Novel Protein sim. GBank glj4928451[gb]AAD34036.1[AF15179] CGI-40 protein [Homo sapiens]	MHC		264488, 264489, 65274572, 56182375, 22278996, 22278997, 22278999, 264259, 60432289, 26331826, 35696052, 264107, 264508, 264509, 264905, 264908, 264907, 264908, 52844045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264688, 21908765, 21908766, 21908767, 35695917, 265020, 265022, 52844150, 264691, 264692, 33657023, 264693, 27468261, 35695783, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264636, 264639, 264663, 264483, 264585, 264586, 264486, 264567
2085	95351528 (4189, 4190)	Novel Protein sim. GBank glj1363238[ptt]A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	
2086	94118760 (4191, 4192)	Novel Protein sim. GBank glj3834423 (AF070688) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi15174501[re]NP_008051.1 PLYF1 - zinc finger protein, subfamily 1A, 1 (Hkeros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264692, 33657109, 18108370, 264636, 264483 56894075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi4758203[re]NP_004081.1 pDUSP - dual specificity phosphatase 3 (varicella virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi12695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi13681189[emb]CAB165141 - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:CO8179 comes from this gene; cDNA EST EMBL:CO8337 comes from this gene; cDNA EST EMBL:CO8929 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nud_rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 26146498, 264908, 265008, 265009, 264910, 264591, 60432229, 60433358, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108374, 35898423, 264558, 83373044, 87189518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gi4589468[db]BAA76761.1  - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi13874149[emb]CAA97423.1  - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35698286, 264259, 35698052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433358, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	85413576 (4205, 4206)	Novel Protein sim. GBank gi14240159[db]BAA74858.1  - (AB020642) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278998, 264259, 29331824, 29331825, 35698052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27466262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000



2105	94848080 (4209, 4210)	Novel Protein sim. GBank gij1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g8.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....	UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52844045, 264510, 264511, 285007, 264512, 265009, 60170831, 60432229, 33857402, 60433356, 264595, 60433438, 264758, 33857084, 87168474, 265010, 87168559, 285017, 285019, 285019, 264782, 18108351, 284684, 18108354, 264288, 264688, 52844229, 18108359, 21908765, 21908766, 21908787, 21908788, 21908789, 35895917, 285020, 265022, 60170815, 52844150, 284682, 33857023, 264693, 33857109, 60431528, 18108374, 85274781, 35895855, 264635, 60170394, 264639, 264538, 18108385, 18108387, 58526486, 87168518, 60432113, 264564, 264568, 264567, 285006, 285019, 284908, 264639
2108	83385475 (4211, 4212)	Novel Protein sim. GBank gij3881524[emb]CAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]	UNCLASSIFIED	264905, 264908, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264784, 284786, 264787, 264788, 264789, 264693, 264629, 35895855, 264632, 264634, 264635, 264638, 264639, 83373044, 284488
2107	78822682 (4213, 4214)	Novel Protein sim. GBank gij3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gij235927 from S. cerevisiae. [Arabidopsis thaliana]	UNCLASSIFIED	18108348, 264789, 18108370, 18108374, 284555, 284556, 284557, 284558, 284584
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gij2143639[ptf]156542 - calmodulin-binding protein - rat	UNCLASSIFIED	284786, 35895917, 264630, 264587, 284486
2109	80478719 (4217, 4218)	Novel Protein sim. GBank gij4426629[gj]AAD20459] - (AF100980) protocadherin [Rattus norvegicus]	UNCLASSIFIED	264508, 264908, 264591, 264682, 22279002
2110	87728075 (4219, 4220)	Novel Protein sim. GBank gij3327184[dj]BAA31680] - (AB014585) KIAA0885 protein [Homo sapiens]	UNCLASSIFIED	265008
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gij4757890[ref]NP_004328.1pc8OR - chromosome 8 open reading frame 1	UNCLASSIFIED	66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21908789, 55811957, 265020, 265021, 33857109, 60170394, 264558, 85274572, 264689, 264691, 264692, 60432113
2112	87283783 (4223, 4224)	Novel Protein sim. GBank gij4426629[gj]AAD20459] - (AF100980) protocadherin [Rattus norvegicus]	UNCLASSIFIED	
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gij3327184[dj]BAA31680] - (AB014585) KIAA0885 protein [Homo sapiens]	UNCLASSIFIED	
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gij3327184[dj]BAA31680] - (AB014585) KIAA0885 protein [Homo sapiens]	UNCLASSIFIED	
2115	80983785 (4229, 4230)	Novel Protein sim. GBank gij4757890[ref]NP_004328.1pc8OR - chromosome 8 open reading frame 1	UNCLASSIFIED	

2116	88258367 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35686286, 22278999, 56182181, 29331824, 29331825, 29331827, 35689052, 284907, 56182435, 285008, 284591, 55812038, 55811386, 87188559, 264288, 284369, 21908768, 29148629, 33857023, 35685763, 55811576, 35696423, 18108385
2117	87788804 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	28331824, 284511, 265009, 33109954, 285017, 285018, 264288, 284689, 265020, 284692, 58528488, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1078307 (prijB56573) - nuclear pore complex glycoprotein p82 - African clawed frog		glycoprotein	284258, 284905, 264907, 284908, 284510, 284511, 285009, 284910, 285010, 284602, 284288, 284788, 284693, 263967, 263972, 284838, 284559
2119	86993317 (4237, 4238)	Novel Protein sim. GBank gij4321407 (gbAAD15748) - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	284683, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gij485527 (refNP_005480.1) pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - Src homology domain 2	eph	284091, 284259, 28331828, 29331828, 285017, 284604, 264288, 284885, 285020, 284691, 18108370, 55810764, 284555, 284636, 80432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 (refNP_004888.1) pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	284601, 284766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gij4828551 (gbAAD34036.1) (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 284907, 56182435, 285007, 284910, 285010, 285018, 284686, 285020, 55811576, 284555, 284637, 18108382, 83373044, 18108383, 18108394, 56528488, 284985, 284587
2123	86787888 (4245, 4246)	Novel Protein sim. GBank gij2224551 (dbjBAA20764) - (AB002302) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108386, 264757, 265011, 18108351, 284691, 284634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5688455 (dbjBAA83011.1) - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 284806, 284907, 264591, 284639, 284583
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gij728831 (prijP39188) (ALU1_HUMAN - III) ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	284258, 284505, 284907, 284511, 85658542, 284783, 21806785, 35695917, 264636, 264488
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539284 (embjCAB39853.1) - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284488, 284489, 29331827, 35696052, 284905, 284509, 284908, 284909, 284510, 285009, 284591, 284592, 284593, 33857402, 284594, 284595, 284596, 284758, 284601, 284603, 285018, 284604, 284605, 284760, 284881, 284782, 284883, 284784, 284684, 284288, 284685, 284689, 80170815, 33857023, 33857109, 55810764, 284635, 284838, 284637, 284638, 284639, 83373044, 284584, 264586

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gll4868435[gb]AAD31315.1[AF14323] - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35693286, 28331826, 35696032, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 285006, 284511, 284512, 285007, 285009, 284910, 284758, 285011, 284600, 284601, 284604, 284762, 284763, 284766, 284687, 284768, 284769, 284889, 35695917, 284690, 284891, 284892, 284893, 284629, 18108374, 35695855, 284832, 284634, 284635, 284636, 284637, 284638, 284639, 18108385, 284563, 284594, 284567, 58182575, 35696288, 58182181, 28331824, 60432289, 35696052, 284905, 284907, 68712502, 284908, 284909, 284510, 284512, 285009, 284910, 284591, 55812038, 285018, 284784, 284288, 284369, 284687, 284788, 55811957, 284692, 18108368, 284628, 284832, 284634, 284635, 284637, 58182323, 284639, 18108384, 18108388, 284563, 284567
2128	87414282 (4255, 4256)				58182575, 35696288, 58182181, 28331824, 60432289, 35696052, 284905, 284907, 68712502, 284908, 284909, 284510, 284512, 285009, 284910, 284591, 55812038, 285018, 284784, 284288, 284369, 284687, 284788, 55811957, 284692, 18108368, 284628, 284832, 284634, 284635, 284637, 58182323, 284639, 18108384, 18108388, 284563, 284567
2129	95102089 (4257, 4258)		UNCLASSIFIED		68714117, 284828, 284595, 55812038, 55811150, 55811957, 284693, 18108374, 283978, 65274791, 18108381, 83373044, 22279000
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gll2648265 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		283981
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gll1086866 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]		Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	284488, 22278988, 284259, 29331827, 28331828, 35696052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 285006, 284511, 285007, 284910, 284591, 284592, 284595, 284758, 21906754, 33109954, 87168474, 265011, 284600, 284601, 284605, 285018, 284760, 18108351, 284681, 284782, 284784, 284288, 284684, 284766, 284688, 284687, 284768, 284769, 284688, 21908769, 284690, 52644150, 284691, 284693, 18108370, 284628, 284629, 18108372, 18108374, 35696423, 35695855, 284631, 284634, 284635, 284636, 284555, 284637, 18108380, 284639, 284556, 58182323, 56528488, 284564, 284565, 284566, 284567
2132	95381096 (4263, 4264)	Novel Protein sim. GBank gll56889373[dbj]BAA82873.1 - (AB028944) KIAA1021 protein [Homo sapiens]		Contains protein domain (PF00122) - ATPase associated with E1-E2 ATPase	

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gll4220489 (AC006089) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52846365, 52646842, 56894075, 35896286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21908754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264368, 264288, 52644229, 56181582, 21908785, 21806786, 21908787, 21908788, 21908789, 55811957, 35895917, 265020, 265021, 60170815, 33857023, 33857109, 60431528, 18108374, 35898423, 65274791, 35695855, 264634, 60431650, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264568
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gll3875351[emb]CAB084151 - (Z96047) DY3.6 [Caenorhabditis elegans]			56181886, 35696286, 21908754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264886, 21908768, 35695917, 265020, 33857023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gll5686559[db]BAA83063.11 - (AB028034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264759, 52646317, 265011, 87188559, 264601, 18108351, 264448, 264883, 264684, 264689, 18108359, 264691, 33857023, 264692, 35695763, 264829, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84348479 (4271, 4272)	Novel Protein sim. GBank gll2662167[db]BAA237151 - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637718 (4273, 4274)	Novel Protein sim. GBank gll4884110[emb]CAB43282.11 - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264809, 33109954, 264763, 21908768, 80170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gll5174779[db]AAD40696.11 - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPass_associated	264259, 29331828, 35696052, 264908, 265006, 265017, 265018, 18108351, 264289, 21908768, 33857023, 33657109, 264628, 18108374, 35695855, 264634, 264559, 264556, 264557, 264558, 264559
2139	94843682 (4277, 4278)	Novel Protein sim. GBank gll3550821[emb]CAA771351 - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 8569542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33857023, 18108364, 55811576, 83373044, 18108385, 56526486, 264482

2140	87845655 (4279, 4280)	Novel Protein sim. GBank glj417283[gbjAAD20418] - (AC007019) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265008, 264759, 265018, 264448, 264288, 21908768, 53811857, 265021, 33857023, 27488265, 35898423, 264636, 264558, 264557, 264559, 264566
2141	79823888 (4281, 4282)		UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank glj2135786[pij]S53382 - mucin 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 28331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank glj2078483 (U43200) - antifeeze glycopeptide AFGP polypeptide precursor [Boreogadus salda]	UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264908, 264908, 264591, 265011, 87188559, 264600, 265018, 264288, 264768, 21908765, 21908767, 55811576, 35898423, 85274791, 22278002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank glj1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264909, 60433356, 264688
2147	80432911 (4293, 4294)	Novel Protein sim. GBank glj3080399[embj]CAA18718.1] - (AL022803) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264807, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank glj728837[sp]P39194[ALU7_HUMAN - III] ALU SUBFAMILY SQ WARNING ENTRY III	UNCLASSIFIED	264593
2149	87382022 (4297, 4298)	Novel Protein sim. GBank glj119883[sp]P20893[FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)]	glycoprotein	29331824, 29331828, 35688052, 264758, 87168474, 265018, 52644150, 33857109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank glj5420387[embj]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21908768, 264488
2151	95353241 (4301, 4302)	Novel Protein sim. GBank glj5689407[dbj]BAA82887.1] - (AB028958) KIAA1035 protein [Homo sapiens]		22278998, 56894075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35688052, 29331828, 264508, 264511, 60433356, 264758, 264598, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21908765, 21908768, 21908768, 265020, 60170816, 33857109, 33857182, 33857349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank glj3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	89313371 (4305, 4308)	Novel Protein sim. GBank gll4758704/rfjnp_004216, 1pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278998, 22278998, 22278999, 264259, 29331822, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265018, 264760, 264288, 264389, 264768, 264887, 264789, 52644229, 21908768, 21908788, 356985917, 33857023, 33857109, 35698585, 264631, 264632, 264635, 264636, 264638, 18108385, 264483, 264584, 264488
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gll225150/prjl1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264084, 265009, 265019, 264288, 21908787, 356985917
2155	87424072 (4308, 4310)			UNCLASSIFIED	18108392, 18108398, 22278998, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264886, 265020, 264693, 264628, 56182323
2156	84265205 (4311, 4312)	Novel Protein sim. GBank gll3970966 (ACQ04974) - spa-1- like; similar to AF026504 (PID:32555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)				264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gll1076211/pirj[S50765 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264598
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gll4650844/dbj[BAA77027.1] - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bnd	29331822, 264112, 285008, 264691, 33857023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gll2878925/dbj[BAA24826] - (AB007887) KIAA0437 [Homo sapiens]			264634
2161	87739131 (4321, 4322)				265008
2162	84318528 (4323, 4324)	Novel Protein sim. GBank gll1504006/dbj[BAA13202] - (D88968) simliarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	85274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264784, 264288, 264766, 264686, 264788, 264789, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264587
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gll3876537/emb[CAA98270] - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278998, 264093, 264683, 33857023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264585

2165	94328169 (4328, 4330)	Novel Protein sim. GBank gl 1086784 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284908, 29331830, 58182435, 285009, 21908754, 33657084, 285011, 285018, 284448, 284288, 284389, 21908765, 21908768, 21908769, 285020, 285021, 284691, 284692, 33657023, 95274820, 35695855, 284558, 60170394, 83373044, 60432113, 22278998, 66714117, 52845158, 22278994, 22278998, 66714117, 29331828, 52844045, 285018, 285019, 284389, 21908765, 21908767, 21908768, 21908769, 285021, 285022, 284693, 27488262, 35695763, 18108376, 58528486, 87168518, 284587
2168	87618934 (4331, 4332)	Novel Protein sim. GBank gl 2708522[emb CAA75816] - (Y15885) ubiquitin activating enzyme [Drosophila melanogaster]		ubiquitin	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gl 2224713[db BAA20840] - (AB002384) KIAA0388 [Homo sapiens]		UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2169	86999334 (4335, 4336)	Novel Protein sim. GBank gl 4321407[gb AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00684) - ABC transporter transmembrane region.	transport	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2170	87888937 (4337, 4338)	Novel Protein sim. GBank gl 5108521[gb AAD39741.1] - (AF10538) K-Ci catantransporter KCC4 [Homo sapiens]		UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2171	80194050 (4341, 4342)			UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2172	85452460 (4343, 4344)			UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2173	87038740 (4345, 4346)	Novel Protein sim. GBank gl 4308681[gb AAD15478] - (AC008930) R33423.1 [Homo sapiens]		UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587
2174	95003286 (4347, 4348)	Novel Protein sim. GBank gl 2483778[sp Q09456]YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5		UNCLASSIFIED	56182575, 35696268, 29331824, 29331826, 28148498, 58182435, 285008, 285009, 284592, 284593, 33657402, 33109954, 285011, 285017, 285018, 18108351, 284389, 21908764, 21908765, 21908768, 29148827, 21908769, 52844150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 284587

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi1263287 (U47855) - fibroin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35896052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 285008, 285007, 264512, 265008, 264910, 264591, 264594, 264595, 264598, 264758, 55812038, 265011, 264800, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21806788, 55811957, 35895917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35896423, 65274791, 35895855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264584, 264585, 264586, 264486, 264597
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi1728637[epiF3919]ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - Penapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35896286, 22278996, 22278999, 29331826, 29331827, 35896052, 29331828, 33656970, 29331830, 284910, 33657402, 264758, 52844298, 87188559, 265018, 284689, 21808765, 21908787, 21908789, 35895917, 52844150, 264690, 33657023, 33657109, 52845129, 33657182, 27486261, 27486262, 33657349, 18108378, 18108377, 35895855, 87168518, 60432113, 264404, 22278900, 264486 18108392, 22278997, 22278999, 284093, 33657402, 265018, 264448, 264766, 264689, 21908787, 21908788, 21908789, 265021, 33657023, 18108370, 18108374, 60432113, 222789002
2177	94128842 (4353, 4354)	Novel Protein sim. GBank gi15454072[refNP_008416.1]pSLU7 - step II splicing factor SLU7		kinase	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35895855, 22278902, 60424299, 264760, 264628, 264632
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi1473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	
2179	87316275 (4357, 4358)			UNCLASSIFIED	



2180	95351397 (4359, 4360)	Novel Protein sim. GBank gi 3122317 sp P90848 KMIH-DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	5264507, 22278994, 35698286, 22278997, 22278998, 264259, 52845090, 29331822, 29331824, 29331825, 29331826, 29331828, 33658970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21908754, 87188474, 87168559, 265017, 265018, 265019, 264783, 264682, 264683, 264684, 264288, 264686, 21908765, 21908768, 21908769, 265020, 265021, 265022, 52844150, 33657023, 33657109, 27488265, 33657349, 18108374, 35688423, 35695855, 263881, 60170394, 18108385, 56526486, 87168518, 60432113, 22278000, 264482, 264568, 264567, 264486, 29331827, 264389, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIIID 100 KD SUBUNIT (TAFII100)			
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1  - (AJ243459) proteophosphoglycan [Leishmania major]			
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873406 gb AAC77482.1  - (U17129) unknown [Rhodococcus erythropolis]			
2184	87760680 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF081346) - Edp1 protein [Mus musculus]			
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106958 gb AAD39908.1 AF11381 - (AF113815) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		inf	29331822, 29331825, 29331826, 56182435, 265011, 264885, 264886, 21908788, 18108370, 264829, 264831, 264636, 264557, 29331824, 264907, 86712502, 264757, 265018, 264288, 264692, 56526486
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2684625 emb CAA16972  - (AL021811) putative protein [Arabidopsis thaliana]		ATPase_associated	264259, 29331822, 29331824, 29331828, 56182435, 264592, 55812038, 264780, 264786, 55811957, 33657023, 55811578, 56182323, 264583
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264808, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264881, 264768, 264769, 35694917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264586, 264486
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107818 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108388, 56994075, 264259, 29331824, 29331825, 68714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22278000, 22278002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452337 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01398) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264389, 264288, 263987

2190	87639197 (4378, 4380)	Novel Protein sim. GBank gij132575jplP29315[RINI_RAT - RIBONUCLEASE INHIBITOR]		nucleaseinhib	22278998, 22278999, 28331822, 28331824, 28331826, 285008, 284910, 60170831, 55812038, 52844296, 285010, 285018, 284685, 284688, 56181562, 21908769, 35695917, 285022, 60170394, 22279000, 28331825, 28331826, 28331830, 284510, 284511, 284910, 284593, 284594, 284556, 284559, 284558
2191	95198828 (4381, 4382)	Novel Protein sim. GBank gij5327002[emb]CAB46272.1] - (Y18503) XAP-5-like protein [Homo sapiens]			
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600jplP34400[Mi10 CAEEL - MIG-10 PROTEIN]	Contains protein domain (PF00169) - PH domain		
2193	84140073 (4385, 4386)	Novel Protein sim. GBank gij5420389[emb]CAB46880.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181880, 28331825, 28331827, 284508, 284909, 285008, 284592, 60432229, 284288, 284684, 284766, 35695917, 33657023, 60431602, 60431528, 55810784, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113, 284592
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763[emb]CAA15685.1] - (AL009191) /prediction=(method:; /match=(desc:; /motif=(desc:; [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35696052, 285008, 21908754, 285017, 35695917, 285021, 285022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gij5262487[emb]CAB45889.1] - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 284259, 28331822, 66714117, 60432289, 28331827, 35696052, 28331828, 284508, 52844045, 56182435, 284510, 265007, 285008, 285009, 60433438, 55812038, 285010, 285011, 284448, 284288, 284686, 284687, 52844229, 21908765, 21908766, 21908767, 35695917, 285022, 284891, 33657023, 284693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 284636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929587[gb]AAD34044.1]AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			284768, 284769, 21908765, 21908766, 21908767, 28148827, 55811857, 35696286, 285020, 22278998, 285021, 284259, 33657023, 284693, 28331824, 35696052, 28331828, 18108370, 35695855, 284113, 285008, 284910, 60432229, 56182323, 33657402, 284758, 63373044, 21908754, 285018, 285019, 22279002, 284482, 284448, 284585, 284288, 284369
2198	88080914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953.1 [Homo sapiens]		UNCLASSIFIED	

2199	68054355 (4397, 4398)	Novel Protein sim. GBank gl 2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				284105, 284110, 284112, 284688, 55811957, 33857023, 284892, 263967, 20281071, 56528486
2200	67405385 (4399, 4400)	Novel Protein sim. GBank gl 3043634[db][BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct			28331824, 284763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gl 3913470[sp]Q57314[DPBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2]	Contains protein domain (PF00108) - short chain dehydrogenase			29331824, 35696052, 284903, 284907, 33857402, 55811386, 285017, 285018, 285019, 284288, 21906788, 35895917, 285020, 285022, 33857023, 33857108, 27488281, 18108370, 35898423, 35895855, 284555, 284556, 83373044, 87188518, 60432113
2202	91872385 (4403, 4404)	Novel Protein sim. GBank gl 5282665[emb][CAB43787.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED			284489, 284259, 29331824, 60432289, 35898052, 264905, 264909, 284592, 285017, 285018, 285019, 18108351, 284782, 284448, 284389, 284288, 264768, 21908765, 21908768, 284690, 284691, 284692, 33857109, 284634, 284636, 284555, 284639, 284558, 284559, 83373044, 18108385, 284404, 22279002, 284482
2203	87781832 (4405, 4406)	Novel Protein sim. GBank gl 172845[sp]P46828[R825_RABIT - RAS-RELATED PROTEIN RAB-25]	Contains protein domain (PF00071) - Ras family	glycoprotein		52846365, 56894075, 284259, 29331822, 29331826, 29331827, 29331828, 284910, 285010, 285011, 87168559, 285018, 285019, 284605, 284288, 21908768, 35895917, 33857023, 284892, 33857109, 35895783, 18108376, 284638, 22279000, 284566, 284567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gl 121038[sp]P28348[GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN GT], ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gl 4589480[db][BAA78768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00066) - dna_rna_bind Zinc finger, C2H2 type			18108394, 18108397, 56182575, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 284606, 285007, 285008, 285009, 60432228, 285010, 285011, 285018, 284883, 264288, 284389, 284686, 21908768, 21908769, 284690, 284691, 284893, 18108388, 55811576, 65274791, 284634, 18108381, 18108384, 60432113, 22279002, 284583, 284568, 284581
2206	20620008 (4411, 4412)	Novel Protein sim. GBank gl 4557753[ref]NP_000372.1[pmid]1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED		29331822, 56182181, 29331827, 35896052, 52844045, 285006, 285019, 56181562, 55811957, 265021, 33857023, 35895763, 35895855, 60170394, 60432113, 284568, 284606, 285019, 18108351, 21908769
2208	88100930 (4415, 4416)	Novel Protein sim. GBank gl 3986748 (AF103228) - tuftelin [Bos taurus]		struct		284112, 285009, 284691, 18108385, 18108374, 284634, 20281166

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 726837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	284603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 726837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	284685, 284686, 18108365, 22278002, 284482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA08214  - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 284092, 284094, 29331822, 68714117, 29331826, 29331828, 284907, 52844045, 265009, 60170831, 21908754, 87188559, 265017, 285018, 18108351, 284683, 18108354, 264369, 284766, 284687, 52644229, 21908765, 21908768, 21908767, 21908768, 265021, 33657109, 18108370, 18108374, 284636, 56182323, 18108384, 18108387, 87168516, 284585
2213	91218309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB48678.1  - (AJ243458) proteophosphoglycan [Leishmania major]			58182575, 22278996, 22278997, 35696052, 284805, 68712502, 284908, 284828, 58182435, 284112, 265008, 60431735, 60433438, 21908754, 265010, 285011, 285017, 265018, 265019, 18108351, 264765, 21908765, 21908768, 21908769, 265020, 265021, 284693, 284629, 263974, 263976, 18108379, 55811576, 284556, 284637, 284558, 83373044, 22278002, 284482, 284483

2214	95381453 (4427, 4428)	Novel Protein sim. GBank gij4504325[re]NP_000173.1pHADH - hydroxyacyl-Coenzyme A dehydrogenase/3-ketolacetyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52844507, 18108394, 56182575, 22278994, 22278995, 35698286, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 62645080, 28331822, 29147620, 28331824, 66714117, 28331825, 60432289, 28331826, 28331827, 35698052, 28331828, 20281100, 264509, 284907, 68712502, 264908, 28331830, 52844045, 58182435, 264510, 265006, 264511, 264512, 285007, 285008, 265009, 60170831, 264593, 60433358, 60433438, 33109954, 33657084, 52844288, 87188474, 265010, 265011, 18108351, 264448, 264682, 264763, 284288, 264687, 52844229, 264889, 21908765, 21908766, 21908767, 21908768, 21908769, 35698917, 285020, 285021, 285022, 284532, 60170815, 264690, 52844150, 264691, 33657023, 284892, 18108384, 33857109, 33657182, 27488262, 27488264, 27488265, 35695763, 18108370, 264629, 60431526, 18108374, 18108378, 55810764, 35698423, 35695855, 264634, 264636, 52844332, 264638, 264558, 60170394, 18108381, 58182323, 63373044, 18108385, 18108387, 18108388, 56528488, 87188518, 60432113, 22278002, 264482, 264564, 264565, 284566, 264809, 265008, 264555, 264558, 87188518
2215	95418208 (4428, 4430)	Novel Protein sim. GBank gij1947160 (AF000288) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614048 (4431, 4432)	Novel Protein sim. GBank gij1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]		264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gij5031707[re]NP_005503.1pGARP - glycoprotein A repetitions, predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264558
2218	85518264 (4435, 4436)	Novel Protein sim. GBank gij3878838[emb]CAA88953] - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:700719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35698423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gij1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108378

2220	95354165 (4438, 4440)	Novel Protein sim. GBank gl 4507261 ref NP_003145.1 pSTAT - elatetherin			264486, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264508, 264905, 264906, 264907, 26331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265008, 264593, 264594, 60433356, 264595, 55812038, 264758, 85658542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264764, 264368, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263976, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	86080827 (4441, 4442)	Novel Protein sim. GBank gl 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264680, 264693, 264628, 263974, 263976, 55811576, 264555, 264636, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gl 3878005 emb CAA84789  - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES... Novel Protein sim. GBank gl 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans] Novel Protein sim. GBank gl 4826524 emb CAB42852.1  - (AL040848) hypothetical protein [Homo sapiens]	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265008, 265009, 264757, 21906754, 18108351, 264693, 18108374, 18108385
2225	85749484 (4449, 4450)			transport	22278994, 22278995, 22278999, 52644045, 264600, 265019, 21906765, 21906769
2226	86878953 (4451, 4452)				264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 26148629, 26148784, 27486261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gl 806978 (U16800) - fibronectin protein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264081, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264638, 83373044, 264563
2229	88080831 (4457, 4458)	Novel Protein sim. GBank gl 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gij226154iprj 1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21908765, 21908766, 21908767, 21908769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21908754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	86060837 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328 1 [Homo sapiens]		UNCLASSIFIED	
2232	87762561 (4463, 4464)	Novel Protein sim. GBank gij5281316ipb AAD41478.1 AF133124 - transcription factor IIC63 [Homo sapiens]		transcript factor	18108394, 56182575, 22278995, 35695288, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265008, 265007, 265008, 264910, 264759, 55812038, 264803, 265018, 265019, 18108351, 264882, 264764, 264683, 264388, 264288, 264686, 264687, 264689, 21908765, 21908768, 21908767, 21908769, 29148629, 35695917, 264680, 52644150, 264881, 33657023, 264693, 18108370, 18108374, 55811578, 35695855, 264839, 18108385, 264564, 264808, 33657402, 265018, 264288, 264688, 265020, 264635, 18108385
2233	87755282 (4465, 4466)	Novel Protein sim. GBank gij4248733ipb AAD13780 - (AF109377) kIIPp [Mus musculus]			
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559ipb P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)		kinase	56182435, 264388, 264688, 21908765, 265020, 264693, 264558, 56526486
2235	91012318 (4469, 4470)	Novel Protein sim. GBank gij4972734ipb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675iprj B53814 - p20 protein - human	Contains protein domain (PF00011) - eph Hsp20/alpha crystallin family		264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264835, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264781, 264782, 264783, 264784
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734ipb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21908765, 21908768, 21908767, 21908768, 21908769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21908754, 18108387, 60432113, 22276000, 265018, 22279002, 264482, 18108351, 264288

2238	9498857 (4475, 4478)		Contains protein domain (PF00286) - Viral coat protein	264509, 264907, 264628, 264634, 264564
2239	87798688 (4477, 4478)			29331825, 265009, 264389, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4478, 4480)	Novel Protein sim. GBank gij2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	264468, 65274572, 66182375, 35698266, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 5264045, 56182435, 264511, 265007, 265008, 265009, 80433356, 80433438, 55812038, 21908754, 33657084, 55811388, 265018, 265019, 18108351, 264683, 264288, 264788, 264687, 264688, 264769, 21908765, 21908768, 21908769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35698423, 35695855, 87188518, 22278000
2241	80031951 (4481, 4482)	Novel Protein sim. GBank	UNCLASSIFIED	264893, 264829
2242	81228075 (4483, 4484)	Novel Protein sim. GBank gij2484312 [spj70541] E2BQ, RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21908754, 265010, 265011, 265017, 265018, 265019, 264448, 264389, 264288, 52644228, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 27486284, 18108374, 35695855, 264834, 264637, 56182323, 83373044, 56526486, 87188518, 264584
2243	78802028 (4485, 4486)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	UNCLASSIFIED	264604
2245	95318545 (4489, 4490)		Contains protein domain (PF00534) - Glycosyl transferases group 1	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 80433438, 264758, 21908754, 265011, 264603, 264764, 264687, 21908767, 21908768, 21908769, 55811957, 265022, 264691, 264629, 35698423, 264638, 18108387, 80432113, 22279000, 22279002, 264568



2246	94846710 (4491, 4492)	Novel Protein sim. GBank gl 4996086[db][BAA78326.1] - (ABD28089) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278985, 35688288, 22278996, 22278997, 22278999, 264259, 35686052, 264108, 264905, 264907, 265006, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21908765, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265022, 27488264, 18108370, 18108374, 65274781, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gl 854065[emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52845158, 52846385, 52845080, 35686052, 33656970, 52846317, 33857084, 265017, 21908768, 21908769, 35695917, 33857108, 52845129, 33857182, 27486261, 27486262, 33657349, 27486285, 18108387
2248	95412888 (4495, 4496)	Novel Protein sim. GBank gl 4756502[ref][NP_004123.1]pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	264488, 264259, 264907, 26331830, 264909, 265007, 265009, 264595, 21908754, 65274444, 264603, 265019, 264762, 264448, 264288, 264689, 21908768, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264488
2249	94885662 (4497, 4498)	Novel Protein sim. GBank gl 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - eph		264766, 264628, 264636, 264637
2250	78827508 (4499, 4500)	Novel Protein sim. GBank gl 3738140[emb][CAA21241] - (AL031852) velyl-tma synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	284908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gl 3218467[emb][CAA07090.1] - (AJ008529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	284259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264780, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264558, 264557, 264558, 264559, 264586
2252	87735887 (4503, 4504)	Novel Protein sim. GBank gl 4929325[gb][AAD33953.1]AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - synthase ATP synthase subunit D		264082, 264094, 264259, 26331822, 66714117, 26331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433358, 265010, 18108351, 21908767, 21908768, 264691, 263974, 263977, 264488, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gij4502847[re]NP_001271.1pCIRB - cold Inducible RNA-binding protein	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264569, 18108394, 18108398, 56182575, 58994075, 35698286, 22278999, 264094, 60432049, 26331822, 29331824, 29331825, 29331826, 60432268, 29331827, 29331828, 35698052, 264108, 264508, 264508, 264806, 264907, 29331830, 66712502, 264908, 264909, 264510, 265008, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433358, 60433438, 264758, 65658542, 265010, 265011, 87188558, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 21908765, 21908767, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263989, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35698423, 35698555, 264630, 264634, 264635, 264638, 264556, 263981, 264638, 56182323, 60170394, 264556, 18108381, 18108382, 83373044, 18108385, 87188518, 60432113, 22279002, 264482, 264564, 264565, 264486, 264557, 18108391
2255	91010548 (4509, 4510)	Novel Protein sim. GBank gij5541865[emb]CAB51072.1] - (AL098656) hypothetical protein [Homo sapiens]	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	63274572, 56182575, 22278997, 22278999, 264258, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264908, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264503, 264595, 21908754, 33109954, 87188474, 265011, 265017, 265019, 264682, 264764, 264369, 264288, 264768, 264685, 264886, 264768, 21908765, 21908766, 21908768, 21908769, 265020, 60170815, 52844150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264638, 52844332, 56182323, 22279000, 22279002, 264768, 264688, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gij3327174[id]BAA31655] - (AB014580) KIAA0880 protein [Homo sapiens]		UNCLASSIFIED	
2257	80086235 (4513, 4514)			UNCLASSIFIED	22278998, 22278999, 264681, 21908765, 21908768, 264587
2258	88090518 (4515, 4516)	Novel Protein sim. GBank gij3025446 (AC004628) - R32184_2 [Homo sapiens]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2258	95384155 (4517, 4518)	Novel Protein sim. GBank gl 4884140 emb CAB43276.1  - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108386, 65274572, 56182575, 22278897, 22278998, 264258, 28331822, 29331827, 284905, 66712502, 284908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87186559, 18108351, 264448, 284883, 264288, 264369, 56181562, 265021, 60170615, 264850, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22278000, 22278002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gl 3080863 (AC004614) - similar to f-espandin proteins AB008086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 284908, 35698423, 284511, 284635, 55812038, 264758, 265018, 265019, 264805, 284760, 284583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gl 3334526 emb CAA18138  - (AL021308) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91638282 (4523, 4524)	Novel Protein sim. GBank gl 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278998, 28331822, 28331825, 80432288, 29331827, 35698052, 264508, 66712502, 52844045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265018, 264288, 264389, 21908785, 21908787, 55811857, 35695917, 52844150, 33657023, 33657109, 55811578, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gl 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 284907, 264828, 52844150, 18108381, 284693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gl 1657601 (U86220) - unknown [Nannocyathus exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 284905, 264509, 284906, 284907, 284908, 284909, 35695855, 284510, 264511, 264512, 265007, 265009, 264638, 264639, 284757, 284758, 18108385, 265011, 284780, 284584, 284565, 264784, 264566, 264486, 284788
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gl 477072 pir J48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	284689, 264910, 264784
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gl 3150478 (AF087212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 284448, 284883, 284288, 264689, 21908765, 21908788, 35695917, 265021, 18108374, 284638, 22278000, 22278002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gl[3560229]emb[CAA20687.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35698286, 264259, 29331824, 29331825, 35698052, 29331828, 284805, 284509, 284907, 284908, 284909, 284512, 285009, 284910, 284593, 33657402, 285010, 285018, 284762, 284448, 284288, 284389, 284768, 32644229, 35695917, 284691, 33657023, 18108392, 33657108, 35698423, 284634, 18108381, 87188518, 284588
2268	85683867 (4535, 4536)	Novel Protein sim. GBank gl[728832]ep[39189]ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	cadherin	284488, 284259, 284508, 284595, 285010, 285017, 284768, 18108385, 284486
2269	86177977 (4537, 4538)	Novel Protein sim. GBank gl[103418]pr[1]ST1785 - Tcd37 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED	56182575, 60432049, 265007, 265009, 284591, 87188559, 284805, 18108351, 21906764, 265020, 284628, 60431528, 284638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)			284763
2271	91010392 (4541, 4542)		cyto450	284909, 56182435, 265008, 55812038, 55811957, 33657023, 284693, 33657109, 55810784, 55811578, 56182323
2272	84208220 (4543, 4544)		UNCLASSIFIED	284905, 284908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gl[4176370]AC005059 - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin	52645156, 22278996, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 28331826, 29331827, 35698052, 284909, 285006, 284593, 60433438, 21908754, 285018, 284889, 21908765, 21908766, 21906767, 21908769, 285021, 285022, 60170815, 284691, 33657023, 284693, 33657109, 27488284, 18108376, 35698423, 35695855, 284630, 52644332, 284558, 56182323, 22278902
2274	91840217 (4547, 4548)	Novel Protein sim. GBank gl[1480112]emb[CAA67981] - (X99842) HP1-8P74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 284908, 52644045, 284511, 285008, 265009, 80170831, 284591, 21908754, 33109954, 285011, 265016, 18108351, 284448, 284288, 284684, 284768, 21908765, 21908768, 21908767, 21908768, 52644150, 284693, 18108364, 35695763, 18108374, 35698423, 284634, 284557, 284638, 52644332, 83373044, 18108385, 56528488, 87188518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gl[3165408]AC004755 - (fos37502_2 [Homo sapiens])	Contains protein domain (PF00122) - E1-E2 ATPase	
2276	11287447 (4551, 4552)		transport	
			UNCLASSIFIED	284555, 284556

2277	18084123 (4553, 4554)	Novel Protein sim. GBank gij280079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF005580) - Leucine Rich Repeat	glycoprotein	2227899, 35696052, 265008, 285019, 284388, 285020, 265022, 59810784, 284404, 22279002
2278	94133079 (4555, 4556)	Novel Protein sim. GBank gij2818702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278987, 28331828, 60433358, 60433438, 21908754, 265018, 33657023, 284639, 83373044, 284565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gij119714 [sp]P13983 [EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)]		UNCLASSIFIED	284766, 284565
2280	84238723 (4559, 4560)				
2281	95293048 (4581, 4582)	Novel Protein sim. GBank gij424029 [dbj]BAA74928.1] - (A8020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 285010, 285019, 265020, 284092, 284259, 29331822, 29331824, 29331826, 35696052, 284107, 284808, 284908, 52844045, 265006, 33657402, 60433358, 264758, 265011, 285019, 284681, 284683, 284684, 284686, 21908785, 21908787, 21908788, 21908789, 60170815, 284690, 52844150, 18108382, 284692, 18108388, 18108374, 263978, 284631, 18108381, 284558, 18108385, 59528486, 22279000, 284566, 284567
2282	87602828 (4583, 4584)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	284488, 284259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21908787, 21908788, 55811957, 33657023, 52845129, 33657109, 33657182, 27488282, 283972, 55811578, 87168518, 20281159, 80424178, 58182575, 22278994, 35696286, 22278997, 22278999, 28331822, 29331824, 58182181, 29331825, 29331827, 35696052, 29148499, 284905, 68712502, 284908, 265007, 265009, 60432229, 284593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 285019, 55811150, 284683, 264369, 284288, 284898, 21908785, 21908787, 21908788, 29148627, 21908789, 55811957, 265020, 285022, 33657182, 27488281, 18108370, 284628, 18108374, 55810784, 18108378, 55811578, 35696423, 35695855, 284630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22278000, 284482, 284587
2283	95322368 (4565, 4566)	Novel Protein sim. GBank gij2495729 [sp]Q82558 [Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)]		UNCLASSIFIED	

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gi2498787 sp Q84311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAAD)			60424179, 52844507, 18108394, 52846842, 22278994, 35698286, 22278986, 22278987, 22278989, 284259, 80432048, 28331822, 28331824, 28331825, 60432289, 28331826, 28331827, 35698052, 28331830, 52844045, 56182435, 33657402, 60433438, 33109954, 21908754, 85658542, 87188559, 285018, 285019, 55811150, 284682, 284389, 21908765, 21908768, 21908787, 21908788, 21908789, 55811957, 35695917, 285020, 285021, 60170815, 33657023, 33657182, 27488262, 27488264, 27488265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 284482, 284584
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gi3342234 (U83909) - nuclear antigen EBNA-1 (Carcopilline herpesvirus 15)		collagen	35696052, 284905, 284907, 284908, 284909, 284512, 285009, 284910, 284595, 284780, 18108351, 284682, 284763, 284685, 284768, 284686, 284768, 284683, 284628, 35695855, 284631, 284634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 58182435, 60170831, 284591, 60432229, 284592, 284593, 284594, 284595, 55812038, 284596, 87168474, 35695917, 284692, 55811578, 284555, 284557
2287	82866896 (4573, 4574)	Novel Protein sim. GBank gi630805 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01381) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	284682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	22278995, 56994075, 22278997, 22278999, 284259, 60432289, 284508, 284512, 285008, 33657402, 285017, 285018, 285019, 18108351, 284448, 21908765, 21908768, 21908767, 21908768, 33657023, 284557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi2887487 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	284683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi3253120 (AC005175) - R31449_3 [Homo sapiens]		strudl	18108394, 284907, 285008, 285009, 33109954, 52846317, 285010, 18108351, 284681, 284688, 284692, 18108370, 18108374, 18108385

2292	94328634 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1  - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	58182575, 35886286, 56894075, 29331824, 29331825, 35886052, 58182435, 60433438, 55812038, 33108954, 87188474, 87188559, 265018, 18108351, 264763, 264448, 264369, 264288, 58181592, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33857023, 264693, 65274620, 33857109, 27486284, 264829, 53810764, 55811576, 35885855, 58182323, 58528486, 87188518, 22278000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF088921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - sinut Leucine Rich Repeat		264488, 18108397, 35886286, 264092, 264259, 29331822, 29331826, 264806, 264908, 264511, 264512, 265009, 264610, 18108351, 264764, 264369, 264288, 264885, 264766, 265020, 265022, 264534, 35886423, 264631, 264637, 18108381, 58182323, 264639, 18108385, 264404, 264563, 264565, 22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35886052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33857109, 18108376, 35886423, 35885855, 264634, 22279000, 22279002, 264363, 264488
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2082680 (U88884) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - nuclease Exonuclease		22278998, 60432289, 264682, 264683, 263974, 263978
2295	95312200 (4589, 4590)			UNCLASSIFIED	264488, 65274572, 58182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35886052, 264907, 264908, 52644045, 58182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33857402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264768, 21906765, 21906767, 21906768, 21906769, 55811857, 265020, 265021, 264690, 264691, 33857023, 264692, 264693, 33857109, 55811576, 58182323, 80170394, 83373044, 18108385, 58528486, 264564, 264488
2296	80030781 (4591, 4592)				transcriptfactor
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5888501 db BAA83034.1  - (AB028005) KIAA1082 protein [Homo sapiens]			

2298	85312207 (4595, 4598)	Novel Protein sim. GBank gl 3875051 emb CAB02849  - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D85564 comes from this gene; cDNA EST EMBL:D89048 comes from this gene; cDNA EST yk368b12.3 comes from this gene; cDNA EST yk368b12.5 comes from this gene ...	collagen	60424179, 56181686, 22278995, 35696268, 22278998, 22278998, 22278999, 264480, 264259, 29331822, 29331824, 66714117, 60424289, 35696052, 29331828, 66712502, 56182435, 264510, 265008, 60433438, 21908754, 33109954, 55811388, 265010, 265018, 55811150, 264782, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21908767, 29148629, 55811957, 29148784, 35695917, 265020, 18108382, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22279000, 264482, 264587, 264488
2299	80193720 (4597, 4598)		UNCLASSIFIED	264369
2300	94124348 (4599, 4600)	Novel Protein sim. GBank gl 2443888 (AC002284) - Unknown protein [Arabidopsis thaliana]		264488, 22278998, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168558, 264600, 265018, 264760, 264782, 18108351, 264764, 264788, 264789, 21908768, 21908767, 35695917, 265021, 264691, 33657023, 35695783, 18108370, 18108374, 35696423, 35695855, 264631, 264638, 264638, 18108385, 22279002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gl 2143837 pir l 84505 - calcium-dependent actin-binding protein - rat	struct	264608, 264758, 265017, 21908765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gl 2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gl 4884194 emb CAB43220.1  - (AL049946) hypothetical protein [Homo sapiens]	struct	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264782, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gl 2484162 p Q10005 YRY1_CAEEL - HYPOTHETICAL 39.8 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	UNCLASSIFIED	264259, 29331824, 21908767, 33657182, 33657349
2305	90835811 (4609, 4610)	Novel Protein sim. GBank gl 4972688 gb AAD34738.1  - (AF132150) unknown [Drosophila melanogaster]		65274572, 22278998, 264908, 265006, 21908769, 264681, 264488



2308	95334940 (4611, 4612)	Novel Protein sim. GBank gi 4929595 gb AAD34043.1 AF15180 - (AF15180) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264486, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33857402, 21906754, 85698542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264768, 21908785, 21908766, 21908787, 21908768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35698423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486
2307	79415283 (4613, 4614)	Novel Protein sim. GBank gi 4759732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4759732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		synthase	35698286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21908754, 264288, 264680, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070  - (Z99842) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72844 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432048, 29331822, 29331826, 60432289, 68712502, 60432228, 60433356, 60433436, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21908766, 21908768, 265020, 264691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi 2137337 pir j148281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir j148281 - gene mCBP protein - mouse		transcriptfactor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265008, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264686, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35698423, 20281071, 264632, 264636, 18108385, 18108387, 87168516, 22278000, 264563, 264486

2312	87548881 (4823, 4824)	Novel Protein sim. GBank gll2811284 (AC002550) - Unknown gene product [Homo sapiens]		56182575, 56994075, 35686286, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52844045, 60432228, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52844228, 21906765, 21906768, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486281, 27486284, 35686423, 35685855, 18108385, 22278990, 22278992, 263981
2313	80042533 (4825, 4828)	Novel Protein sim. GBank gll3043626[db][BAA25477] - (AB011123) KIAA0551 protein [Homo sapiens]		52844507, 52846365, 52848842, 22278996, 22278997, 22278998, 264259, 52845080, 29331822, 29331824, 60432228, 29331826, 29331827, 29331828, 35686052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906768, 21906769, 35685917, 52844150, 33657023, 33657109, 52845129, 33657349, 35685763, 18108374, 35686423, 35685855, 52844332, 22278990, 22278992, 264563, 264567
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gll5598714[emb][CAB51401.1] - (AL035398) dJ79817.2 (CGI-51) [Homo sapiens]	UNCLASSIFIED	52844507, 52846365, 52848842, 22278996, 22278997, 22278998, 264259, 52845080, 29331822, 29331824, 60432228, 29331826, 29331827, 29331828, 35686052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906768, 21906769, 35685917, 52844150, 33657023, 33657109, 52845129, 33657349, 35685763, 18108374, 35686423, 35685855, 52844332, 22278990, 22278992, 264563, 264567
2315	80430119 (4629, 4630)		UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385, 52844507, 52845156, 52846365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 35686052, 29331828, 284906, 264807, 29331830, 52844045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906794, 52846317, 33109954, 33657084, 52844286, 87168474, 265010, 87168558, 265017, 265018, 265019, 264681, 264783, 264448, 264683, 264389, 52844229, 21906764, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 35685917, 265020, 265021, 52844150, 33657023, 18108362, 52845129, 33657182, 33657349, 35685763, 18108370, 18108376, 35686423, 35685655, 264631, 264556, 52844332, 83373044, 18108385, 18108387, 87168518, 60432113, 22278990, 264566, 264567
2316	94312181 (4631, 4632)	Novel Protein sim. GBank gll5531827[gb][AAD44488.1] - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain	52844507, 52846365, 52848842, 22278996, 22278997, 22278998, 264259, 52845080, 29331822, 29331824, 60432228, 29331826, 29331827, 29331828, 35686052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906768, 21906769, 35685917, 52844150, 33657023, 33657109, 52845129, 33657349, 35685763, 18108374, 35686423, 35685855, 52844332, 22278990, 22278992, 264563, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 284910, 60432229, 284686, 264687, 264688, 264689, 284558, 18108385
2318	79698979 (4635, 4636)			UNCLASSIFIED	285006, 264910
2319	95101781 (4637, 4638)			UNCLASSIFIED	264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 264259, 52845080, 26331825, 26331826, 26331827, 26331828, 26331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21808754, 52644286, 87188474, 265011, 87188559, 265017, 265018, 265019, 18108351, 284448, 18108354, 264288, 264369, 52644228, 21808764, 21808765, 21808766, 21808767, 21808768, 21808769, 265021, 265022, 52644150, 33657023, 52845129, 33837109, 27486284, 33857349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 63373044, 18108385, 56526486, 87188518, 264584, 264585, 264586
2320	91822428 (4639, 4640)			kinase	22278994, 60432049, 60432289, 26331827, 264511, 265008, 52846317, 265017, 265019, 21808765, 18108372, 18108387, 22278902, 264486, 264687, 18108394, 264689
2321	94320377 (4641, 4642)	Novel Protein sim. GBank g 1728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII Novel Protein sim. GBank g 3673837 emb CAB02700  - (261029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154): cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01082 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...		UNCLASSIFIED	21808765, 18108397, 18108398, 21808767, 21808768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 284555, 264636, 264558, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264689, 60433356, 264559, 60433438, 26331824, 18108365, 18108346, 18108384, 26331825, 18108385, 33109954, 26331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 284448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87603165 (4643, 4644)	Novel Protein sim. GBank g 5678957 emb CAB51685.1  - (AL109830) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264838

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi2494162 epiQ10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00228) - DnaJ domain	eph	22278984, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21908754, 85658542, 87168474, 265011, 87168559, 265017, 285019, 264780, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21908765, 21908767, 21908768, 55811957, 35695917, 265021, 33657023, 18108382, 27468262, 55811578, 264631, 264555, 83373044, 87168518, 60432113, 22279002
2324	86633607 (4647, 4648)				264532, 264593, 265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi15419865 embjCAB48377.1  - [AL098732] hypothetical protein [Homo sapiens]		ATPase-associated	265020
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi231885 spP29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00087) - Cytochrome P450	cyto450	265006, 264796, 35695855, 56182323
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi14240227 dbjBAA74892.1  - [AB020678] KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]		UNCLASSIFIED	264259, 264508, 264905, 264908, 264907, 264908, 265007, 264512, 264810, 264758, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264636, 264639, 264486
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi1169343 epiP42209 DIF6_MOUSE - DIFF8 PROTEIN	Contains protein domain (PF00735) - Cell division protein	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264892, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2330	87333398 (4659, 4660)			UNCLASSIFIED	265017, 264695, 60432113, 264088
2331	86680463 (4661, 4662)	Novel Protein sim. GBank gi5678136 b AAD46674.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi12104452 embjCAB08779  - (Z95397) unknown [Schizosaccharomyces pombe]		ATPase-associated	35696265, 22278998, 29331824, 60424269, 265006, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264566
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi13879985 embjCAA92891.1  - (Z89318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:CO7930 comes from this gene; cDNA EST EMBL:CO9483 comes from this gene; cDNA EST yk41568.3 comes from this gene; cDNA EST yk41568.5 comes from this gene; cDNA EST...		UNCLASSIFIED	56182575, 56994075, 26331826, 26331828, 264107, 33657402, 87168559, 264693, 35695917, 265021, 33657023, 263976
2334	94318768 (4667, 4668)	Novel Protein sim. GBank gi14966270 gb AAB52261.2  - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	56182575, 29331825, 21908768, 264636, 83373044

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gl 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00812) - struct	18108351, 21906769, 264555
2336	95186121 (4671, 4672)	Novel Protein sim. GBank gl 1929056 emb CAA72805  - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	kinase	264807, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gl 4495063 emb CAB39181.1  - (Z85988) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED	35698286, 22278999, 56182181, 29331825, 60424289, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906788, 35695917, 264891, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gl 2224689 db BAA20829  - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	18108394, 28331822, 66714117, 60432289, 264808, 56182435, 265009, 60433438, 264586, 265010, 265019, 18108354, 264288, 264389, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gl 3873550 emb CAA22127  - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35698286, 264592, 264369, 264661, 264558
2340	90937716 (4679, 4680)			
2341	87752681 (4681, 4682)			65274572, 22278994, 35698286, 22278997, 22278999, 264259, 29331822, 60432289, 29331828, 26331830, 265009, 33657402, 33109954, 265017, 265018, 264788, 264685, 21906789, 35695917, 264691, 264692, 35696423, 87188518, 22279000
2342	95334966 (4683, 4684)	Novel Protein sim. GBank gl 3874563 emb CAB02797  - (Z81042) similar to Yeast hypothetical protein YEY8 like; cDNA EST yk208h5.3 comes from this gene; cDNA EST yk208h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - kinase	264259, 264808, 264909, 264682, 22279000, 264488, 65274572, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331828, 60432289, 35698052, 264905, 264509, 29331830, 265008, 60170831, 60432229, 60433356, 87188474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21908766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810784, 35696423, 55811576, 264556, 264558, 18108395, 60432113, 264553, 264584, 264585, 264568, 264587, 264907, 264512, 265011, 264683
2343	87754448 (4685, 4686)	Novel Protein sim. GBank gl 492974 gb AAD34131.1 AF15189 - (AF15189) CGI-138 protein [Homo sapiens]	UNCLASSIFIED	
2344	79953198 (4687, 4688)		UNCLASSIFIED	264758
2345	94319789 (4689, 4690)	Novel Protein sim. GBank gl 2508307 sp P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	264488, 264259, 66712502, 264759, 83373044, 264586

2348	84131820 (4691, 4692)	Novel Protein sim. GBank gll1255411 (U53153) - one short region of weak similarity to <i>S. cerevisiae</i> protease A inhibitor 3 (SP-P01094) and another short region of weak similarity to <i>S. cerevisiae</i> glucose repression mediator protein (SP-P14922) [ <i>Caenorhabditis elegans</i> ]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35698286, 22278998, 264259, 35698052, 29331828, 33657402, 60433396, 33108954, 87168559, 264603, 265019, 18108351, 264881, 264686, 21908768, 285021, 33657109, 55811576, 35698585, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811576
2348	85198133 (4695, 4696)	Novel Protein sim. GBank gll1928056[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [ <i>Lycopersicon esculentum</i> ]		kinase	18108394, 35698286, 264259, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264286, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35698423, 264631, 264635, 264638, 264637, 264638, 264639, 83373044, 18108385, 264587, 264488
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gll4884108[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35698052, 29146499, 264909, 264369
2350	88280594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33108954, 21908754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21908768, 21908767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	86868042 (4701, 4702)	Novel Protein sim. GBank gll728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY III		kinase	56182575, 264909, 265006, 264558
2352	87337198 (4703, 4704)	Novel Protein sim. GBank gll731637[sp]P38780[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gll1346955[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337198 (4707, 4708)	Novel Protein sim. GBank gll731637[sp]P38780[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	81638788 (4708, 4710)	Novel Protein sim. GBank gl 4938503 emb CAB43881.1  - (AL078485) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - dna_ma_bind RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	56994075, 22278996, 35686286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 284905, 284908, 265008, 264758, 87188474, 265010, 265017, 264687, 21908765, 21908767, 21908769, 264691, 264692, 263987, 18108370, 87188518, 22278000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gl 5138320 gb AAC0377.1  - (AF092135) PTD014 [Homo sapiens]		52844507, 22278995, 35686286, 22278996, 22278997, 22278998, 22278999, 284259, 28331824, 66714117, 28331825, 60432289, 35686052, 28331828, 284908, 66712502, 284512, 265007, 265008, 60170831, 60432229, 60433358, 60433438, 264758, 52846317, 33109854, 21908754, 59811386, 87188474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264389, 264288, 264686, 264768, 21908785, 21908768, 21908767, 21908768, 21908768, 265021, 60170819, 33857109, 27486284, 35695783, 55810764, 18108378, 35698423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 58526488, 284404, 60432113, 22279000, 264482, 264563, 264568, 264488, 284587
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gl 4928741 gb AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]	UNCLASSIFIED	284488, 264769, 18108394, 264258, 29331822, 18108370, 18108374, 264610, 285017, 264482, 264563, 264762, 264565, 264568, 264389, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gl 4218005 AC008135  - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	UNCLASSIFIED	22278997, 22278999, 284509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833988, 18108374, 264556, 18108385, 264482
2359	87755858 (4717, 4718)	Novel Protein sim. GBank gl 1086830 UA1264  - coded for by C. elegans cDNA yk208.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g8.5; coded for by C. elegans cDNA yk208.5; coded for by C. elegans cDNA yk18g12....	UNCLASSIFIED	35686286, 22278998, 284905, 264511, 265007, 265008, 60433438, 264288, 264686, 21908768, 265020, 264692, 35695855, 264558, 56528486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gl 3881545 emb CAA93779  - (Z68804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	22278997, 28331826, 263981, 22278000
2361	84232181 (4721, 4722)	Novel Protein sim. GBank gl 748487 U23514  - No definition line found [Caenorhabditis elegans]		22278995, 22278999, 264512, 265009, 264757, 21908785, 65274820, 18108370, 60431528, 18108374, 264635, 60170394, 284482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gi1171083 sp P19708 MYSB.ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278898, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264862, 264883, 264369, 21908765, 21908768, 21908768, 60432113, 22279000, 22278002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gi1854085 emb CAA58337  - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gi15639830 gb AAD45886.1 AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00369) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278996, 56994075, 35698286, 22278997, 22278998, 264259, 66714117, 29331825, 35698052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21908754, 87168474, 265010, 87168558, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264786, 18108358, 264689, 18108359, 21908765, 21908766, 21908767, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35698423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486, 22278996, 22278998, 22278999, 264907, 264609, 264910, 33657402, 264758, 264600, 264786, 264687, 264689, 21908768, 21908767, 21908768, 21908769, 265021, 33657023, 33657109, 83373044, 264556, 52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264768, 264689, 21908766, 21908769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264566
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gi1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278996, 22278998, 22278999, 264907, 264609, 264910, 33657402, 264758, 264600, 264786, 264687, 264689, 21908768, 21908767, 21908768, 21908769, 265021, 33657023, 33657109, 83373044, 264556, 52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264768, 264689, 21908766, 21908769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gi1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35698286, 21908768, 56810764, 65274781, 264567
2368	94322190 (4735, 4736)				264628



2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5380901[dbj BAA02158.1] - (AB020343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52844507, 52848842, 35696286, 264092, 264094, 52845080, 35696052, 264107, 29331830, 52844045, 285008, 285007, 285009, 52844298, 52844229, 264889, 21908765, 21908768, 35695917, 285020, 52844150, 283987, 33857109, 27486285, 35695763, 18108370, 263974, 18108374, 18108378, 52844332, 283981, 18108385, 264508, 264908, 284598
2370	79804120 (4739, 4740)			UNCLASSIFIED	264369
2371	57280408 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87842413 (4743, 4744)	Novel Protein sim. GBank gij4588582[dbj BAA78813.1] - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	29331826, 285010, 285019, 35695917, 284634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij5105131[dbj BAA0445.1] - (AF000061) 248aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - UNCLASSIFIED 3' exoribonuclease family	UNCLASSIFIED	285008, 265007, 265008, 265009, 285011, 264788, 35695917, 35695855, 263981, 264557, 264585
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij1331115[sp P47758]SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	60432049, 29331824, 264907, 52844045, 284512, 60433358, 21908754, 52844298, 87188559, 284448, 21908765, 21908768, 21908769, 33857023, 18108368, 55811578, 52844332
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1331115[sp P47758]SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	284259, 29331830, 264908, 264910, 265009, 60433438, 21908754, 265017, 265018, 285019, 264882, 264288, 284685, 21908767, 283972, 35695855, 87168518, 60432113
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2845435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	284095, 29331822, 22278997, 22278999, 66714117, 29331825, 29331826, 29331828, 33856970, 28148498, 29148499, 284508, 285008, 285007, 285008, 285009, 60170831, 285010, 265011, 265018, 55811150, 18108351, 284764, 264288, 21908767, 21908768, 29148627, 29148629, 265021, 33857023, 33857109, 18108370, 18108374, 18108379, 35696423, 284558, 83373044, 18108385, 18108388, 56528486, 22279000, 22279002, 284593
2377	95319889 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb AAD41238.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 28331826, 80432289, 29331827, 56182435, 264510, 285009, 60433356, 87168474, 285011, 285018, 264288, 21908765, 33857023, 264557, 56182323, 83373044, 18108385, 22279002, 284482
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U00942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	285017, 264288, 21908768
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	

2380	88923062 (4759, 4760)	Novel Protein sim. GBank gi 4502839 ref NP_001845.1 pcCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	284908, 284910, 285011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi 4455809 emb CAC38555  - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR/Romalin Organization Modifier) domain	helicase	58182575, 284081, 284093, 284259, 29331825, 284105, 284908, 80433356, 21908784, 285017, 285019, 284883, 284288, 284885, 284688, 284687, 284691, 284692, 284693, 59811578, 284638, 284597 29331824, 60432289, 284905, 284596, 21908784, 284789, 285022, 284693, 283987, 33657109, 284629, 284831, 284558, 83373044, 60432113, 284482 285009, 21908785, 21908788
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276  - (AF119716) dMI-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 db BAA19005  - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	
2384	95354768 (4767, 4768)	Novel Protein sim. GBank gi 2482851 (AF018252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	struct	284488, 52844507, 52845158, 52846385, 35898286, 22278999, 52845080, 29331824, 29331828, 35898052, 29331828, 284906, 284828, 52844045, 285008, 285008, 285009, 33109954, 33657084, 52844286, 285011, 285017, 285018, 284883, 52844229, 21908785, 21908787, 21908788, 285020, 52844150, 33857023, 284893, 65274820, 52845128, 33857109, 33857182, 27488281, 27488282, 27488284, 33857349, 27488285, 35895783, 18108374, 35895855, 284634, 284555, 284558, 284557, 52844332, 284558, 284559, 18108385, 22278900, 22279002 284488, 52844507, 52845158, 284887, 52846385, 22278995, 22278998, 22278997, 22278999, 284289, 52845080, 29331822, 29331828, 35898052, 52844045, 285008, 285007, 285008, 285009, 284910, 80432228, 80433356, 52846317, 21908784, 285018, 284448, 284683, 284686, 284687, 284689, 21908785, 21908786, 21908787, 21908789, 55811857, 285021, 285022, 284690, 284691, 284692, 65274620, 33657109, 18108370, 284631, 52844332, 22279000, 22279002, 284563, 284585, 284587 284488, 22278995, 22278996, 22278997, 284259, 28148498, 284112, 284511, 80170831, 60432228, 284595, 80433438, 87188474, 87188559, 284682, 21908765, 21908768, 21908767, 21908769, 28148828, 35895917, 285021, 284690, 33657109, 284628, 18108376, 83373044, 60432113, 22278900, 284564, 284566, 284487
2385	95419485 (4769, 4770)			UNCLASSIFIED	
2386	94742648 (4771, 4772)	Novel Protein sim. GBank gi 4828888 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	

2387	14987890 (4773, 4774)		UNCLASSIFIED	284634
2388	11424604 (4775, 4776)		UNCLASSIFIED	284595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gll4758058[ref]NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	284488, 22278998, 22278999, 284509, 284895, 284908, 284907, 284908, 284909, 285008, 284511, 284512, 284810, 284591, 21908754, 284601, 284604, 284761, 18108351, 284784, 284288, 284766, 284768, 284789, 21908765, 21908768, 284692, 284693, 35898423, 284635, 284636, 284555, 83373044, 22278000, 284488
2390	94320912 (4776, 4780)	Novel Protein sim. GBank gll1644239[dbj]BAA12223] - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	52844507, 56182575, 22278995, 35898286, 22278996, 22278997, 22278998, 29331822, 29331825, 29331826, 35898052, 284905, 52844045, 285008, 284758, 284759, 33108954, 52844296, 85658542, 285011, 265017, 285018, 284605, 52844229, 21908765, 21908767, 21908768, 21908769, 35895917, 52844150, 33857023, 33857109, 33857349, 35895763, 18108370, 18108374, 18108376, 35898423, 35895855, 284555, 52844332, 56182323, 60170394, 83373044, 58528486
2391	80036184 (4781, 4782)		UNCLASSIFIED	263978
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gll4240169[dbj]BAA74863.1] - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	35898286, 35898052, 284508, 284905, 284509, 284906, 284907, 284908, 284909, 284510, 284511, 284512, 284910, 265009, 284591, 284758, 284800, 284604, 284782, 284448, 284784, 284369, 284766, 284788, 284789, 284889, 35895917, 284628, 18108374, 283978, 35898423, 35895855, 284631, 284634, 284635, 284636, 284637, 284638, 60170394, 284639, 284565, 264486

2393	95302633 (4785, 4788)	Novel Protein sim. GBank gjk4506867[refINP_000983.1]pRPLP - ribosomal protein, large, PO	Contains protein domain (PF00488) - Ribosomal protein L10	ribosomalprot	18108392, 60424178, 284489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278998, 22278997, 22278998, 284093, 60432049, 284259, 29331822, 29147620, 20281098, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 284508, 284509, 284905, 284907, 284908, 66712502, 52844045, 284828, 284909, 56182435, 284112, 284113, 284510, 285008, 284511, 285007, 285008, 285009, 284910, 284591, 284593, 60433356, 284595, 60433438, 52846317, 33109954, 21908754, 55811386, 285010, 285011, 285017, 285018, 285019, 284881, 284762, 18108351, 284763, 284882, 284764, 284883, 284389, 284288, 18108354, 284766, 284886, 284687, 284688, 284689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29148629, 29148794, 35695917, 285021, 285022, 33657023, 284692, 284693, 18108384, 33657109, 18108388, 27486281, 27486282, 33657349, 35685763, 18108370, 263972, 284829, 18108374, 263977, 18108376, 263978, 55810784, 35696423, 35695855, 284634, 60431850, 284555, 284637, 284557, 263981, 284559, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 285008, 284592, 55811386, 285010, 285011, 285017, 285019, 284448, 284683, 284288, 21908765, 21908768, 21908769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108375, 55810764, 55811576, 35696423, 60170394, 18108385, 284584, 284586, 284587
2394	94323268 (4787, 4788)	Novel Protein sim. GBank gjk4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99878 (P1D:G3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gjk512756[gb AAD47836.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_ma_bind	284259, 29331824, 284910, 284288, 285021, 83373044, 18108387, 284563, 284566

2398	95096700 (4791, 4792)	Novel Protein sim. GBank gi 106322 p H34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - nuclease Leucine Rich Repeat	52846355, 18108397, 56182575, 35698288, 22278997, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284108, 284907, 29331830, 68712502, 284110, 60170831, 264591, 33857402, 60433438, 55812038, 33109954, 21908754, 33857084, 87188474, 265017, 265018, 265019, 284760, 284448, 284288, 284768, 52844228, 21908768, 21908767, 265020, 265021, 60170815, 264692, 33857023, 65274620, 52845129, 33857182, 27488282, 27488284, 27488285, 284629, 18108374, 35698423, 35698555, 284631, 284556, 52844332, 284558, 83373044, 18108388, 87168518, 22279002, 284482
2397	87280854 (4793, 4794)			52844507, 52845156, 56182575, 264259, 29147620, 284905, 264907, 264908, 264909, 284910, 284758, 52844288, 284603, 284604, 284762, 284881, 284764, 18108357, 284769, 21908788, 284893, 284628, 284635, 284638, 284639, 284684
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258809 (AC005178) - H53 GS1 (Homo sapiens)	UNCLASSIFIED	
2399	87738985 (4797, 4798)	Novel Protein sim. GBank gi 766117 (L41834) - nuclear protein [Ensis minor]	UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 66714117, 60432289, 284908, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87188474, 284600, 285017, 285018, 265019, 284764, 284765, 21908785, 21908786, 21908787, 21908789, 35895917, 265020, 265022, 60170815, 33857023, 18108370, 18108374, 284556, 60170394, 284558, 87168518, 22279000, 22279002, 284564, 284566, 284487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1  - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	21908766, 52846842, 56994075, 33657182, 27488282, 52844288, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gl 2352822 gb AA689285.1  - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	52644507, 52645156, 52644228, 264688, 21908784, 21908785, 52646365, 52646842, 21908786, 21908787, 21908788, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 285020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 28331824, 33657109, 52645129, 28331826, 33657182, 28331827, 35696052, 27466281, 27466282, 33656970, 33657349, 27466285, 35695763, 264108, 264905, 35698423, 35695955, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644298, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gl 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]		
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gl 4829575 gb AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00082) - C-type lysozyme/alpha-lactalbumin family	22278999, 35698052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gl 2315796 (AF018685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase family	35696286, 28331826, 35696052, 265008, 265018, 21908789, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gl 464178db BAA03591  - (D14853) polyprotein [Hepatitis C virus]	UNCLASSIFIED	35696286, 28331822, 265007, 21906754, 265017, 265018, 265019, 264783, 264389, 21906785, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	86084501 (4811, 4812)	Novel Protein sim. GBank gl 2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - struct CAP-Gly domain	52646342, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264389, 264685, 264686, 21908788, 21908789, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465003 (4813, 4814)		UNCLASSIFIED	264685, 264686
2408	87381503 (4815, 4816)	Novel Protein sim. GBank gl 423442 pi IS33513 - gene Fil protein - mouse	UNCLASSIFIED	264910, 265010, 264448, 264557

2409	84741770 (4817, 4818)	Novel Protein sim. GBank gll1178801[sp]P45988[YNZ8, CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T08A5.6 IN CHROMOSOME III]		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29148498, 52844045, 60433438, 33857084, 87168474, 264760, 21906787, 29148627, 29148629, 52844150, 33857023, 263987, 20281089, 18108374, 20281071, 58182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gll4966282[gb]AACJ8052.21 - (UB4849) Contains similarity to P1am domain: PF00848 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00808) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gll3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264369, 33857108, 58182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gll54103338[gb]AADX3038.11 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278998, 29331827, 264807, 265011, 265017, 285018, 285019, 18108351, 21906788, 285020, 33857109, 264559, 18108385
2413	84133820 (4825, 4826)	Novel Protein sim. GBank gll5282705[emb]CAB45778.11 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00039) - Intermediate filament proteins	struct	264488, 284259, 29331828, 264508, 264905, 264309, 264906, 264907, 264908, 264510, 264511, 264512, 285008, 285009, 264910, 265011, 264682, 264764, 264768, 264686, 264768, 264688, 265021, 33857023, 18108370, 264628, 35895855, 264832, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264568, 264587, 264488
2414	84312590 (4827, 4828)	Novel Protein sim. GBank gll1082340[pir]S52863 - DNA- binding protein R kappa B - human		ubiquitin	52645158, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 58994075, 22278998, 35898286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35898052, 33856970, 29331830, 264909, 60433356, 33857402, 264594, 52846317, 21906754, 33857084, 265010, 87168558, 285017, 285018, 285019, 284369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906785, 21906786, 21906787, 29148627, 21906789, 285020, 265021, 60170815, 33857023, 264693, 52845128, 33857109, 33857182, 27486281, 27486282, 27486285, 33857349, 18106370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52844332, 264638, 264558, 58182323, 83373044, 18108385, 87168518, 22278902

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gij423915 pir A45438 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21908754, 265018, 264687, 264689, 21908769, 55811957, 265021, 264690, 264691, 33657023, 264693, 33698423, 56182323, 58526486
2416	94116336 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54485 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265008, 60432228, 21908754, 87168559, 265019, 264882, 21908768, 21908769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264588
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284008 pir S18732 - autoantigen, 84K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264584
2421	87805345 (4841, 4842)	Novel Protein sim. GBank gij224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]		transport	18108392, 18108394, 18108398, 264906, 265008, 265010, 18108351, 18108374, 18108385
2423	88036390 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331828, 60432289, 29331828, 265008, 265009, 60433356, 21908754, 265017, 265018, 265019, 21908768, 21908769, 21908769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 22278997, 60432049, 264259, 29331828, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264768, 21908768, 55811857, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415991 (4849, 4850)	Novel Protein sim. GBank gij2077932 dbj BAA16879  - (D86558) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87813945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AA853003.1  - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21908767, 18108370, 18108374, 263976



2427	87622693 (4853, 4854)	Novel Protein sim. GBank g f4680695 g b AAD27737.1 AF13286 - (AF132862) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	(ribosomalprot	284259, 20281099, 35898052, 285008, 284594, 285011, 284780, 18108351, 284682, 284883, 284389, 284684, 284886, 284887, 284889, 21908786, 284681, 284692, 18108374, 18108377, 284557, 284639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank g f1537070 (U83840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278998, 35898052, 21908754, 284288, 21908785, 21908788, 21908789, 35895917, 285020, 283972, 22278002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank g f601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 284808, 284909, 284511, 285008, 21908754, 285017, 285018, 285019, 284448, 284683, 284288, 21908785, 21908788, 285021, 284683, 18108381
2430	86848827 (4859, 4860)	Novel Protein sim. GBank g f3860729 emb CAA14630  - (AJ235270) CELL DIVISION PROTEIN FTSJ (fts-J) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein	UNCLASSIFIED	284112, 284631
2431	87648884 (4861, 4862)	Novel Protein sim. GBank g f3860729 emb CAA14630  - (AJ235270) CELL DIVISION PROTEIN FTSJ (fts-J) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		28331828, 29331827, 35898052, 29148499, 284905, 284908, 284681, 284288, 284689, 21908785, 284692, 35898423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank g f3876387 emb CAA93287  - (Z89380) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89268 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	284634, 284558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank g f2224593 db BAA20784  - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	284589, 284805, 285018, 284762, 284683, 284691, 284558, 284557, 284639, 284558
2434	19520148 (4867, 4868)				284583
2435	20759044 (4869, 4870)			UNCLASSIFIED	284555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank g f1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	285008, 284758, 285010, 284689, 27486261, 283972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank g f3641352 (AF081234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 285007, 285009, 285017, 284760, 284685, 284693, 284565
2438	94143473 (4875, 4876)	Novel Protein sim. GBank g f3860014 (AF091086) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	28331828, 284508, 284805, 284509, 284906, 284907, 284908, 284909, 284511, 285008, 284512, 284910, 285009, 284591, 33657402, 21908754, 285011, 284760, 284764, 284685, 284688, 284788, 35895917, 33857023, 284693, 284631, 284632, 56182323, 284556, 83373044, 284563, 284584, 284585, 284586, 284587

2439	94850850 (4877, 4878)	Novel Protein sim. GBank gl 4283519 gb AAD15345  - (AC004044) small nuclear riboprotein Sm-D1 (Arabidopsis thaliana)	Contains protein domain (PF01423) - UNCLASSIFIED Sm protein	60424178, 18108397, 56182575, 56181886, 56984075, 22278998, 35698286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 86714117, 29331825, 60432288, 29331826, 29331827, 29331828, 35698052, 29146488, 264509, 264905, 264906, 52644045, 60431735, 33109854, 21808754, 33657084, 55811386, 52644298, 87168474, 265017, 265018, 285019, 18108351, 264448, 264288, 264768, 52644229, 56181582, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 33657023, 33657109, 33657182, 27486282, 27486284, 33657349, 27486285, 35695783, 18108370, 60431528, 263977, 55810764, 35698423, 85274791, 35695855, 60431850, 56182323, 60432113, 22278000, 22279002, 264587
2440	87641733 (4878, 4880)		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264807, 264510, 265018, 285019, 264448, 264389, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gl 3024889 pf 56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIA0288 (HAG116)	UNCLASSIFIED	264488, 264629, 16108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gl 4508013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - UNCLASSIFIED Leucine Rich Repeat	22278998, 22278999, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gl 1170858 pf Q02975 KID1_RA1 - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - UNCLASSIFIED KRAB box	264908
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gl 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - UNCLASSIFIED bZIP transcription factor	264259, 18108382, 18108383, 18108385, 22278000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gl 2135950 pf S58222 - PQ-rich protein - human		264259, 35698052, 264369, 18108381
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gl 4753887 emb CAA05408.2  - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - UNCLASSIFIED WAP-type (Whey Acidic Protein) 'four-disulfide core'	265011, 264889, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gl 4885613 ref NP_005409.1 pST5  - suppression of tumorigenicity 5	cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 285018, 264692, 85274620, 60431528, 85274791, 56182323

2448	87748680 (4895, 4898)			UNCLASSIFIED	22778996, 22278997, 22278998, 29331826, 35698052, 264107, 264110, 87168474, 87188559, 18108351, 21906787, 21906789, 27486282, 263978
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gll728637 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		cadherin	284259, 264828, 265007, 284595, 265021, 56526488
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	81014563 (4801, 4802)	Novel Protein sim. GBank gll1710021 sp P35280 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 68714117, 29331828, 29331828, 35698052, 264907, 68712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906787, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	81230509 (4803, 4904)	Novel Protein sim. GBank gll1504034 db BAA13216  - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264983
2453	84201088 (4805, 4806)	Novel Protein sim. GBank gll2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D48802 (PID:g1369908) [Homo sapiens]	Contains protein domain (PF00580) - Leucine Rich Repeat	ngf/ncp	264509, 264512, 18108385
2454	95310691 (4807, 4808)	Novel Protein sim. GBank gll1076802 p H549915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 68714117, 29331827, 264508, 264509, 264903, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264803, 264604, 264760, 264781, 264762, 18108351, 264784, 264785, 264786, 264688, 264768, 264769, 264534, 264691, 264682, 33657023, 264693, 33657109, 264628, 263978, 35698055, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264583, 264584, 264486
2455	95288301 (4809, 4810)	Novel Protein sim. GBank gll543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264486, 22278998, 264259, 35698052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906786, 21906787, 21906769, 29148629, 35698117, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264583, 264584, 264586, 264587
2458	88166700 (4811, 4812)	Novel Protein sim. GBank gll2586630 (AC003079) - Ankyrin-like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ankyrin Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gll3025447 (AC004528) - R32184_3 [Homo sapiens]	UNCLASSIFIED	58181688, 264905, 264907, 264511, 264598, 5581388, 264882, 264884, 264885, 264887, 264891, 33857023, 264893, 35695855, 264636, 264555, 56182323, 264558, 56528486, 264563
2458	85075304 (4915, 4916)	Novel Protein sim. GBank gll2384942 (AF022885) - Similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	264681, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gll5441942[gblAAD43187.1]AC004897 supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gll4929701[gblAAD34111.1]AF15187 - (AF151874) CGI-116 protein [Homo sapiens]	kinase	85274572, 35688286, 22278996, 22278997, 80432049, 29331822, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 29331828, 33858970, 29146499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 264891, 33657023, 27486261, 18108374, 35695855, 87168518, 80432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gll4428882[gblAAD20833] - (AF126082) Arf-like 2 binding protein BART1 [Homo sapiens]	UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86988002 (4923, 4924)	Novel Protein sim. GBank gll5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264809, 264758, 264884, 18108374, 264637, 18108385
2463	84386543 (4925, 4926)	Novel Protein sim. GBank gll5052518[gblAAD38588.1]AF14561 - (AF145613) BcDNA GH03108 [Drosophila melanogaster]	UNCLASSIFIED	264691, 264586
2484	91219857 (4927, 4928)	Novel Protein sim. GBank gll5410300[gblAAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	protease	264489, 52648842, 22278995, 35695286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35698052, 29331828, 264509, 52644045, 264510, 264511, 264512, 285008, 60170831, 264593, 52846317, 33109954, 33657084, 265017, 265018, 265019, 264782, 264448, 264784, 264288, 264768, 21906765, 21906768, 21906767, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22278002, 264488

2465	85357483 (4928, 4930)	Novel Protein sim. GBank gi 4506401 ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - oncogene Eukaryotic protein kinase domain	1810392, 52844507, 52845156, 52846385, 22278994, 22278995, 35698288, 22278998, 22278998, 264259, 29331822, 29331824, 29331825, 60424289, 80432289, 29331827, 35698032, 29331828, 264907, 29331830, 52844045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33857402, 60433438, 55812038, 21908754, 33109954, 285010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264787, 21908765, 21908767, 21908768, 55811957, 35698917, 265020, 265021, 60170615, 52844150, 33657023, 52845128, 33857109, 27488261, 27488264, 35695763, 264626, 263972, 18108374, 35695855, 264636, 264637, 80170394, 58526488, 87168518, 60432113, 264583, 264584, 264586, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi 4321819 gb AAD15788.1  - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		
2467	85059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005595) - F18801.1, partial CDS [Homo sapiens]	UNCLASSIFIED	56894075, 264908, 21906768, 33657023
2468	87614686 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pir I58108 - gene [DMR-N9 protein - mouse (fragment)]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat	29331824, 52844045, 265008, 264910, 265019, 21908765, 21908769, 265021 264288, 264628
2469	86284397 (4937, 4938)	Novel Protein sim. GBank gi 5420389 emb CAB46860.1  - (AJ243480) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264592, 264692, 264555, 264558, 264557, 264558, 264559, 18108389, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 emb CAB46424.1  - (AL088749) DKFZp434G153 [Homo sapiens]	UNCLASSIFIED	65274572, 35698288, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95080811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]	UNCLASSIFIED	264092, 60432049, 28331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421508 (4945, 4946)	Novel Protein sim. GBank gi 4538008 emb CAB39830.1  - (AL049461) putative protein [Arabidopsis thaliana]		80424179, 65274572, 22278999, 60424289, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264688, 265021, 264692, 65274620, 60431528, 65274791, 264558, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]		65274572, 56984075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gll1218486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284259, 29331822, 265008, 265007, 285010, 285011, 284448, 284288, 284389, 284685, 284686, 18108357, 264768, 18108382, 284693, 18108370, 18108374, 18108379, 35688423, 83373044, 18108383, 18108385, 284584, 284585, 284587
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gll3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	284259, 60424289, 66714117, 284905, 285006, 284511, 265008, 265009, 284758, 285010, 285011, 18108351, 284681, 284389, 284288, 284689, 21908767, 285020, 18108374, 284639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	285017
2479	94314562 (4957, 4958)	Novel Protein sim. GBank gll1844232 [dbj]BAA11082] - (D87086) N-WASP [Bos taurus]		UNCLASSIFIED	56984075, 22278989, 21906754, 264682, 21906785
2480	95295605 (4959, 4960)			UNCLASSIFIED	284905, 284907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gll5689489 [dbj]BAA83018.1] - (AB028989) KIAA1066 protein [Homo sapiens]	collagen	UNCLASSIFIED	85274572, 56182575, 22278987, 284084, 284259, 29331822, 29331824, 68714117, 28331827, 35686052, 284508, 284905, 284906, 284907, 284908, 52844045, 284909, 58182435, 265008, 264910, 33657402, 55812038, 284758, 265010, 285011, 285017, 285018, 284760, 284762, 18108351, 264764, 284288, 284766, 284986, 284768, 21908788, 55811957, 265020, 264691, 264692, 264693, 284628, 55811576, 264630, 284634, 264635, 284636, 284637, 284556, 264558, 56182323, 83373044, 60432113, 22278002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gll321249 [pir]S28407 - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 284508, 284905, 284509, 284908, 284907, 284908, 284511, 284591, 284768, 284693, 284631, 284632, 284636, 284638, 284639, 284583
2483	87731583 (4965, 4966)			UNCLASSIFIED	284488, 22278985, 284083, 284095, 60432049, 60433356, 60433438, 284448, 284288, 263967, 18108370, 18108385, 18108388, 284482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gll728831 [sp]P39188 [ALU1] HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	kinase	UNCLASSIFIED	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gll1185367 (U23281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278985, 22278986, 22278987, 22278989, 284259, 60432048, 29331824, 60432289, 29331827, 285007, 284910, 284593, 284600, 284603, 284604, 285018, 284448, 284288, 284685, 284686, 284758, 284689, 35695917, 285022, 284692, 284693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gii2862167[db][BAA23715] - (AB007803) KIAA0443 [Homo sapiens]			265017, 264555
2487	85343105 (4973, 4974)	Novel Protein sim. GBank gii484559[sp]P35287[RB14_RAT RAS-RELATED PROTEIN RAB-14]	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35688286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265008, 264511, 265008, 265009, 60433436, 21908754, 33108954, 87188558, 265018, 264681, 264288, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35688423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264583, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gii486439[emb]CAB43355.1] - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264688, 264693, 55811576, 22279002
2490	88089609 (4978, 4980)	Novel Protein sim. GBank gii2588624 (AC003083) - Rap2 Interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	81242116 (4981, 4982)	Novel Protein sim. GBank gii728632[sp]P39169[ALU2_HUMAN - IIII] ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	264259, 29331826, 265008, 264782, 18108370, 18108376, 18108379
2492	85308202 (4983, 4984)	Novel Protein sim. GBank gii3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21908784, 21908788, 264692, 60431528, 87188518, 60432113, 22279000

2493	95422415 (4985, 4986)	Novel Protein sim. GBank gl 4240307 db BAA74932.1  - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432048, 26331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264805, 264509, 264908, 264807, 29331830, 264909, 264510, 265006, 264511, 285007, 264512, 285008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264805, 265019, 55811150, 264762, 18108351, 264891, 264448, 264683, 264389, 264288, 18108355, 18108357, 264687, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 264691, 264692, 33657023, 33657348, 18108370, 18108374, 18108376, 55810784, 18108379, 65274791, 264830, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264568, 264486
2494	30783118 (4987, 4988)	Novel Protein sim. GBank gl 5420389 emb CAB46880.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284907, 284601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gl 5420389 emb CAB46880.1  - (AJ243460) proteophosphoglycan [Leishmania major]	collagen	263994, 22278997, 35696032, 284509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264784, 264288, 264685, 264768, 264769, 264689, 265020, 264692, 65274620, 264629, 55810784, 35696423, 55811578, 264636, 264637, 18108385, 22279000, 264584, 264587, 264486
2496	80018785 (4991, 4992)	Novel Protein sim. GBank gl 4808220 emb CAB42832.1  - (AL022316) dJ11715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2497	91723554 (4993, 4994)		UNCLASSIFIED	52644507, 22278996, 22278999, 28331824, 29331828, 33657402, 21908754, 87168474, 285019, 264389, 264689, 21908765, 21908766, 21908767, 21908768, 265020, 33657023, 18108376, 18108387
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gl 200503 (U47824) - B [Homo sapiens]	UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2499	94685125 (4987, 4988)	Novel Protein sim. GBank gl 3510234 (AC005561) - R31237.1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264909, 55812038, 264631, 264637, 264558



2500	94849324 (4898, 5000)	Novel Protein sim. GBank gij3881275[emb]CAA21725] - (AL032655) predicted using GeneFinder, similar to Inositol monophosphatase family; cDNA EST yk255a11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645158, 22278995, 56994075, 35698286, 22278998, 264259, 52845080, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52844286, 87188474, 87188559, 264603, 264661, 264448, 264883, 264288, 264389, 52844229, 264889, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 52844150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87188518, 22279002
2501	94303886 (5001, 5002)	Novel Protein sim. GBank gij4929815[gb]AAD34068.1[AF15183] CGI-73 protein [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	dna_rna_bind	65274572, 56182575, 35698286, 22278998, 56994075, 22278997, 60432048, 264259, 29331822, 29331824, 29331826, 29331827, 35698032, 264905, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 285007, 264910, 264591, 60432229, 33657402, 80433356, 264595, 55812038, 264758, 264598, 87188474, 87188559, 264800, 264601, 264602, 265017, 264604, 265018, 264805, 265019, 18108351, 264448, 264389, 264288, 264786, 18108357, 21908765, 21908768, 21908767, 21908769, 29148629, 35695917, 264692, 33657023, 264629, 35698423, 55811576, 35695855, 264630, 264834, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87188518, 60432113, 22279002, 264368
2502	90893718 (5003, 5004)	Novel Protein sim. GBank gij3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like: similar to P22059 (PID:g128308) [Homo sapiens]	Contains protein domain (PF01237) - UNCLASSIFIED Oysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264835, 264555, 264556, 264557, 264558, 56182323, 264559, 87188518, 264563, 264482
2503	87878345 (5005, 5008)	Novel Protein sim. GBank gij2198974[emb]CAA72638] - (Y11898) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87686708 (5007, 5008)	Novel Protein sim. GBank gij550420[emb]CAA48220] - (X88101) trg [Rattus norvegicus]			264488, 52844507, 52845156, 52846842, 22278994, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264808, 264808, 52844045, 265009, 60433336, 33857402, 60433438, 264595, 33109954, 87168474, 265017, 265018, 264448, 264288, 264766, 52844229, 21908765, 21908766, 21908767, 21908768, 52844150, 264892, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52844332, 58182323, 18108387, 87188518, 60432113, 22279002, 264584
2505	8760559 (5008, 5010)			UNCLASSIFIED	264488, 52844507, 52845156, 52846365, 65274572, 22278995, 36994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331828, 29331828, 264508, 56182435, 264112, 264593, 60433356, 55812038, 21908754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 265022, 60170815, 33857023, 27486264, 18108378, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264585
2506	87232328 (5011, 5012)	Novel Protein sim. GBank gij2137562[pil]49635 - mouse Dhml protein - mouse		nuclease	264488, 263984, 264592, 264595, 264369, 264886, 264768, 35695917, 35696423, 264563
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[ref]NP_006035.1[pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		22278995, 22278999, 60432049, 264259, 29331828, 265008, 265007, 60433438, 33857084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21908765, 21908769, 55811857, 265020, 265022, 27486281, 33857349, 18108377, 35695855, 60432113, 22279002, 264563, 264585
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[emb]CAB42889.1] - (AL031447) DJ128A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264558, 264567

2510	95421378 (5018, 5020)	Novel Protein sim. GBank gl 3293537 gb AAC25762.1  - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331828, 33656970, 284908, 66712502, 285007, 284910, 60170831, 60432229, 60433356, 60433438, 21908754, 87188474, 285017, 285018, 284448, 284288, 21908767, 21908768, 21908769, 55811957, 35695917, 285020, 285022, 284891, 33657023, 284693, 85274820, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 284555, 58182323, 83373044, 60432113, 22279002, 265017, 21908764, 265020, 284692
2511	67384281 (5021, 5022)	Novel Protein sim. GBank gl 4323152 gb AAD18228.1  - (AF098863) Ets-protein Spi-C [Mus musculus]			
2512	68084771 (5023, 5024)	Novel Protein sim. GBank gl 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 284259, 29331825, 29331826, 29148499, 284907, 284909, 285008, 284591, 60432228, 21908754, 284763, 284683, 284766, 18108357, 284689, 21908769, 284693, 18108370, 263972, 18108374, 284558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gl 3004857 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424178, 52845156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424268, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 285017, 284448, 284389, 56181562, 21908766, 21908767, 21908768, 21908769, 285020, 285021, 33657023, 18108366, 33657109, 27486281, 27486282, 33657349, 18108374, 55810784, 35696423, 58182323, 284558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gl 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87894509 (5029, 5030)	Novel Protein sim. GBank gl 3757727 emb CAA18783  - (AL022727) dJ8018.7 (olfactory receptor-like protein (hs8M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	lim7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	284259, 29148498, 284905, 284288, 29148829, 35695917, 27489281, 284634
2517	87784988 (5033, 5034)	Novel Protein sim. GBank gl 4220527 emb CAA23000  - (AL035356) putative protein (Arabidopsis thaliana)		UNCLASSIFIED	284091, 29331824, 29331825, 29331826, 29331828, 35696052, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284511, 284910, 33657402, 284757, 33108954, 285017, 285018, 284605, 284760, 284762, 284763, 284768, 284769, 33657109, 33657182, 284628, 55811576, 35698423, 284631, 284634, 284637, 284638, 284639, 87168518, 22279002, 284584

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gi 4928591 gb AAD34058.1 AF15181 - (AF151819) CGI-81 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 284909, 284511, 285007, 60432228, 60433358, 60433438, 58812038, 285010, 285017, 284446, 284288, 264889, 21806768, 21806769, 285022, 52644150, 284693, 18108370, 263972, 284555, 56182323, 83373044, 18108385, 60432113, 264088 264259, 66714177, 29331826, 29331827, 29331828, 264907, 68712502, 285008, 265008, 264594, 265010, 265011, 285018, 264288, 21806768, 265020, 60431528, 55811576, 65274791, 284632, 284555, 284636, 22279002, 284584 284259, 284808, 284810, 284682, 21806769, 285020, 284563
2519	94328180 (5037, 5038)	Novel Protein sim. GBank (AC004893) similar to KIAA0768, similar to PID:g3882253 [Homo sapiens]	kinase		
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_008035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		284488, 264489, 263984, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 284906, 284907, 66712502, 284511, 285008, 285007, 284591, 284592, 264593, 264594, 284595, 264596, 284681, 264448, 284763, 284682, 264784, 264684, 264369, 284288, 284685, 264686, 21806768, 55811957, 284692, 284693, 27486261, 18108370, 284628, 264629, 18108374, 55811576, 35698423, 35698555, 284632, 284558, 18108385, 65274727, 60432113, 284563, 284564, 284585, 284586, 284587 284489, 22278997, 20281171, 21806754, 35695917, 263967, 263976, 263981, 20281169 263969
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		
2523	95340467 (5045, 5046)				
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gi 1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		35694075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 284512, 285008, 60170831, 33657402, 265010, 87168559, 285019, 284288, 21806768, 21806769, 35695917, 285020, 265021, 265022, 52644150, 284691, 33657023, 33657109, 27486281, 35698423, 65274791, 264559, 83373044, 56528486, 87168518, 284587

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gl 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278998, 60432049, 60432289, 29331828, 284805, 285008, 55812038, 21908754, 265018, 264369, 21908783, 21908786, 21908787, 21908789, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gl 4589628 [db BAA78836.1] - (AB023209) KIAA0982 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	60424179, 264768, 264667, 284769, 284689, 65274572, 21908787, 58183575, 21908788, 21908789, 55811957, 22278994, 22278995, 35696288, 35695917, 22278996, 22278997, 265020, 22278998, 285021, 22278999, 265022, 264690, 264691, 60432049, 264259, 60432289, 29331828, 29331827, 29331828, 284097, 33657023, 29331822, 29331824, 27486282, 284508, 284509, 284905, 284907, 18108370, 66712502, 60431528, 264828, 264908, 18108372, 18108374, 56182435, 18108376, 55810784, 55811576, 35696423, 35695855, 265008, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 284555, 264592, 60431735, 284638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52648317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22278000, 265018, 265019, 264584, 18108351, 264448, 284566, 264289, 264486, 284587, 264766, 264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gl 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22278002
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gl 2085786 (AC002066) - similar to zinc finger 5 protein from Gallus gallus, U51640 (P1Dg1399185) [Homo sapiens]	Contains protein domain (PF00861) - BTB/POZ domain	dns_ma_bind	
2529	86670826 (5057, 5058)	Novel Protein sim. GBank gl 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	
2530	80259978 (5059, 5060)				284369, 264558
2531	87768931 (5061, 5062)			UNCLASSIFIED	28331822, 29331824, 60432289, 264508, 264509, 284906, 265011, 264769, 21908768, 33657023, 87168518, 22279000, 284593
2532	87419776 (5063, 5064)	Novel Protein sim. GBank gl 2664625 [emb CAA16972] - (AL021811) putative protein [Arabidopsis thaliana]			
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gl 437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gll3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	UNCLASSIFIED	284259, 35698052, 284905, 285017, 21908769, 285020, 285022, 33657109, 22278000
2535	91225058 (5069, 5070)	Novel Protein sim. GBank gll4488311 (emb CAB37992) - (AL031432) dJ485N24.2.1 (PUTATIVE novel protein) (isoform 1) (Homo sapiens)		65274572, 35698286, 60432289, 29331828, 68712502, 285008, 60432228, 285017, 285018, 285019, 284288, 284369, 284689, 21908768, 285020, 285021, 284636, 60170394, 22278002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gll7288386 (p39193) ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III	kinase	18103368, 56182375, 35698286, 22278997, 22278999, 60432049, 284259, 29331824, 29331826, 29331827, 29331828, 284905, 284511, 285009, 284910, 284598, 52846317, 18108351, 284681, 284683, 18108354, 284288, 284687, 284768, 284689, 21908765, 21908766, 21908767, 285021, 52845129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87188518, 60432113, 22279000, 22279002, 284567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gll4557028 (pNP_003913.1) pHERC - guanine nucleotide exchange factor p32	ubiquitin	65274572, 35698286, 29331822, 29331825, 29331827, 29331828, 35698052, 284905, 68712502, 284909, 285008, 285011, 284760, 284288, 284685, 35698917, 60170815, 284681, 33657023, 65274820, 33657109, 18108374, 35698423, 35698585, 284636, 284558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)		UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 28148499, 284908, 284112, 60170831, 87168559, 284804, 285019, 284685, 284768, 87168518, 22278000, 284565, 284566
2539	84144816 (5077, 5078)		UNCLASSIFIED	22278997, 29331828, 285008, 285009, 284758, 285010, 18108351, 284683, 284288, 21908765, 35698917, 285020, 18108374, 284587
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gll1362647 (pirl S53878 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura))	UNCLASSIFIED	22278997, 29331828, 285008, 285009, 284758, 285010, 18108351, 284683, 284288, 21908765, 35698917, 285020, 18108374, 284587
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gll171858 (pP54787T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION)	UNCLASSIFIED	284488, 284768, 284689, 284511, 20281771, 284634, 284635, 284691, 284639, 29331824, 284603, 284604, 284905, 284907, 284908, 284768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AAD40850.1 AF083110 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646365, 52646842, 65274572, 22278994, 35698286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35698052, 33656970, 264907, 264909, 52644045, 264510, 265008, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644288, 265010, 265011, 265018, 265019, 18108351, 264883, 264288, 264885, 264887, 52644229, 264789, 21908768, 21908767, 21908769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486281, 27486284, 33657349, 35695783, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1  - (AL088723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		65274572, 58182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264389, 264288, 264684, 264768, 264689, 21908765, 21906787, 21908769, 60170815, 264692, 264693, 55811578, 65274791, 264636, 264558, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218548 (5087, 5088)	Novel Protein sim. GBank gi 2498110 sp Q83181 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264688, 264687, 264689, 21908765, 265020, 265021, 18108370, 18108374, 18108378, 18108381, 18108385, 18108387, 56528486, 22279000, 264482, 264563, 264567
2545	87742645 (5089, 5090)	Novel Protein sim. GBank gi 3327048 cbj BAA3159.1  - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264908, 265008, 60170831, 265017, 264389, 21908787, 60170815, 264692, 33657109
2546	88083861 (5091, 5092)	Novel Protein sim. GBank gi 2996032 (AF054588) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143868 (5083, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34084.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	UNCLASSIFIED	264488, 18108394, 52646842, 18108397, 56182575, 22278999, 56984075, 22278998, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35698052, 29331826, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906784, 52646317, 265010, 265011, 264800, 264801, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906785, 21906786, 21906787, 21906788, 29148627, 21906789, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27486281, 18108370, 18108374, 55810764, 55811576, 35698423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22278002, 264564, 264568, 264486
2548	66179079 (5085, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35698266, 56984075, 22278997, 22278999, 264259, 29331822, 26331824, 29331825, 29331826, 60432289, 26331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 35657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22278000, 22279002, 264563, 264567
2549	94186893 (5087, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - struct LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265016, 264688, 21906784, 21906785, 21906786, 21906787, 21906788, 265020, 265021, 52644150, 264691, 18108368, 60431802, 18108376, 35698423, 56182323, 18108387, 264587
2550	87775584 (5089, 5100)	Novel Protein sim. GBank gi 2143886 pir J152523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638



2551	95308400 (5101, 5102)	Novel Protein sim. GBank gl 4337103 gb AAD18079  - (AF129756) NG28 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 284905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 285018, 284605, 265019, 284288, 21906766, 21906768, 21906769, 265020, 60170815, 284693, 33657109, 35696423, 284638, 56182323, 83373044, 22279000
2552	85332820 (5103, 5104)			UNCLASSIFIED	56182375, 35696286, 29331824, 29331826, 35696052, 29331828, 284508, 284907, 56182435, 285008, 284591, 33109954, 284760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811578, 35696423, 35695855, 56182323, 284558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gl 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DCCR REGION		UNCLASSIFIED	284686, 284488, 263976, 284768, 29331826, 35696052, 35696423, 284601, 284511, 284602, 284910, 284634, 284760, 284555, 284762, 284908, 284592, 284891, 284566, 284908, 284684, 284567, 284909, 284768
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gl 728835 sp P39192 ALU5_HUMAN - III ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 284508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gl 4884319 emb CAB43260.1  - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gl 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 284509, 33657402, 284683, 284684, 284766, 284889, 33657023, 33657109, 35695855, 284558, 284567, 284595
2557	79437803 (5113, 5114)				
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gl 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 284908, 284511, 285018, 284448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gl 4539999 emb CAB39618.1  - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 284288, 284765, 284766, 284769, 21906765, 21906766, 60432113, 284482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gl 5051399 emb CAB44995.1  - (AL078630) 573K1.3 (nm17M1-4) (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gl 5326825 gb AAD42056.1 AF044955 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331826, 29331827, 29331828, 285007, 60432229, 87168559, 285017, 285018, 285019, 284689, 21906768, 21906769, 35695917, 285020, 33657023, 33657109, 18108374, 284634, 284559, 18108385, 87168518, 22279002

2562	07845539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21908785, 55811957, 60170615, 33657023, 264693, 35895855, 87188518, 264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	80085497 (5125, 5126)	Novel Protein sim. GBank gi 4886447[emb]CAB43371.1] - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352844[sp]P47179 YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR		sulfoltransferase	264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530906 (5129, 5130)	Novel Protein sim. GBank gi 628012[pi]A53933 - myosin I	Contains protein domain (PF00063) - struct	UNCLASSIFIED	86714117, 264909, 283978, 264632, 18108370, 35695855, 264558, 264558, 18108383
2566	80224956 (5131, 5132)	myr 4 - rat	Myosin head (motor domain)		18108383
2567	88143580 (5133, 5134)	Novel Protein sim. GBank gi 460009[sp]P34548 YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	265020, 60170615
2568	91233089 (5135, 5136)				60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810784, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313784 (5137, 5138)	Novel Protein sim. GBank gl 2599560 gb AAB84168.1  - (AF029874) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcript factor	18108394, 56182575, 56181886, 22278995, 22278996, 56994075, 35896286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35896052, 264905, 264908, 56182435, 265008, 265009, 264910, 60432229, 284592, 60433356, 60433438, 21908754, 87188559, 265017, 265018, 265019, 264682, 264448, 264288, 21908765, 21908766, 21908767, 21908768, 29148827, 21908769, 35895917, 265021, 265022, 52644150, 284690, 264891, 264692, 264693, 65274620, 263987, 35895763, 20281089, 263974, 18108374, 55810764, 35898423, 35898585, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 58528486, 87168518, 22279000, 22279002, 264566
2570	94138754 (5139, 5140)	Novel Protein sim. GBank gl 4758954 ref NP_004587.1 ppp2 - protein phosphatase 2 (lumeny 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278998, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35896052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 284689, 285020, 265021, 264691, 264692, 264693, 18108374, 35895855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gl 732218 sp P34609 YO60. CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gl 4884319 emb CAB43280.1  - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35896286, 29331827, 35896052, 264100, 264104, 264110, 264592, 21905754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35895855, 60170394, 264559, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank gi1399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 60424179, 65274572, 56182575, 56181886, 22278995, 56994075, 22278987, 60432049, 264259, 29331822, 29331824, 29331825, 60432286, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21908765, 21906766, 21908767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170815, 264690, 52644150, 264691, 264692, 33637023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56162323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21908765, 21908768, 21908768, 55811957, 60170815, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	94748814 (5147, 5148)	Novel Protein sim. GBank gi13334882 (AC003308) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi14929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		UNCLASSIFIED
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi14680681 gb AAD27730.1 AF13295 - (AF13295) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - ubiquitin	264259, 35696052, 264908, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35698423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi14337103 gb AAD18079  - (AF129756) NG26 [Homo sapiens]	Ubiquitin carboxyl-terminal hydrolases family 2	UNCLASSIFIED
2578	87786841 (5155, 5156)			UNCLASSIFIED
2579	87282879 (5157, 5158)			UNCLASSIFIED

2580	88168788 (5159, 5180)	Novel Protein sim. GBank gi 2568828 (AC003080) - Similar to KIAA0289; 80% similarity to AB002297 (PID:g224539) [Homo sapiens]			265007, 265018, 264762
2581	87888048 (5181, 5182)	Novel Protein sim. GBank gi 4406642 gb AA020049  (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	5694075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87168539, 21908769, 265022, 35695855, 263981
2582	87788789 (5183, 5184)	Novel Protein sim. GBank gi 2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112 emb CAA16521.1  (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	56181688, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430841 (5167, 5168)			UNCLASSIFIED	264808, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi 2738151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91228138 (5171, 5172)				
2587	80430943 (5173, 5174)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264782, 264288, 21908766, 21908767, 21908769, 265022, 264691, 83373044, 58528486, 22278002
2588	80074385 (5175, 5176)			UNCLASSIFIED	264908, 265019, 264768, 264693, 55811576, 56182323
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 302159 emb CAA71415  (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	264564
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi 2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264768, 35698423, 264636
2591	94192187 (5181, 5182)	Novel Protein sim. GBank gi 5702202 gb AAD47189.1 AF129166 (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	22278995, 29331830, 265008, 265010, 265017, 264639
					264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22278002

2592	95332848 (5183, 5184)	Novel Protein sim. GBank gi 3024898 sp Q80936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432288, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 59812038, 18108348, 21908754, 265011, 87168559, 265017, 265019, 264784, 264369, 284288, 264786, 285021, 60170615, 33657023, 33657109, 264628, 35698423, 35695855, 284557, 284638, 60170394, 56182323, 83373044, 56526486, 87188518, 264563, 264482, 264585
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]	im7		22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 284389, 21908768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34034.1 AF15181 - (AF151817) CGI-59 protein [Homo sapiens]	UNCLASSIFIED		264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 284760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567 264892
2595	78581878 (5189, 5190)	Novel Protein sim. GBank gi 4309881 gb AAD15478  - (AC008930) R33423_1 [Homo sapiens]	UNCLASSIFIED		22278999, 264259, 265018, 264448, 265021, 60431528
2596	87538637 (5191, 5192)		UNCLASSIFIED		264905, 264509, 264908, 284762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264488
2597	94784089 (5193, 5194)	Novel Protein sim. GBank gi 1001351 db BAA10838  - (D84008) hypothetical protein [Synecocystis sp.]	UNCLASSIFIED		22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264891, 33657023, 33657109, 18108370, 18108374, 264564, 264585
2598	87842888 (5187, 5188)	Novel Protein sim. GBank gi 3941737 (AF103719) - BAT2 [Mus musculus]	MHC		264766, 264769, 21908768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22278999, 264568 35696286, 264093, 284288, 21906769, 35698423, 35695855
2600	87787848 (5199, 5200)	Novel Protein sim. GBank gi 4283521 gb AAD15347  - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Kinase receptor WD domain, G-beta repeat		

2601	81243070 (5201, 5202)	Novel Protein sim. GBank gij728837ispjP39194JALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 28331822, 29331824, 60432289, 29331826, 28331827, 264908, 285007, 285008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 285020, 60170615, 264693, 33657109, 18108370, 18108376, 56182323, 18108381, 18108385, 22278902, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank (AF131801) Unknown [Homo sapiens]			264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 285009, 60433356, 264757, 60433438, 284759, 33657084, 87168474, 265010, 285011, 87168559, 265017, 265018, 265019, 264448, 264883, 18108354, 284288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264893, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264638, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gij3122367ispjQ61211LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264259, 35696052, 264508, 264806, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264585
2604	94876801 (5207, 5208)	Novel Protein sim. GBank gij5454030rejinP_008488.1pRRP2 - RAS-related on chromosome 22		oncogene	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264756, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2605	94316756 (5209, 5210)	Novel Protein sim. GBank (AB013721) mltaugmin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	
2606	87748408 (5211, 5212)				

2607	87827742 (5213, 5214)	Novel Protein sim. GBank gl 4828626 gb AAD30202.1  - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 68712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21908765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264839, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gl 2226005 (U49873) - ORF2: function unknown [Homo sapiens]			264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21908765, 21908767, 21908769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2609	94843781 (5217, 5218)	Novel Protein sim. GBank gl 3024889 pp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264636, 87168518, 60432113, 22278999, 265017, 264684, 21906768, 22279000
2610	86177654 (5219, 5220)	Novel Protein sim. GBank gl 4336855 gb AAD17989  - (AF108473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcript factor	
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gl 3876761 emb CAA92994  - (Z88780) predicted using Genefinder; Similarly to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gl 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gl 5533081 gb AAD45009.1 AF16118 - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52644229, 21906765, 33657109, 27486284, 18108370, 263972, 264555, 60432113, 264768, 18108394, 264692, 264683, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264768
2615	87361986 (5229, 5230)			UNCLASSIFIED	



2616	87428895 (5231, 5232)	Novel Protein sim. GBank glij3876761[emb CAA92894] - (Z68760) predicted using GeneFinder. Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - isomerase FKBP-type peptidyl-prolyl cis-trans isomerases	22278995, 22278997, 22278998, 60432049, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21908765, 21908767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264587
2617	86976888 (5233, 5234)	Novel Protein sim. GBank glij728831sp P39188 ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III	kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank glij3319282 (AF049103) - Huntingtin Interacting protein [Homo sapiens]	Contains protein domain (PF00397) - UNCLASSIFIED WW domain	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 68712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21908754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264889, 21908765, 21908766, 21908767, 35695917, 265020, 265022, 33657023, 264892, 33657108, 264628, 18108374, 35695855, 18108381, 83373044, 18108365, 18108388, 55826486, 264563
2619	87684000 (5237, 5238)	Novel Protein sim. GBank glij2431772 (U68411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - dehydrogenase Iron-containing alcohol dehydrogenases	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank glij322587[gb AAD16097] - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00828) - UNCLASSIFIED PHD-finger	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35686286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 68712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21908765, 21908768, 35695917, 52844150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 264594, 264638
2621	80263495 (5241, 5242)	Novel Protein sim. GBank glij4557341[ref NP_001174.1 pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit]		264488, 264908, 264807, 264908, 264512, 265007, 264756, 35695917, 264634, 264636, 264583, 264482
2622	81780390 (5243, 5244)	Novel Protein sim. GBank glij3880355[emb CAB05289] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148829
2623	91693906 (5245, 5246)			

2624	91638308 (5247, 5248)	Novel Protein sim. GBank glj3880355[emb](CA05298) - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278998, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29146499, 68712502, 52644045, 285007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265018, 264448, 264286, 21908765, 21908766, 21908767, 29148629, 35695917, 265021, 265022, 27486285, 18108370, 60431528, 55811576, 35695855, 58182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank glj2887429[dbj](BAA24857) - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 264511, 263981
2626	18533797 (5251, 5252)	Novel Protein sim. GBank glj487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank glj89462[pir](J27307) - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278998, 265007, 265009, 284448, 21908767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank glj3123552[emb](CAA18609) - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278997, 22278999, 284259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 285008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21908765, 21908768, 265022, 65274781, 264638, 18108387, 87168518, 22279002
2629	87376480 (5257, 5258)	Novel Protein sim. GBank glj4929595[gbj](AAD34058.1)(AF15182) - (AF151821) CGI-63 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265008, 284766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	78188364 (5259, 5260)			UNCLASSIFIED	284636, 18108385
2631	94845908 (5261, 5262)	Novel Protein sim. GBank glj321605[pir](JQ1161) - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - Zinc finger, CCHC class	dna_ma_bind	52644507, 52645156, 52646385, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 284448, 284288, 284369, 284768, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21908769, 35695917, 265020, 52844150, 33657023, 52645129, 33657109, 33657349, 35695763, 35696423, 65274781, 33657182, 27486281, 27486282, 27486285, 35695855, 284634, 264637, 52644332, 58182323, 60432113, 284566, 264486
2632	38730414 (5263, 5264)				264685

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gij1139548jBAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264886, 29148829, 33657023, 264693, 33657182, 35895763, 55811578, 264639, 56182323, 83373044, 18108385, 56526468, 87168518, 22279000, 22279002, 264565
2634	87330921 (5287, 5288)	Novel Protein sim. GBank gij5441611jemb[CAB48854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	22278997, 264259, 29331824, 56714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148829, 18108376, 55811578, 35695855, 87168518, 22279000, 264569, 29331822, 29331828, 265008
2635	86823144 (5269, 5270)	Novel Protein sim. GBank gij4680863jgAAD27721.1jAF132946) CGI-12 protein [Homo sapiens]		60170831, 264681, 264765, 264685, 29148827, 21906769, 29148784, 265022, 60170815, 264635, 18108385, 56526468, 22279002, 264567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3878148jemb[CAB07846] - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW:P43618); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52845080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264908, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52844296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264887, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 35895917, 265021, 60170815, 264681, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264594, 264565, 264566, 264488, 264567
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gij4758208jrefjNP_004081.1lpDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	

2638	84326733 (5275, 5278)	Novel Protein sim. GBank gij4829889jgbAAD34105.1(AF15186 - (AF151868) CGI-110 protein [Homo sapiens])	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 56182575, 22278995, 22278996, 35698286, 22278997, 22278998, 264259, 60432048, 29331822, 60424268, 29331826, 35696052, 29146498, 284905, 52644045, 58182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264769, 52844229, 58181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33857109, 35695763, 18108374, 55810784, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95381346 (5277, 5278)	Novel Protein sim. GBank gij2190007jbjBAA20355 - (AB004109) phosphatidylserine synthase II [Cricetulus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 284909, 264512, 33857402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33857109, 264628, 35696423, 264555, 264639, 264563, 264584, 264565, 264586, 284488
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gij3155516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 87.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906768, 35695763, 284636, 284637, 18108387
2641	11868834 (5281, 5282)	Novel Protein sim. GBank gij2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gij4490304jembjCAB38785.1 - putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264259, 29331822, 33857402, 265019, 264369, 264691, 264634, 56526488, 22279002
2643	87843981 (5285, 5286)	Novel Protein sim. GBank gij3789797jbjAAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 284684, 264685, 264686, 29148627, 264680, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	98177671 (5287, 5288)	Novel Protein sim. GBank gij3789797jbjAAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl. recpt	264107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank gij1706722jbpP49749jEVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	Novel Protein sim. GBank gij1706722jbpP49749jEVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 264632, 83373044

2847	91212878 (5283, 5294)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 284259, 29331822, 56182181, 29331825, 60424269, 60432228, 35696052, 66712502, 284908, 285007, 55812038, 33109954, 21908754, 33857084, 265018, 264448, 264288, 56181562, 21908765, 21908766, 21908768, 21908769, 35695917, 285020, 285021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264584
2848	87600587 (5295, 5298)				29148498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2849	84128783 (5287, 5298)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1668171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432228, 66712502, 56182435, 60170831, 60432229, 33857402, 33109954, 21908754, 265017, 264686, 264688, 21908765, 21908768, 60170815, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2850	87297533 (5299, 5300)	Novel Protein sim. GBank gij5360271[dbj BAA81908.1] - (AB029335) HRPET-3 [Halocynthia roretzi]			264685
2851	88088745 (5301, 5302)	Novel Protein sim. GBank gij4240225[dbj BAA74891.1] - (AB020875) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Lamhin G domain		29331824, 29331826, 28331827, 265007, 55812038, 21908754, 18108366, 18108384, 22279002, 264587
2852	10343125 (5303, 5304)	Novel Protein sim. GBank gij4493956[emb CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa: Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....		UNCLASSIFIED	264682
2853	87798735 (5305, 5306)			UNCLASSIFIED	285018, 18108370, 18108387, 264566
2854	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 285021, 283976, 55810764, 65274791, 56182323, 83373044, 65274727
2855	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272[emb CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcriptfactor	56182575, 56181686, 264092, 264259, 56182181, 60432228, 264907, 33857402, 55812038, 21908754, 87168559, 265017, 264448, 264369, 264288, 21908765, 21908766, 21908767, 21908768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2856	84562801 (5311, 5312)	Novel Protein sim. GBank gij3043718[dbj BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank glj56959509[dbj BAA83038.1] - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	264693
2658	80602454 (5315, 5316)	Novel Protein sim. GBank glj3688088 (AC005757) - R3281_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331828, 29331828, 265019, 264683, 21908788, 35695917, 284693, 35695855, 284637, 87168518, 264486, 264567
2659	87600765 (5317, 5318)	Novel Protein sim. GBank glj5420387[emb CAB46879.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	284909, 264910, 265018, 264369, 264769, 21908789, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank glj728837[sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21908765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22278000, 22278002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank glj4758048[ref NP_004739.1 PCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331828, 29331827, 29331828, 264905, 264909, 264593, 33108954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21908765, 21908768, 265022, 264691, 33657023, 27486282, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank glj3874714[emb CAA91263] - (Z68494) similar to choline dehydrogenase, cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264555, 264556, 264558, 264486
2663	87780823 (5325, 5326)	Novel Protein sim. GBank glj5106958[gb AAD39908.1 AF113615] - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	Contains protein domain (PF00008) - EGF-like domain	oncogene	264908, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518329 (5327, 5328)	Novel Protein sim. GBank glj1369670 (U56977) - Notch homolog Scalloped wings [Lucilia cuprina]		UNCLASSIFIED	35696286, 22278998, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21908765, 21908766, 21908767, 21908768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2665	87770662 (5328, 5330)	Novel Protein sim. GBank glj4884408[emb CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264556, 22279002
2666	87828472 (5331, 5332)	Novel Protein sim. GBank glj5106958[gb AAD39908.1 AF113615] - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567
2667	87422720 (5333, 5334)	Novel Protein sim. GBank glj2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0584.1			

2668	81216716 (5335, 5336)	Novel Protein sim. GBank gi15454186 ref NP_008327.1 pZYG  - ZYG homolog	UNCLASSIFIED	56181686, 35696286, 22278998, 22278999, 56182181, 29331824, 60424299, 29331825, 35696052, 29331828, 68712502, 56182435, 60433356, 284758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 284448, 284369, 284288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 284682, 33657109, 35695763, 60431528, 18106374, 35698423, 55811578, 264634, 60431850, 83373044, 18108385, 87168518, 22278000, 284583, 264564
2669	85415721 (5337, 5338)	Novel Protein sim. GBank gi12147012 pir JC4899 - proline rich protein - rat		284488, 264688, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170815, 52644150, 60432049, 264259, 284691, 33657023, 284692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331828, 29331827, 35696052, 29331828, 29146488, 29146499, 284905, 284908, 52644045, 284909, 58182435, 35696423, 65274781, 35695855, 265006, 284910, 284635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi1723523 sp Q10362 YD8B_SCHPO - HYPOTHETICAL 84.9 KD PROTEIN C2E12.11C IN CHROMOSOME 1	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi14768277 gb AAD29444.1 AF064255 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646642, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 284288, 265021, 33657023, 33657109, 33657182, 27486281, 27486282, 27486285, 18108378, 18108385
2672	87398123 (5343, 5344)	Novel Protein sim. GBank gi14966348 gb AAD34677.1 AC00634 - (AC00634) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	UNCLASSIFIED	284787

2873	87430748 (5345, 5346)	Novel Protein sim. GBank gi 5457337 emb CAB41505.2  - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - polymerase Poly(ADP-ribose) polymerase catalytic region.	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264583
2874	94847721 (5347, 5348)	Novel Protein sim. GBank gi 4768824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	264468, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2875	79563835 (5349, 5350)		UNCLASSIFIED	264691
2876	78628393 (5351, 5352)		UNCLASSIFIED	264906, 265008
2877	94328600 (5353, 5354)	Novel Protein sim. GBank gi 1079042 pir S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264480, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52644045, 265008, 285007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21908769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33857109, 27486284, 27486285, 33657349, 35695763, 18108370, 18108374, 18108377, 55811578, 35698423, 35695855, 83373044, 18108387, 22279000, 22278002, 264584



2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi 86780 pir A04045 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52846842, 35696286, 22278999, 264259, 29331825, 35696052, 284508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21908754, 265010, 265011, 87188559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264882, 264683, 264784, 264288, 264766, 264687, 264768, 264769, 264689, 21908765, 21908767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108384, 18108385, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264488, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi 1709233 sp P07514 INCSR_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264568, 264258, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi 4586604 db BAA76824.1  - (AB023187) KIAA0980 protein (Homo sapiens)	Contains protein domain (PF00036) - EF hand	struct	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264784, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264784, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi 423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 58528486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi 5114351 gb AAD40286.1  - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264909, 264769, 264635, 264638

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gl 4886489 emb CAB43385.1  - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	68054289 (5369, 5370)	Novel Protein sim. GBank gl 3342728 (AC005331) - R31341_2 [Homo sapiens]	UNCLASSIFIED		
2686	67628690 (5371, 5372)	Novel Protein sim. GBank gl 4650844 gb BAA77027.1  - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - struct Kelch motif		264259, 29331822, 60432289, 29331827, 29331830, 284909, 284512, 284596, 264769, 284534, 264555, 264556, 264557, 264558, 60170394, 284559, 284486
2687	87988183 (5373, 5374)	Novel Protein sim. GBank gl 5281314 gb AAD41475.1 AF133123 - transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108398, 22278996, 35696286, 22278997, 29331826, 29331828, 68712502, 21906754, 265011, 264760, 264761, 264763, 284689, 21906765, 35696423, 264559, 18108385, 264563
2688	79859584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gl 3880023 emb CAA97339  - (Z73086) Similarity to yeast hypothetical protein (Swiss Prot accession number Q08685); cDNA EST EMBL:D72882 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264908, 284908, 56182435, 284512, 284910, 285009, 60433438, 21906754, 18108351, 284682, 284683, 284767, 21906765, 21906766, 21906768, 33657023, 33657182, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gl 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gl 4107276 emb CAA67130  - (X88506) acyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 284564, 264568
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gl 3513303 (AC005594) - R26884_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438607 (5385, 5386)			UNCLASSIFIED	264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gl 3122400 sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gl 4972740 gb AAD34765.1  - (AF132177) unknown [Drosophila melanogaster]		collagen	35696288, 56994075, 22278999, 264259, 35696052, 29331830, 285011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263978, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264566
2696	87674040 (5391, 5392)	Novel Protein sim. GBank gl 728831 sp P39189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21906768, 18108370, 18108372

2697	91838472 (5393, 5394)	Novel Protein sim. GBank gij5689473dbj BAA03020.1  - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87188474, 265010, 265011, 87188559, 264601, 265017, 265018, 265019, 264781, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21908768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87188518, 22279002, 264583, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gij841318 (U22818) - mutant sterol regulatory element binding protein-2 [Crictetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 285019, 264288, 21908765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52844150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22278000
2699	87700650 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gij5174395 ref NP_006006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181582, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gij1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264585, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gij2605867 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264558, 264557, 264558, 264559
2703	87649514 (5405, 5408)	Novel Protein sim. GBank gij5689399 dbj BAA02893.1  - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00842) - Zinc finger C-x8-C-x5-C-x3-H type (and similar)		80432288, 265007, 21908765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335894[gb AA863284] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278895, 22278898, 29331828, 29148499, 264805, 264908, 264907, 52844045, 264511, 33857402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264887, 264789, 265021, 264691, 264692, 18108382, 264693, 18108370, 18108374, 264634, 264835
2705	87771745 (5408, 5410)				264489, 264508, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264586, 264486
2706	94328789 (5411, 5412)	Novel Protein sim. GBank gij3255852[emb CAA18621.1] - (AL021728) /prediction=(method;; /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278984, 50894075, 22278897, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264809, 52844045, 56182435, 265008, 265007, 60433438, 55812038, 21908754, 52844298, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21908786, 21908789, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33857023, 264692, 264693, 65274620, 27466264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417284 (AC004381) - Unknown gene product [Homo sapiens]			22278986, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52845129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bb 147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264389, 264288, 264765, 264693, 264565
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127.1 [Homo sapiens]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2710	87627878 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gij3122400[sp]O358a2IMUG_MOUSE · MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264768, 21908784, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 284508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87188518, 87168474, 87188559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264784, 264568, 264288, 264766 264488, 35696288, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433358, 265010, 285019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87188518, 60432113 66714117, 264908, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gij5081315[gb]AAD39343.1[AF076607] prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	- transferase	
2713	86003084 (5425, 5426)	Novel Protein sim. GBank gij2477513 (AC002398) - F25985_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5428, 5430)	Novel Protein sim. GBank gij4321988[gb]AAD158971 - (AF067430) Smarcat1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264638
2716	86003088 (5431, 5432)	Novel Protein sim. GBank gij2477513 (AC002398) - F25985_3 [Homo sapiens]		glycoprotein	264031, 264259, 29331822, 66714117,
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gij3327046[gb]BAA315911 - (AB014516) KIAA0818 protein [Homo sapiens]			264908, 264369, 264693, 264558, 264563 264593, 264558
2718	79604082 (5435, 5436)				264693
2719	86180423 (5437, 5438)	Novel Protein sim. GBank gij746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87188559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gji1335873 (U46889) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	18108374, 60424179, 264489, 56182435, 21908765, 21908766, 35698423, 22278997, 265020, 265022, 265005, 265008, 264092, 264636, 60432229, 284691, 284692, 33657023, 284693, 33657402, 83373044, 29331824, 18108366, 60424269, 29331826, 18108385, 52845129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 285019, 22278002, 284905, 264482, 284563, 264906, 18108351, 284681, 18108370, 29331830, 264908, 66712502, 32844045, 284909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gji4928663 [gb]AAD34092.1 [AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023	22278995, 35698286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21908766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 58182323, 22278000
2722	91638607 (5443, 5444)	Novel Protein sim. GBank gji3212997 [gb]AAC23434.1 - (AC004987) match to ESTs AA667999 (NID:g2826700), AA185485 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040854 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - oncogene TBC domain	35696286, 22278999, 21906754, 265017, 264762, 264288, 21908765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)			UNCLASSIFIED
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gji4880881 [gb]AAD27730.1 [AF13295 - (AF132955) CGI-21 protein [Homo sapiens]		ubiquitin
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gji3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gji3342738 (AC005328) - R28660_1, partial CDS [Homo sapiens]		MHC

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - synthase RNA pseudouridylate synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696032, 29331828, 33656970, 284509, 66712502, 284910, 33657402, 60433438, 264758, 55812038, 21908754, 33657084, 55811386, 265018, 265019, 264767, 21908765, 21908767, 21908769, 55811957, 35695917, 52844150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486285, 33657349, 55811576, 35696423, 35695855, 264830, 60431850, 264638, 56182323, 87168518, 60432113, 22278000, 264564, 264565	
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811957, 35695855, 285021, 284690, 284558, 264259, 284557, 29331822, 284559, 284448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408089 emb CAB16300  - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 284259, 60432289, 66712502, 56182435, 284448, 264288, 264369, 55811957, 285021, 284557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264887, 29331824, 29331826, 35696032, 284107, 56182435, 265008, 265009, 284592, 60431735, 265011, 264601, 265017, 18108351, 284288, 29148627, 55811957, 265021, 284690, 18108388, 18108374, 284557, 284558, 284559, 18108387, 56526486, 264566, 264488
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KO PROTEIN C26A3.1.1 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696032, 265008, 284758, 264762, 284448, 284288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399  - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 285006, 265008, 264910, 265009, 264690, 284555, 284259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 284448, 283972, 284369, 284567
2733	87363060 (5465, 5466)	Novel Protein sim. GBank gi 4519621 dbj BAA76670.1  - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	28331825, 264509, 284809
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gi 4519621 dbj BAA76670.1  - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	60424179, 52844507, 56182575, 284259, 29331828, 284907, 264510, 284910, 60433356, 265019, 55811150, 264681, 284763, 284687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712338 (5469, 5470)	Novel Protein sim. GBank gll3850589 (AC005278) - ESTs gblT21278, gblT45403, and gblAA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278998, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264537, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264903, 264628, 264629, 263978, 264632, 264564
2737	87604528 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gll2558501[gb]BAA22896] - [D83850] hepaloma-derived growth factor [Mus musculus]			264488, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gll5420387[emb]CAB46679.1] - [AJ243459] proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gll3417386[emb]CAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 80432228, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264368, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657108, 18108370, 18108374, 55810764, 35695855, 264634, 80431850, 264639, 58182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gll3242764 (AC005154) - similar to protein U28928 (PID:g881308) [Homo sapiens]		UNCLASSIFIED	22278998, 52644045, 52644229, 21906768, 21906769, 265020, 80170815, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gll4758412[ref]NP_004472.1pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GallNac-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264805, 264758, 55812038, 264368, 29146627
2743	87827991 (5485, 5486)	Novel Protein sim. GBank gll4468311[emb]CAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264908, 264908, 265006, 80433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 80432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gll3880433[emb]CAA91399] - (Z86521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL.C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00163) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331828, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 284482, 264448, 264486, 264369, 264288



2745	87740125 (5488, 5490)	Novel Protein sim. GBank gl 4405795 gb AAD19826  - (AF038863) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - helicase domain Helicases conserved C-terminal domain	35698286, 284509, 284905, 284907, 284908, 284909, 264510, 264512, 265008, 264758, 284801, 285017, 284804, 284783, 264288, 264886, 284769, 284693, 35698423, 35695855, 264634, 264636, 264563, 284564, 284565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gl 4758738 ref NP_004680.1 pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 284907, 284908, 284909, 52644045, 265008, 60170831, 264596, 55812036, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 285020, 264690, 33657023, 284693, 33857109, 18108368, 18108374, 264558, 18108385, 22278000, 264563
2747	94112877 (5493, 5494)	Novel Protein sim. GBank gl 4557803 ref NP_000262.1 pNPC1 - Niemann-Pick disease, type C1	glycoprotein	284569, 52644507, 18108394, 22278995, 35698286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35698052, 264907, 284908, 284909, 265009, 33109954, 55811386, 87188474, 265010, 87188559, 264603, 265019, 264760, 264686, 264768, 21906789, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35698423, 35695855, 264556, 58182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gl 4191272 emb CAA09984  - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.	65274572, 29331828, 284112, 284511, 265019, 264760, 264767, 264768, 264789, 21906768, 21906769, 285020, 27486262, 58526488, 87188518, 22278000
2749	97346307 (5497, 5498)			264259, 284908, 284510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87338344 (5499, 5500)	Novel Protein sim. GBank gl 1872498 U74297  - PIUS [Oryctolagus cuniculus]	UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 284595, 33657084, 265011, 265019, 18108351, 264288, 284686, 264769, 264689, 55811957, 284693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)		UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gl 3041859 AC004534  - OG-2 homeodomain protein-like; similar to U65067 (PID:gl1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	

2753	941138972 (5505, 5508)	Novel Protein sim. GBank gij3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 284288, 56181562, 21908767, 21908788, 265021, 264693, 18108374, 65274791, 284632, 56182323, 22278002, 264583, 264587
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gij53428 (U13736) - calmodulin-like protein [Plum salinum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35686052, 29331828, 264808, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21906765, 21908767, 265022, 33657023, 264693, 56182323, 18108382, 22278000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gij2986653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465808 (5511, 5512)			UNCLASSIFIED	264594
2757	85381590 (5513, 5514)	Novel Protein sim. GBank gij1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	eph	85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gij3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gij2072200 (U84863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 284508, 56182435, 21908754, 55811957, 284628, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gij4814573 (emb) CAB-3885_1 - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	nuclease	22278998, 29331822, 29331830, 265010, 265019, 264288, 21908765, 21908768, 21908769, 265020, 56182323, 22279002, 264563
2762	87592698 (5523, 5524)	Novel Protein sim. GBank gij3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264806, 264909, 265008, 285007, 264757, 265010, 265011, 265017, 265018, 18108351, 264448, 264683, 284686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108385, 33657109, 18108388, 18108370, 18108381, 18108382, 18108384, 18108388, 87168519
2763	87539888 (5525, 5526)	Novel Protein sim. GBank gij3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264369, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gij2805843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FOGY family of carbohydrate kinases		52648842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 284905, 284907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27486282, 56182323, 56526486, 87168519, 264487

2765	94315105 (5529, 5530)	Novel Protein sim. GBank gl 4698672 emb CAA17688.2  - (AL022016) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])		264488, 65274572, 22278995, 35698286, 22278998, 22278999, 264259, 29331822, 29331824, 35698052, 264508, 284509, 284905, 284908, 284907, 284908, 284909, 284512, 284910, 285009, 284592, 284595, 284798, 59812038, 33109954, 285010, 87188558, 284600, 285018, 264760, 264761, 284762, 284763, 284448, 264764, 284288, 284766, 284767, 284768, 56181562, 21908764, 21908765, 21908768, 35695917, 285021, 284681, 284682, 33657023, 33657109, 284628, 18108370, 284629, 18108374, 55811576, 35698423, 35695855, 284631, 284634, 284635, 284636, 284637, 284638, 284558, 284839, 83373044, 87188518, 22279000, 22279002, 284563, 284482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gl 5441611 emb CAB46854.1  - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	294488, 65274572, 60432289, 264907, 264909, 284511, 264512, 60433356, 264288, 264885, 264688, 35695917, 265022, 264693, 264628, 65274791, 284635, 284555, 284556, 264557, 284638, 264558, 284559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gl 1079451 pir A55463 - tropomodulin, skeletal muscle - chicken	struct	264112, 263974, 264558
2768	94322238 (5535, 5538)	Novel Protein sim. GBank gl 5441322 emb CAB4672.1  - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]	UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 284508, 264509, 264905, 284906, 284907, 29331830, 284908, 284909, 284510, 284511, 284512, 265008, 264810, 285009, 284591, 284592, 264593, 33657402, 284594, 284595, 264757, 264596, 285011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 284686, 284768, 18108357, 284769, 284689, 21908768, 21908769, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 284629, 18108374, 35698423, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284555, 284638, 284639, 83373044, 284563, 284564, 284565, 284566, 284486, 284567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gl 5419859[emb CAB46375.1] - (AL086725) hypothetical protein [Homo sapiens]		Iubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264891, 33657023, 264692, 33657109, 18108374, 55811576, 264834, 264836, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21908765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gl 5701865[emb CAB52157.1] - (AL108736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 29331822, 29331824, 29331825, 264369
2771	98084071 (5541, 5542)	Novel Protein sim. GBank gl 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264768, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264486
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gl 4885531[ref NP_005465.1 ]pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	18108374, 264686, 264687, 263976, 56182435, 264889, 55810764, 21906766, 35696423, 55811576, 65274791, 56181886, 55811957, 35695855, 264110, 265021, 264112, 265022, 265008, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264737, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27466261, 29331828, 35696052, 55811386, 264107, 60432113, 285017, 55811150, 18108351, 264681, 264908, 18108370, 264484, 264682, 20281059, 264448, 66712502, 264683, 264764, 264288, 264684, 264768, 263974, 22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21906768, 21908767, 21906769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22278999, 264482
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gl 3288888 (AC005253) - R28445_1 [Homo sapiens]		UNCLASSIFIED	
2774	87619908 (5547, 5548)	Novel Protein sim. GBank gl 465852[sp P34388]YLS3 CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	

2775	95307987 (5548, 5550)	Novel Protein sim. GBank gi 4688132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - ribosomal prot Ribosomal protein S7p/S5e	264488, 22278985, 56994075, 22278998, 35699286, 22278998, 22278999, 264258, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264682, 264389, 264288, 18108354, 52644228, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2776	87701557 (5551, 5552)			56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21908754, 55811386, 265017, 265019, 264448, 264288, 21906765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 265022, 60170615, 55810764, 55811578, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)		UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)		UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]	UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35696052, 265006, 264512, 264448, 264288, 29148827, 18108364, 20281149, 18108370, 264629
2780	94678397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pHGX - HPK/GCK-like kinase	Contains protein domain (PF00780) - Kinase GNH domain	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF089502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - ubiquitin Ubiquitin carboxyl-terminal hydrolase family 2	60424178, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 58181562, 21908765, 21906768, 21908768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - struct Leucine Rich Repeat	65274572, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264780, 264683, 264288, 264766, 264685, 264686, 264768, 52644229, 264689, 21908768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5568)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		tm7	264809, 264628, 263878, 263981
2784	87614360 (5567, 5568)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gij2134933[pri]S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 285020, 264564
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gij2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901268 (5573, 5574)	Novel Protein sim. GBank gij5174507[re]NP_006020.1[pMA1] - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108385, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 284908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080844 (5575, 5576)	Novel Protein sim. GBank gij3252828 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gij2495728[sp]Q92556[Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)]		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gij510172[emb]CAB45135.1] - (AJ242978) p821 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264258, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264784, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gij2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	85083783 (5583, 5584)	Novel Protein sim. GBank gij2854163[gb]AAC02581.1] - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 284259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264906, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 285010, 285011, 285017, 285018, 265019, 264682, 264448, 264288, 264369, 264768, 52644229, 21906765, 21906768, 265020, 285021, 33657023, 263974, 18108374, 65274781, 35695855, 264638, 264556, 264558, 56182323, 83373044, 18108385, 56526488, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2785	85334888 (5588, 5590)	Novel Protein sim. GBank gi 5454148 ref NP_006348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35698288, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331828, 29331827, 35698032, 29331826, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33108954, 85658542, 265018, 265019, 264288, 264866, 21908764, 21908765, 21908768, 21908768, 21908769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526466, 60432113, 22279002, 264482, 264563, 264484, 264567
2786	94848857 (5591, 5592)	Novel Protein sim. GBank gi 4680851 gb AAD27715.1 AF132940 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264480, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264598, 21908754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274781, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22278000, 264563, 264564, 264565, 264566, 264567
2787	95110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1  - (AF143858) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 26148498, 264509, 264508, 56182435, 264757, 21908754, 265010, 265017, 265019, 264681, 264682, 264683, 264688, 21908765, 21908767, 21908768, 21908769, 26148629, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22278002, 264563
2788	88198003 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264486, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264489, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331828, 35696052, 29331828, 264909, 60433356, 33657402, 33108954, 87168474, 264448, 52844229, 21908766, 21908767, 21908768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000, 264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264686, 60170815, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264558, 264559, 87188518, 264564, 264566, 264567, 265007, 264687
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74828.11 - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter		264448, 35695855
2803	79577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC00658 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED - peptidase	264639 264566
2805	87398488 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87888951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148628, 265022, 52644150, 56182323



2807	91720702 (5813, 5814)	Novel Protein sim. GBank gl 468310 emb CAB37891  - (AL031432) dJ468N24.1 (PUTATIVE novel protein similar to Predicted yeast and worm proteins) [Homo sapiens]	UNCLASSIFIED	52644507, 52645156, 52846842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 35698032, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433358, 264594, 60433438, 52846317, 21908754, 33109954, 33657084, 52844296, 87168474, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52844229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 52844150, 33657023, 52645128, 33657109, 33657182, 27486261, 27486262, 27486284, 27486285, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87188518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gl 5541863 emb CAB51071.1  - (AL096857) hypothetical protein [Homo sapiens]	MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gl 2772561  - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:g118965) [Homo sapiens]	ATPase_associated	18108351
2810	87259032 (5619, 5620)			
2811	91235845 (5621, 5622)		UNCLASSIFIED	284569, 22278996, 284091, 284259, 29331828, 29146499, 29146629, 29148784, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gl 3284583 (AC005189) - match to ESTs H87759 (NID:g118943) and AA085546 (NID:g182873) [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 66712502, 264693
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gl 4240273 db BAA74815.1  - (AB020699) KIAA0892 protein [Homo sapiens]	UNCLASSIFIED	264106
2814	90980908 (5627, 5628)	Novel Protein sim. GBank gl 3548791 (AC005620) - R33590.1 [Homo sapiens]	UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87188518, 60432113
2815	78774521 (5629, 5630)		transcription factor	85274572
2816	85366228 (5631, 5632)	Novel Protein sim. GBank gl 5420389 emb CAB46880.1  - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284907, 284909
			UNCLASSIFIED	284486, 35696286, 29331825, 29331828, 264508, 284509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21908765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gl 1203846 (U56986) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263878, 264634, 264638, 264639, 264584, 264565, 264566, 264488, 264597
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gl 549986 (U13149) - possible apospory-associated protein [Pennisetum dillare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87783527 (5637, 5638)	Novel Protein sim. GBank gl 4929773 (gb AAD34147.1) AF15209 - (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	264909, 264511
2820	87785744 (5639, 5640)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	UNCLASSIFIED	16108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264638
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gl 2224671 (db BAA20820) - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21908765, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)	Novel Protein sim. GBank gl 3659683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			264760
2826	94311805 (5651, 5652)	Novel Protein sim. GBank gl 3659683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906768, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35698423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320518 (5653, 5654)	Novel Protein sim. GBank gi 398144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284488, 263994, 264489, 65274572, 29331822, 68714117, 29331827, 29331828, 264508, 264905, 264509, 264806, 264907, 264908, 264909, 264310, 265008, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21908754, 285011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264890, 264691, 264692, 264693, 263972, 264629, 35895855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264593, 264584, 264565, 264566, 264587, 264488, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35896052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264768, 264686, 55811957, 18108370, 18108374, 55810784, 35898423, 55811578, 56182323, 83373044, 87168518, 22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 68712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906785, 21906789, 21906769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264585, 264485, 265008, 265019, 264639, 22279002
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680889 gb AA027734.1 AF13295 - (AF132959) CGI-25 protein [Homo sapiens]			
2830	86087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1  - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772  - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1  - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	284259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87768482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 284907, 284909, 265008, 265007, 265018, 265019, 264682, 264288, 21906766, 21906787, 55811957, 35895917, 18108374, 56182323, 22279000, 22279002
2838	87775382 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 284567
2839	85799317 (5677, 5678)			UNCLASSIFIED	284555
2840	87774663 (5678, 5680)	Novel Protein sim. GBank gij1575515 (U84899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			284509, 264511, 265011, 264288, 264769, 265020, 264634, 264638, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj]BA420780] - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35895855, 264631, 264559, 264563, 264567
2842	80080088 (5683, 5684)				264600
2843	91012404 (5685, 5686)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp]Q08879[FBL, MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321718 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	29148498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5308263[gb]AAD41995.1[AC00623] - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij339676 (AC005390) - R31180.1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 284568
2848	87612843 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264450, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264688, 264628, 264629, 264555, 264638, 264556, 264557, 264638, 264558, 264559, 284563, 264566, 264567
2849	86084203 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623638 (5699, 5700)			UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321819[gbjAA015788.1] - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35895855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U86308) - similar to drosophila membrane protein PATCHED SP-P18502 (PID:g128645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - Kinase WW domain		56182575, 55811150, 264690, 27486262, 27486285, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079086) [Homo sapiens]	Contains protein domain (PF01344) - dna_ma_bind Kelch motif		35686286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723858 (5709, 5710)	Novel Protein sim. GBank gij1504040[gbjBAA13218] - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00580) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264908, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486285, 83373044, 22279000, 22279002, 264482
2856	88083359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085548 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486282, 265007, 265009, 285017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044078 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695783, 22279002, 264583
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585[spjP35227]ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00087) - dna_na_bind Zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264908, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gij4325320[gbjAA017331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	21906768, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264829, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264586, 264486, 264567, 60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2880	87532589 (5719, 5720)	Novel Protein sim. GBank gij4469188[emb]CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5'-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 28331822, 28331824, 28331825, 28331826, 28331827, 28331828, 284510, 284511, 33109954, 18108351, 284683, 284765, 284389, 284686, 21908765, 284691, 284692, 284693, 18108388, 22279002, 284482
2881	8688507 (5721, 5722)	Novel Protein sim. GBank gij3941730 (AF108083) - BS4 [Homo sapiens]			284389, 284692
2882	87568585 (5723, 5724)	Novel Protein sim. GBank gij4505013[ref]NP_002310.1[plRN] - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2883	91220421 (5725, 5726)	Novel Protein sim. GBank gij3249088 (AC004473) - Contains similarity to goliatin protein gbjM97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type		56994075, 35696286, 22278998, 28331822, 28331824, 35696052, 28331828, 284106, 284511, 55812038, 33657084, 55811388, 285018, 285019, 21906765, 21906768, 21906769, 35695917, 285020, 285022, 33657023, 33657109, 33657349, 284629, 18108378, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2884	87420030 (5727, 5728)	Novel Protein sim. GBank gij1078451[plRN]A55463 - tropomodulin, skeletal muscle - chicken	struct		284259, 284910
2885	85312191 (5729, 5730)	Novel Protein sim. GBank gij438840 (L18048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2886	95105480 (5731, 5732)	Novel Protein sim. GBank gij585703[sp]Q07068[PMP2_RAT] - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		65274572, 22278998, 22278998, 22278999, 284259, 28331824, 28331827, 28331828, 60433438, 21906754, 285018, 284448, 284764, 52844150, 83373044
2887	86808001 (5733, 5734)	Novel Protein sim. GBank gij4580987[gb]AAD2457.1/AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		284488, 284768, 21906798, 22278998, 285022, 284258, 284508, 284805, 284907, 284511, 284910, 284635, 284636, 284637, 285011, 285017, 285018, 285019, 284583, 284088, 284568, 284764, 284389, 284587, 284486, 284288, 284768

2868	95303283 (5735, 5738)	Novel Protein sim. GBank gl 1282869 emb CAA63923  - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35896052, 29331828, 264508, 52844045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433356, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 285021, 285022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35898423, 35895855, 284632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gl 5306283 gb AAD41995.1 AC00823 - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567, 263981
2872	95312187 (5743, 5744)	Novel Protein sim. GBank gl 112205 pir B39066 - proline-rich protein 15 - rat	kinase	
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35698423, 35698288, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264258, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264908, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	52645507, 52645158, 52646385, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424266, 29331825, 68714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 285007, 265009, 60433358, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 285018, 265019, 264692, 264369, 264288, 264888, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35698423, 56182323, 18108387, 87168518, 60432113, 22278000, 22279002, 264563, 264565
2875	88083726 (5748, 5750)	Novel Protein sim. GBank gij2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1738918) [Homo sapiens]	Contains protein domain (PF00350) - Leucine Rich Repeat	glycoprotein	22278996, 22278997, 22278998, 29331826, 29331828, 29146499, 68712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108378, 18108377, 55811576, 60170394, 22279000, 264487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Fibroblast growth factor	Ig	
2877	84747029 (5753, 5754)	Novel Protein sim. GBank gij4704208 [emb]CAB41846.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]			52646385, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424259, 60432289, 29331827, 35698052, 29331828, 68712502, 52644045, 56182435, 60433356, 33657402, 33857084, 265018, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264658, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij3876775 [emb]CAB03057] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - Uncharacterized protein family UPF0034	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264805, 264509, 264907, 264809, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567



2879	87888122 (5757, 5768)	Novel Protein sim. GBank gll4895145jgb/AAD32752.1] - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - UNCLASSIFIED	18108359, 284259, 284905, 18108370, 284629, 284908, 284909, 18108374, 18108377, 285008, 284910, 284637, 60170394, 284559, 285017, 284564, 284565, 284587, 284684, 284369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gll4880703jgb/AAD27741.1]AF13298 - (AF132988) CGI-32 protein [Homo sapiens]		284488, 52846365, 52846842, 22278994, 35988286, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331828, 29331827, 35988052, 29331828, 284107, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 52844045, 284510, 285006, 284511, 285007, 284512, 285009, 284910, 284594, 21908754, 52846317, 52844289, 87188559, 284600, 284604, 284605, 284760, 284764, 284288, 284766, 284768, 284687, 284769, 21908768, 21908769, 359895917, 285021, 284690, 284692, 33657023, 52845129, 33657109, 33657182, 27486262, 33657349, 284629, 18108374, 35989585, 284634, 284635, 284636, 284637, 284638, 284557, 52844332, 284558, 284559, 83373044, 284404, 22279000, 284563, 284483, 284587, 284486
2881	87850539 (5781, 5782)	Novel Protein sim. GBank gll733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 29331822, 52844045, 21906765, 284639, 60432113
2882	87714387 (5783, 5784)	Novel Protein sim. GBank gll118112 (U41559) - No definition line found [Caenorhabditis elegans]		284488, 22278996, 22278999, 29331822, 29331826, 284908, 60170831, 60433356, 55812038, 284881, 284882, 284886, 284887, 284888, 21908768, 21908769, 284893, 283987, 18108374, 55811576, 56182323, 22279002, 284568
2883	95382875 (5785, 5786)	Novel Protein sim. GBank gll488008jgb/AAD31087.1]AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - UNCLASSIFIED	WD domain, G-beta repeat
2884	87784843 (5787, 5788)	Novel Protein sim. GBank gll2224697jdbj/BAA20832] - (AB002378) KIAA0378 [Homo sapiens]	UNCLASSIFIED	285018, 284634
2885	83008308 (5789, 5770)	Novel Protein sim. GBank gll1255889 (U53344) - T07H8.5 gene product [Caenorhabditis elegans]	complementrecept	284686, 284693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gll9882323jdbj/BAA34521.1] - (AB018344) KIAA0801 protein [Homo sapiens]	Contains protein domain (PF00084) - UNCLASSIFIED	60432048, 284259, 28331828, 284908, 284511, 284595, 60433438, 284596, 285017, 284805, 283969, 283972, 284555, 83373044, 87188518, 284566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gll4508015jre]NP_003447.1]pZNF2 - zinc finger protein 205	transcriptfactor	18108351, 284686, 284629, 284631, 284639, 83373044, 284482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gll4508015jre]NP_003447.1]pZNF2 - zinc finger protein 205	Contains protein domain (PF00086) - UNCLASSIFIED	284488, 284259, 28331828, 284508, 284906, 284593, 284758, 284766, 284769, 18108374, 83373044, 284486

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gl 854065 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264768
2891	88084428 (5781, 5782)	Novel Protein sim. GBank gl 3877750 emb CA801509  - (Z78064) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65885 comes from this gene; cDNA EST EMBL:D89451 comes from this gene; cDNA EST EMBL:D68028 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95418745 (5783, 5784)	Novel Protein sim. GBank gl 4929759 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	56274572, 35696286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263987, 35695855
2893	87788014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755885 (5787, 5788)	Novel Protein sim. GBank gl 5669015 gb AAD46135.1  - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type		transcript factor	264259, 265008, 60433438, 52644286, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gl 3924708 emb CAA84646  - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D78135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gl 4885549 ref NP_005456.1 pPKBG - protein kinase B gamma	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain			18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29148499, 264908, 264908, 265007, 265009, 265018, 265019, 264389, 264685, 264689, 21906786, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gl 4502877 ref NP_001296.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433358, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264568
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

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2907	81211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNA-J-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	eph -	52644507, 56182575, 56181686, 22278995, 56994075, 35698286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811388, 265019, 264682, 264389, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2908	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264892, 18108374, 264556, 264838, 264557, 264558
2909	87420225 (5817, 5818)			eph	264239, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi 45393335 emb CA837483.1  - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4469187 emb CA838415.1  - (AL031588) dJ1163J1.3 (novel protein similar to mouse B98) [Homo sapiens]	glucoamylase		52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265008, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637 gb AAD34079.1 AF15184 - (AF15184) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat		52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264883, 264288, 264686, 265021, 264693, 18108388, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065 emb CAA58337  - (X03413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52644507, 52645156, 52646842, 56182575, 35698286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)				264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_008030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - eph Lectin C-type domain	264569, 264488, 264687, 264768, 21908768, 52846842, 21908767, 21908768, 58182575, 29148629, 35695917, 22278998, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432048, 264692, 52845129, 33657109, 33657182, 29331827, 27486281, 35696052, 29331828, 27486282, 27486284, 27486285, 33657349, 29146498, 29146499, 264908, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433358, 56182323, 18108382, 55812038, 18108385, 33108954, 21908764, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264389, 264288, 264768
2918	95337780 (5831, 5832)	Novel Protein sim. GBank gi 5104851 dbj BA80165.1  - (AF000061) 303aa long hypothetical dTDP-4- dehydrothymine reductase [Aeropyrum pernix]	dehydrogenase	52845156, 65274572, 22278994, 22278995, 35696288, 22278998, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264908, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433386, 52646317, 21906754, 33108954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906768, 21906767, 21906768, 21906769, 55811857, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486282, 27486284, 35695763, 18108376, 55811578, 35698423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454548 (5833, 5834)	Novel Protein sim. GBank gi 3169065 emb CAA19260.1  - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690528 (5835, 5836)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi 2584955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696288, 22278997, 284259, 52845080, 28331824, 29331826, 29331827, 284828, 284909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 285011, 264601, 285017, 285019, 264681, 264687, 21906767, 285021, 52644150, 284690, 284691, 284692, 264693, 33657109, 33657182, 27486262, 27486284, 27486285, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108355, 87168518, 80432113, 35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29146498, 284104, 284105, 264107, 284509, 264110, 264112, 264512, 60433358, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 284555, 263981, 55528488, 87168518, 22278900, 22279002, 264906, 264909, 264511, 265008, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29146627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 284555, 264558, 56182323, 60170394, 22279000, 264486
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gi 4580013 gb AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 285009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52844150, 264691, 284692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22278900, 264563, 264568
2922	87748762 (5843, 5844)	Novel Protein sim. GBank gi 4569514 db BAA76779.1 - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 285009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52844150, 264691, 284692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22278900, 264563, 264568
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gi 483526 emb CAB42898.2 - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 285009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52844150, 264691, 284692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22278900, 264563, 264568
2924	87781967 (5847, 5848)	Novel Protein sim. GBank gi 2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomal prot	265017, 264628, 20281152, 284556
2925	95080120 (5849, 5850)	Novel Protein sim. GBank gi 238898 emb CAB11718 - (Z88980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		58182575, 35696286, 264259, 60432289, 29331827, 284508, 52844045, 284910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 285022, 60170615, 284692, 33657023, 284693, 33657109, 35696423, 65274791, 56182323

2928	95343003 (5851, 5852)	Novel Protein sim. GBank gl 283032 pir j S22456 - hydroxyproline-rich glycoprotein - perennial leontine			29331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2927	80408018 (5853, 5854)				
2928	20452178 (5855, 5856)			UNCLASSIFIED	264559
2929	81622920 (5857, 5858)	Novel Protein sim. GBank gl 3413320 emb CAA06915 - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52845080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52844045, 265008, 33109954, 52844286, 87168539, 264780, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52844045, 56182435, 285008, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 285018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170815, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	84312693 (5881, 5882)	Novel Protein sim. GBank gl 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW/Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52845156, 22278997, 22278998, 29331822, 52845080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906768, 21906769, 21906770, 21906778, 265020, 52844150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264568
2932	79632623 (5883, 5884)				264906, 264907
2933	81720776 (5885, 5886)	Novel Protein sim. GBank gl 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52844045, 56182435, 265007, 285009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52844229, 21906765, 21906768, 21906769, 265022, 52844150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486282, 264628, 87168518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 264448, 264788, 21908784, 21908765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gl[4153662 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811578, 18108387, 60432113, 264563
2937	94853098 (5873, 5874)	Novel Protein sim. GBank gl[5174409ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264908, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52844228, 21908765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264585, 264488, 264567
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gl[3319890 emb CAA76720) - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 285008, 265009, 60432228, 33657402, 60433438, 55812038, 21908754, 65658542, 285010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21908765, 21908767, 21908768, 55811957, 35695917, 265020, 60170615, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263978, 35696423, 35693855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56528486, 60432113, 22279002
2939	87766822 (5877, 5878)	Novel Protein sim. GBank gl[3978900 emb CAA99809) - (Z75547) similar to WD domain, G-beta repeat: cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686



2940	95011103 (5879, 5880)			UNCLASSIFIED	22278986, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264568 284557
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gij3413872jdbjBAA32300j - (AB007824) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gij1172845jlpj46629jRB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gij4829653jgbjAAD34087.1jAF15185 - (AF15185) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 264593, 80433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 284587
2944	95081083 (5887, 5888)	Novel Protein sim. GBank gij4678282jembjCAB41190.1j - (AL049680) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	56994075, 22278998, 60432049, 284259, 29331822, 29331824, 60424289, 60432289, 29331826, 29331828, 264905, 264907, 52844045, 264909, 264511, 265006, 265009, 284594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21908765, 21906766, 21908767, 21906768, 21908769, 265021, 60170615, 52844150, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 58525486, 87168518, 60432113, 22279002, 264482, 264583, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gij72883jlpjP39188jALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424289, 60432289, 35696052, 264908, 285006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264687, 56181562, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 264693, 80431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 284568, 264587

2846	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	284488, 284259, 284508, 284509, 284806, 284907, 284809, 284510, 284511, 285007, 284512, 284910, 284591, 284593, 18108351, 284764, 284288, 284684, 284769, 285021, 284692, 33657109, 284628, 284629, 18108374, 284631, 284634, 284636, 284637, 18108380, 284638, 284639, 83373044, 284555, 284588, 284496, 284587
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1  - (AF056116) Ali-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 29148498, 264508, 29331830, 265007, 265008, 285009, 60432229, 21906754, 285010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AA65654.2  - (AF001533) mitogen-induced [Mus musculus]			52846842, 22278995, 284259, 29331824, 29331825, 29331827, 29331830, 284809, 285007, 285009, 285019, 284763, 284684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 284563, 284567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278996, 22278997, 60432229, 29331826, 29331827, 29331828, 35696052, 28146499, 284104, 284107, 284905, 66712502, 284808, 60433556, 80433438, 87168559, 284764, 52844229, 56181562, 21906767, 21906768, 21906769, 265022, 60170815, 33857023, 35898423, 263981, 264558, 60432113, 22279002
2950	95088870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 Y0J8_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	284488, 35696286, 284259, 35696052, 284907, 285007, 264910, 265017, 265018, 284288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264556, 58526486, 284486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1  - (AJ238248) centaurin beta2 [Homo sapiens]			284693

2952	95329852 (5903, 5904)	Novel Protein sim. GBank gl 5596693 emb CAB51405.1  - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - transcript factor CRA/TRIO domain.	264687, 52645156, 21908766, 21906769, 22278996, 265020, 284890, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33637109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264908, 264907, 29331830, 284908, 284909, 35695855, 264511, 265008, 265009, 264910, 264835, 264836, 60432229, 264838, 60433358, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gl 119522 sp P10858 ISRC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPiP)	Contains protein domain (PF00286) - UNCLASSIFIED Aminotransferases class-V	18108396, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264908, 264807, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52848317, 21908754, 33657084, 52844296, 87168559, 264600, 264760, 264681, 18108351, 264784, 264369, 264288, 264887, 21906765, 21906766, 21908767, 21906768, 21906769, 35695917, 33657023, 18108364, 52845129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264838, 87168518, 264482, 264563, 264565, 29331822
2954	88088288 (5907, 5908)	Novel Protein sim. GBank gl 4885281 ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Igf domain Transforming growth factor beta like domain	
2955	87698428 (5909, 5910)	Novel Protein sim. GBank gl 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 284908, 52844045, 284512, 60432228, 265018, 265019, 55811150, 264789, 21906787, 21906768, 21908769, 265021, 60170815, 55810764, 264567
2956	85788745 (5911, 5912)	Novel Protein sim. GBank gl 4889254 gb AAD27830.1 AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	22278996, 264259, 29331827, 264908, 21906768
2957	90333301 (5913, 5914)	Novel Protein sim. GBank gl 4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor	cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 284448, 264763, 264683, 264288, 264685, 18108357, 29148628, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 58182323, 18108382, 18108385, 18108388, 58526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gl 4240257 dbj BAA74907.1  - (AB020891) KIAA0884 protein [Homo sapiens]		264595, 264596, 264681, 264369, 264629, 264831, 264587

2859	95109420 (5917, 5919)	Novel Protein sim. GBank gij888221 (U33005) - Tctc1 [Mus musculus]	Contains protein domain (PF00568) - oncogene TBC domain	263994, 22278997, 264259, 60432049, 29331828, 29331828, 35696032, 29331830, 68712502, 56182435, 265008, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906787, 21906789, 265020, 60170815, 264692, 27486265, 18108374, 65274791, 35696855, 83373044, 56328486, 60432113
2960	87420081 (5918, 5920)		UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2981	85413416 (5921, 5922)	Novel Protein sim. GBank gij5596846 (emb)(CAB05177.2) - (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - (transcript factor WD domain, G-beta repeat	22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265008, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906789, 265020, 60170815, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2982	87812700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264583, 264585, 264586, 264587, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gij424023 (dbj)(BAA74880.1) - (AB020874) KIAA0887 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21908754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264893, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)		UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2965	80384782 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRMV - Kreiser (mouse) mal- related leucine zipper homolog		transcriptfactor	264259, 29331826, 264508, 264509, 264805, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264829, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264593, 264597, 18108381 60432289, 264682, 264448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi 526275 emb CAB45690.1  - (Xenopus laevis) [Xenopus laevis]			
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264584, 264486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb A034118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		264687, 52645156, 21906765, 52646365, 21906767, 18108398, 35898423, 22278996, 35896286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264636, 264690, 52644150, 264258, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35896052, 27486282, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 264583, 18108351, 264908, 264907, 264448, 66712502, 264568, 264389, 264288, 52646842, 22278998, 22278999, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264508, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264389, 52644229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22278000
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	
2970	86088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2871	94186930 (5941, 5942)	Novel Protein sim. GBank gi1728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII			lm7	264488, 56182575, 35866286, 56894075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21908754, 87188558, 265018, 265019, 18108351, 264889, 21908765, 21908767, 21908768, 265020, 265021, 60170815, 18108364, 264828, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87188518, 264584, 264587 265017, 35695917, 265021, 33657109, 22279002, 264563
2872	86825943 (5943, 5944)	Novel Protein sim. GBank gi1728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII			kinase	
2873	91215301 (5945, 5946)	Novel Protein sim. GBank gi17246789 (AF040642) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2874	91673002 (5947, 5948)	Novel Protein sim. GBank gi1786117 (L41834) - nuclear protein [Ensis minor]			UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278995, 22278996, 35898286, 22276897, 22278998, 22278999, 264259, 52845080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21908754, 55811386, 52644286, 87188474, 87188559, 265017, 265018, 265019, 18108351, 264448, 264389, 264288, 52644229, 18108359, 21908765, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486282, 27488264, 35695763, 18108370, 18108376, 55810784, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87188518, 60432113, 22279000, 264482, 264487
2875	95326213 (5949, 5950)	Novel Protein sim. GBank gi13880812 emb CAA19508  - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00832) - HECT-domain (ubiquitin- transferase).		ubiquitin	29331824, 29331827, 29331828, 264910, 85858542, 265011, 265018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2876	87771202 (5951, 5952)	Novel Protein sim. GBank gi15878136 gb AAD48874.1 AF16093 - (AF160934) BcDNA LD14189 [Drosophila melanogaster]			transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2877	91726254 (5953, 5954)	Novel Protein sim. GBank gi15282751 emb CAB45890.1  - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5958)	Novel Protein sim. GBank gij748549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433358, 60433438, 21908754, 285010, 285011, 265017, 265018, 265019, 264288, 264685, 264688, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2879	91725258 (5957, 5958)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56984075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2880	86298600 (5959, 5960)				265009, 21908767, 263981, 22279000
2881	87376330 (5961, 5962)			UNCLASSIFIED	264629, 264564
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gij4928767 [gb]AAD34144.1 [AF151907] CGI-149 protein [Homo sapiens]			22278995, 56984075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21908765, 21908768, 21908767, 21908768, 21908769, 285020, 265022, 18108365, 33657182, 33657349, 35698423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424179, 52846842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52844045, 265006, 60431735, 87188474, 265018, 265019, 18108351, 264448, 21908765, 21908768, 35695917, 33657023, 52845129, 18108370, 35698423, 83373044, 56526486, 60432113, 264404, 22279002
2884	94136487 (5967, 5968)	Novel Protein sim. GBank gij2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z88297 (PID:g1130819) [Homo sapiens]	ATPase-associated		
2885	87098072 (5969, 5970)	Novel Protein sim. GBank gij103160 [pir]S22128 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810784, 264632, 264635, 60432113
2886	86284861 (5971, 5972)				55811957, 264568
2887	86455934 (5973, 5974)			UNCLASSIFIED	264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gij4679028[gip][AAD27002.1]- (AF077207) HSPC021 [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331826, 60432289, 35698052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264399, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695955, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567 22278996, 22278997, 264905, 264511, 60170831, 264593, 265018, 21906765, 21906767, 21906768, 18108374 265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gij113671[sp]P23964[ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII	kinase	264563
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gij2828838[sp]P87348[RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	264563
2991	94325361 (5981, 5982)		UNCLASSIFIED	264563
2992	85425184 (5983, 5984)		UNCLASSIFIED	264563
2993	94325363 (5985, 5986)		UNCLASSIFIED	264563
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gij2496549[sp]Q506581YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02	transport	264259, 265019, 264889, 18108385 264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565 22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265008, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695955, 83373044, 18108385, 22279000, 264565, 264566 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		65274572, 35696288, 264259, 29331824, 35696052, 29146499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484
2996	91013788 (5991, 5992)	Novel Protein sim. GBank gij2828912 (AC002281) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	



2997	87627440 (5993, 5994)	Novel Protein sim. GBank gi 4589652 dbj BA017684.1  - (AB023221) KIAA1004 protein [Homo sapiens]	homeobox	264488, 56182575, 264258, 66714117, 29331826, 35898052, 264508, 284509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27488261, 18108374, 35696423, 264634, 264635, 264638, 264557, 18108385, 87188518, 52846385, 22278997, 264508, 264908, 18108351, 21908765, 21906767, 18108370, 18108374, 35898423, 264636, 264639
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gi 3947569 emb CAA22252  - (AL034384) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264638, 264557, 18108385, 87188518, 52846385, 22278997, 264508, 264908, 18108351, 21908765, 21906767, 18108370, 18108374, 35898423, 264636, 264639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gi 115408 sp P18835 CC19_CAEEL - CUTICLE COLLAGEN 19	UNCLASSIFIED	56182575, 22278996, 28147620, 29331825, 29146498, 29146499, 264905, 69712502, 265006, 265009, 21906754, 85858542, 18108351, 29148627, 29148829, 60170615, 33837109, 27486262, 18108370, 18108374, 264558, 264557, 264558, 60170394, 18108385, 264563
3000	95089370 (5999, 6000)	Novel Protein sim. GBank gi 1163174 (U32575) - similar to yeast Sec8p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03168; Method: conceptual translation supplied by author [Rattus norvegicus]	UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35898052, 28146498, 264508, 264905, 264908, 264907, 264908, 284508, 284510, 284511, 285006, 285007, 285008, 285009, 264910, 33857402, 264757, 284595, 264598, 264758, 21906754, 265011, 264600, 265017, 285018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33857023, 284693, 33857109, 33857182, 27486261, 264628, 264629, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20788451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi 2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678046), D31562 (NID:g644442), AA158721 (NID:g173515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]	calthapsin	18108394, 52846842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52844296, 265017, 265019, 264288, 265020, 265021, 52844150, 264892, 35695763, 55810764, 35696423, 56182323, 18108387, 284563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi 3589478 (AF085185) - Myosin-IA [Acanthamoeba castellanii]	UNCLASSIFIED	284488, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 284510, 265009, 21908754, 264682, 264688, 33857023, 264565

3003	86848078 (6005, 6006)	Novel Protein sim. GBank gl1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	284512, 264593, 264564, 264567, 264486
3004	8806876 (6007, 6008)	Novel Protein sim. GBank gl2224629[dbj]BA208021 - (AB002342) KIA0344 [Homo sapiens]			29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gl4680859[gb]AAD27719.1[AF13284 - (AF132844) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21906787, 21906788, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3008	87422224 (6011, 6012)	Novel Protein sim. GBank gl3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gl2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)	Novel Protein sim. GBank gl3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	204905, 264593, 264766, 264636
3009	91213387 (6017, 6018)				52646842, 58182575, 22278995, 22278996, 264259, 29331825, 29331828, 29331827, 29331828, 35698052, 264508, 264509, 264907, 58182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109854, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264389, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27466262, 20281149, 18108370, 55811576, 264637, 264558, 264557, 18108381, 264558, 58182323, 264558, 18108385, 18108368, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gl4827370[gb]AAD33084.1[AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27466261, 29331828, 264508, 264909, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 285019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gl5052319[gb]AAD38501.1[AF11883 - (AF118836) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 58182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87763087 (6023, 6024)			UNCLASSIFIED	263972

3013	81238789 (6025, 6026)	Novel Protein sim. GBank gi 3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcript factor	284488, 263994, 35886286, 22278997, 284259, 29331824, 60424269, 66714117, 35696052, 284905, 284908, 284907, 284908, 284909, 56182435, 284511, 284512, 284910, 284591, 284592, 264593, 264594, 33657402, 60433438, 284595, 264598, 55812038, 284758, 33109954, 21908754, 265010, 265018, 264604, 284760, 284682, 284683, 284764, 284389, 284288, 284785, 284786, 284686, 284788, 284687, 21906767, 35695917, 285020, 33857023, 284692, 284693, 33657109, 284628, 284629, 55811576, 35698423, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 83373044, 284563, 284595, 284586, 284587
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gi 3878374 emb CAA93081  - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33318 comes from...		ATPase associated	284760
3015	8695468 (6029, 6030)				
3016	8775945 (6031, 6032)	Novel Protein sim. GBank gi 168818 sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	22278995, 22278996, 22278997, 284259, 29331824, 29331828, 284908, 265007, 265008, 264910, 265011, 265017, 265019, 284891, 33657109, 18108370, 35695855, 264556, 264564
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gi 4389659 db BAA76851.1  - (AB023224) KIAA1007 protein [Homo sapiens]			52844507, 52846842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52844045, 264598, 33657084, 265017, 265019, 52844229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 35695855, 87168518
					284488, 18108397, 22278996, 35696286, 22278999, 284259, 29331822, 60432289, 264908, 29331830, 284909, 56182435, 265008, 265007, 265008, 265009, 284591, 60433358, 60433438, 52846317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 284687, 21908765, 21908766, 21908767, 21908769, 265020, 285022, 65274820, 52845129, 33657109, 33657182, 18108370, 283972, 18108374, 284631, 52844332, 83373044, 18108385, 18108388, 56528486, 87168518, 264404, 60432113, 22279000, 284567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank gll3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264558 264559, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265009, 60432228, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274781, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563
3020	94318251 (6038, 6040)	Novel Protein sim. GBank gll3414809 (AF081529) - fjs [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gll3880889[emb] (CAB09005) - (Z85559) cDNA EST yk23864.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk32996.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264568
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gll416592[sp]P32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108378, 263978, 264635, 264558, 22279000
3024	86875305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906768, 55811957, 35695917, 264690, 264555, 264559, 264593, 55811576
3025	65706829 (6049, 6050)	Novel Protein sim. GBank gll295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			

3028	87643862 (8051, 8052)	Novel Protein sim. GBank gl 3024052 sp p97824 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21908765, 29148627, 263987, 20281149, 20281089, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (8053, 8054)	Novel Protein sim. GBank gl 4929847 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264789, 264889, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 35695917, 265020, 265021, 265022, 52844150, 264682, 33657023, 264693, 52645129, 33657109, 27486281, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56528486, 22279000, 22279002
3028	94231997 (8055, 8056)	Novel Protein sim. GBank gl 308052 emb CAA18650  - (AL022589) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21908765, 21908768, 21908769, 29148629, 35695917, 265021, 265022, 33657109, 27486285, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264584
3029	87619284 (8057, 8058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263989, 18108370, 264558, 22278000, 22279002, 264482
3030	87544928 (8059, 8060)	Novel Protein sim. GBank gl 3757728 emb CAA18782  - (AL022727) dJ80119.1 (olfactory receptor-like protein [Hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	
3031	91677953 (8061, 8062)	Novel Protein sim. GBank gl 4530587 gb AAD22105.1  - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21908765, 21908766, 21908767, 21908768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gi 1019951 (U37429) - similar to M. musculus MERS and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 284907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264288, 21906769, 285021, 284693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi 5031573 ref NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - slrucl Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 284907, 284908, 284909, 265008, 284591, 21908754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695955, 264632, 264635, 284639, 284482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	284908, 284907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486, 264636
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi 3738207 emb CAA21262  - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	284907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 4406580 gb AAD20040  - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi 5360093 gb AAD42865.1 AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	22278996, 22278997, 264259, 284905, 285007, 265009, 80433356, 21906754, 285018, 285019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486282, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 4757128 emb CAB42094.1  - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 28331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 284691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391, 284692, 264556, 18108382, 18108385, 264567
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1  - (AL050037) hypothetical protein [Homo sapiens]	UNCLASSIFIED	
3041	86312357 (6081, 6082)	Novel Protein sim. GBank gi 3876073 emb CAB04122.1  - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolemmal associated protein-2 [Cryptotagus cuniculus]	glycoprotein	264636

3043	87773028 (6085, 6088)	Novel Protein sim. GBank gi 854085 emb CAA58337  - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	3568286, 60424268, 35696052, 284508, 284805, 66712502, 58182435, 5811386, 52844296, 55811150, 35895917, 60170615, 33657109, 18108374, 284634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042278) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COO5 methyltransferase family	glycoprotein	22278998, 22278998, 22278999, 29331824, 56182435, 284511, 285007, 60170831, 60432229, 60433356, 33108954, 18108351, 284288, 35695917, 18108388, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589880 dbj BAA76859.1  - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	264488, 264259, 35696052, 284508, 284905, 284509, 264906, 284907, 284909, 284511, 265006, 284591, 284593, 33108954, 284604, 284784, 284683, 284288, 284766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 284628, 18108374, 35695855, 264630, 264632, 264635, 264563, 284584, 284566
3046	88088247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 284909, 52846317, 55811957, 60432113, 22279000, 22278002, 264482, 264584
3047	95088924 (6093, 6094)			UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 284768, 21906768, 21906769, 35695917, 52844150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629418 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25862.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284102, 29148784
3049	88228655 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_008285.1 pVARS - valy-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 284907, 264758, 87168559, 265018, 284448, 21908768, 285020, 33657109, 35695855, 60432113, 22279000
3050	87643878 (6099, 6100)	Novel Protein sim. GBank gi 4589842 dbj BAA76843.1  - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284259, 29331825, 264909, 285007, 264512, 285019, 284288, 21908768, 265020, 284693, 18108385, 56526486, 87168518, 22279002, 284566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 284693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN	dehydrogenase		284534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947813 emb CAA19463.1  - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gi 107621 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35698286, 35696052, 28331830, 264908, 264909, 264512, 264910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264636, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265008, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 726837 sp P39194 ALU7 SQ WARNING ENTRY IIII		glycoprotein	264488, 264559, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331828, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567



3057	95412748 (6113, 6114)	Novel Protein sim. GBank gij3878119[embjCAA88860] - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353....			284508, 284905, 284907, 284908, 284909, 284510, 284512, 284910, 284592, 284594, 284767, 18108374, 284635, 284555, 284637, 284639, 284583, 284564, 284565, 284486
3058	78646226 (6115, 6116)			UNCLASSIFIED	284693
3059	87829425 (6117, 6118)	Novel Protein sim. GBank gij4588034[gbjAAD25962.1]AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C2HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 284480, 284259, 29331824, 29331825, 29331827, 35896052, 29331828, 285007, 60433438, 285017, 285018, 285019, 284681, 284448, 284288, 284768, 21906765, 21908766, 21906767, 21906769, 29148629, 29148784, 285022, 52644150, 18108370, 284636, 18108385, 284563, 284567
3060	79346681 (6119, 6120)			UNCLASSIFIED	284567
3081	87740984 (6121, 6122)			UNCLASSIFIED	284112, 52644296, 21906768, 33657023, 283974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gij4454690[gbjAAD20863] - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	284908, 265008, 18108351, 284566
3063	80076023 (6125, 6126)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 284558
3064	91241528 (6127, 6128)	Novel Protein sim. GBank gij4240315[gbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52846365, 52846842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 284259, 60432049, 29331824, 68714117, 284508, 284907, 284908, 56182435, 285009, 60432229, 60433438, 55812038, 52844286, 285018, 284682, 284288, 284686, 284768, 284687, 52644229, 284689, 21908768, 284691, 284692, 284693, 18108370, 18108377, 55811576, 284636, 56182323, 284558, 284639, 18108385, 22278990, 22278992
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gij5658743[gbjAAD45960.1]AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencscan [Homo sapiens]		UNCLASSIFIED	284095, 29331824, 60424289, 68714117, 284100, 284907, 285007, 284591, 60432229, 284593, 265011, 285019, 18108351, 284766, 284767, 21906765, 21906768, 284693, 20281069, 22279000, 22279002, 284482, 284586, 284587

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4894268 emb CABA3245.1  - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 68712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264557
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF12185) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264802, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264688, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56528486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264587, 264486
3068	85360851 (6135, 6136)	Novel Protein sim. GBank gi 3878119 emb CAA88860  - (Z49068) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01928) - struct GTPase of unknown function		264112
3069	95412753 (6137, 6138)	EMBL:M89111 comes from this gene: cDNA EST EMBL:D27709 comes from this gene: cDNA EST EMBL:D73788 comes from this gene: cDNA EST yk353...			22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170815, 33657023, 18108370, 18108376, 264634, 264557, 80170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94318173 (6138, 6140)	Novel Protein sim. GBank g 387778 emb CAB05527  - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474b7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk466c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...	Synthase	264488, 22278994, 22278995, 22278996, 59994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21908754, 87168474, 265019, 18108351, 284448, 264683, 264288, 52844228, 264689, 21908765, 21908768, 21908787, 21908769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 284634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	84325573 (6141, 6142)	Novel Protein sim. GBank g 4502425 e NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Igf Thioridoxin	284488, 65274572, 18108398, 22278996, 35695288, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35695052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 264592, 80433358, 33657402, 60433438, 33109954, 52644298, 87188474, 265010, 265017, 264681, 264288, 264685, 284766, 264687, 264769, 284689, 21908765, 21908768, 21908787, 21908768, 21908769, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35695423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264584, 264585, 264586, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564
3072	95115892 (6143, 6144)	Novel Protein sim. GBank g 1263289 (U47856) - fibrin-4 [Araneus diadematus]	transcript factor	

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi134840 sp P2328 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi13418847 (AC004932) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g588461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264567
3075	88085752 (6149, 6150)	Novel Protein sim. GBank gi4557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56525486
3076	87818219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 284891, 264683
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi3023958 sp Q00808 HET1_PODAN - VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat		65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33857182, 27486264, 33657349, 35695783, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi13900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi13875410 emb CAB02876  - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]	transport		29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21908788, 265020, 265021, 264693, 18108378, 264631, 52644332, 22279002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gi15257221 gb AAD41265.1  - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264882, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906755, 21906767, 21906769, 55811957, 35695917, 265020, 60170815, 52644150, 264682, 33657023, 264693, 65274620, 33857109, 27486261, 35695783, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264585, 264484
3081	88084884 (6161, 6162)	Novel Protein sim. GBank gi1728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264807, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264585, 264588
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	68085768 (6165, 6166)	Novel Protein sim. GBank gij868241 (U26488) - C56C10.3 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij476774(pir)A37475 - probable structural component p38 - borna disease virus		22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265008, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264768, 35695917, 265020, 18108374, 35696423, 264631, 264558, 264555, 264556, 264587, 264486, 265011, 264681
3085	67765781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]	UNCLASSIFIED	
3086	87768942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810784, 263981, 18108385, 264487
3087	87482888 (6173, 6174)			52846365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52846317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52845129, 33657182, 27488262, 35695855, 87168518, 264591
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4688146(pbl)AAD27782.1(AF07704) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35696288, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gll1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	50424179, 52845156, 65274572, 56182575, 56181686, 22278995, 35699286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21908754, 33109954, 52646317, 55811386, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265022, 60170815, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486281, 27486265, 35695763, 18108374, 18108376, 55810784, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22279000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gj3873932(emb)(CAB01859) - (Z79598) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264583, 264685, 264788, 264789, 264789, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264583, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gij11710756[sp P15880]RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	284488, 60424179, 18108398, 22278995, 58994075, 22278988, 35698286, 22278997, 22278998, 60432049, 284259, 29331822, 28331824, 28331825, 29331826, 29331827, 35698032, 28331828, 28146498, 28146499, 284508, 284509, 284905, 284906, 284907, 28331830, 284908, 284909, 284113, 284510, 284511, 265008, 284512, 265007, 265008, 284910, 265009, 60170831, 284591, 284592, 60431735, 284593, 284594, 60433438, 284595, 284758, 21908754, 285010, 265011, 284601, 284602, 265017, 284603, 284604, 265018, 284605, 265019, 284760, 284762, 284681, 18108351, 264763, 284682, 264448, 284784, 284683, 284288, 284369, 284765, 284786, 284688, 284767, 284687, 284768, 284789, 284688, 21908764, 284689, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 29148784, 35695917, 265020, 265021, 284534, 60170815, 284690, 284691, 284692, 65274620, 33657109, 27486262, 284628, 284629, 18108374, 263978, 18108377, 35696423, 284630, 284631, 284632, 284634, 284635, 284555, 284636, 284637, 284556, 284638, 284557, 284558, 284639, 60170394, 18108385, 284259, 29331824, 35696052, 284905, 265006, 60432228, 80431735, 284684, 284369, 284288, 284766, 21908767, 35698423, 83373044, 18108389
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gij5002587[emb CAB44347.1] - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED		18108398, 284259, 60432289, 29331827, 284511, 284763, 284288, 284767, 285022, 284691, 284693, 65274791, 56182323, 284584, 284565
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gij400734[sp P31044]PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	

3095	94848182 (6189, 6190)	Novel Protein sim. GBank gjl4877759jgblAAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 (Homo sapiens)	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432048, 66714117, 29331825, 60432289, 35696052, 33656970, 29146498, 264508, 264905, 284509, 29331830, 284909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 284288, 284686, 264768, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 284952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264389, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gjl3882221 dbj BAA34470.1  - (AB018293) KIAA0750 protein (Homo sapiens)	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gjl4468289 emb CAB37981  - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) (Homo sapiens)	Contains protein domain (PF00846) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gjl303603 dbj BAA02145.1  - (D12621) cytochrome P-450L TBV (Homo sapiens)		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 58182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gjl1083784 pir B48013 - proline- rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	78602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632



3102	91220892 (6203, 6204)	Novel Protein sim. GBank gij5305708jbp/AA041781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	struct	35696286, 22278998, 22278999, 29331827, 35696052, 264909, 284512, 285008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21908767, 60170815, 284692, 33657023, 284638, 22278000, 284482, 264564 UNCLASSIFIED
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gij484584isp/P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	35895917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gij5032207 refNP_005698.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	284259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 284905, 284906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 284692, 284693, 284628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 284404, 22279002, 264563, 264565, 264566, 264466, 264567
3106	95381416 (6211, 6212)	Novel Protein sim. GBank gij1938574 (U87190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52844045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264883, 264888, 264687, 264769, 52844228, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264680, 52844150, 264692, 284693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gij3341441 emb CAA76851  - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 285009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 284691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 55526488, 264492, 264487, 56182435, 264288, 264690, 264564
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gij5032207 refNP_005698.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[emb]CAB44347.11 - (Y17454) LSR1 protein [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	strudt	264480, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21908767, 21908768, 264683, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95080716 (6219, 6220)	Novel Protein sim. GBank gij1076211[pir]S50735 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278985, 22278987, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264608, 264510, 265008, 265007, 265008, 265009, 60432228, 33657402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21908768, 21908767, 21908768, 265020, 60170815, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264583, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21908767, 265020, 33657023, 18108385, 18108388, 35696423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3800848 (AC005023) - match to EST AA361117 (NID:2013438) [Homo sapiens]	Contains protein domain (PF000046) - Homeobox domain	homeobox	
3113	88207088 (6225, 6226)	Novel Protein sim. GBank gij2459910 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	im7	18108397, 22278999, 264259, 29331824, 35696052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21908767, 21908768, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22278000, 22279002
3114	78843187 (6227, 6228)	Novel Protein sim. GBank gij4868270[gb]AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	264908, 66182435, 264810, 21908754
3115	94117866 (6229, 6230)	Novel Protein sim. GBank gij5032225[re]NP_005876.1[pw]BSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424176, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812036, 55811386, 265019, 264288, 264689, 21908768, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	78642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21908764, 264690
3117	87771268 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264584

3118	84665848 (8235, 8238)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1  - (Z78018) predicted using GeneFINDER; similar to serine/threonine kinase; cDNA EST YK353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF000008) - Igr EGF-like domain	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 284905, 264908, 28331830, 52844045, 56182435, 264510, 264511, 265007, 265008, 265009, 284757, 52846317, 21906754, 33657084, 52844296, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264882, 284884, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52844150, 264691, 33657023, 284693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35698423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 284488, 265008, 264288
3119	85728796 (8237, 8238)		Contains protein domain (PF003328) - Histidine acid phosphatase	
3120	87344040 (8239, 8240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264488
3121	84110735 (8241, 8242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR  - acrosin		52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52844150, 33657023, 18108374, 264637
3122	11814528 (8243, 8244)		UNCLASSIFIED	284638
3123	86083003 (8245, 8246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g13456860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27488265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766899 (8247, 8248)		UNCLASSIFIED	264805
3125	81216607 (8249, 8250)	Novel Protein sim. GBank gi 4980828 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 28148627, 29148628, 33657023, 33657109, 18108382, 56528488

3128	95337205 (6251, 6252)			UNCLASSIFIED	22278989, 264490, 264259, 60432049, 29331822, 60432289, 29148498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264369, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 3596286, 22278996, 22278999, 29331826, 264908, 60433438, 87168559, 264604, 21908765, 21908769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gjl2629280(emb)(CAA16694.1) - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gjl3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21908764, 265017, 265018, 21908768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gjl3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331826, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566
3130	14983860 (6259, 6260)	Novel Protein sim. GBank gjl3329465 (AF064553) - NSD1 protein [Mus musculus]			264636
3131	95351468 (6261, 6262)	Novel Protein sim. GBank gjl1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 264448, 264766, 21908769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 85274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52844507, 52846842, 52846365, 85274572, 56182575, 22278994, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52844045, 56182435, 284910, 60170831, 60432229, 60433356, 33657402, 55812038, 52846317, 21906754, 52844296, 85658542, 87188559, 285017, 265018, 285019, 264448, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52844150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526466, 87168518, 60432113, 22279002
3133	67379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264685, 264628, 264566
3134	94848818 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	88389356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278998, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi 627101 pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 285019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257647 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 285017, 285018, 285019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811857, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	04130188 (8275, 8276)	Novel Protein sim. GBank gij4406759[gbjAAD20070] - (AC006838) hypothetical protein [Arabidopsis thaliana]			264589, 264488, 264907, 264511, 264593, 33109954, 87188559, 264681, 264684, 264685, 264686, 264687, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (8277, 8278)	Novel Protein sim. GBank gij228938[prj]1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21906785, 265020, 264636, 264557
3140	91222892 (8279, 8280)	Novel Protein sim. GBank gij832[embjCAA37773] - (X53744) 88kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56984075, 35696286, 264908, 264909, 60433356, 21906754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35695855, 264630, 264555, 264568
3141	87323584 (8281, 8282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264369, 21906766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (8283, 8284)	Novel Protein sim. GBank gij2498197[spjQ85245][C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)]	cytochrome		52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29148499, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 264758, 21906754, 264288, 264766, 264687, 52844228, 21906765, 21906767, 21906768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (8285, 8286)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265018, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263978, 55811578, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264488

3144	95330329 (6287, 6288)	Novel Protein sim. GBank glij488446[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264486, 18108396, 22278996, 35696286, 22278997, 22278998, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21908765, 21908766, 21908767, 265020, 265021, 52644150, 27486281, 18108370, 18108374, 35696423, 56182323, 83373044, 22278900, 22278902, 264567
3145	86811657 (6289, 6290)	Novel Protein sim. GBank glij3679709[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from l...	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21908766, 29146827, 21908769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87188518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank glij2135746[pir]S69890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - struct PH domain		264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21908768, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank glij3674279[emb]CAB07315.1] - (Z82825) predicted using GeneFinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	56181866, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22278902
3148	95362169 (6295, 6296)	Novel Protein sim. GBank glij5225322[gb]AAD40851.1[AF08310] siruin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56528488, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank glij4200448 (AF102777) - FYVE finger-containing phospholipase kinase [Mus musculus]	Contains protein domain (PF01363) - eph FYVE zinc finger		29331822, 35696052, 264109, 29146829, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank glij3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - transferase Glutathione S-transferases.		264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264688, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank glij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - oncogene Zinc finger, C2H2 type		29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21908754, 87168559, 264605, 21908768, 52644150, 27486284, 35696423, 22278900

3153	95317289 (6305, 6306)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 52645365, 35688286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87188474, 87188559, 264801, 265019, 264448, 264682, 264784, 264288, 264369, 264768, 21908765, 21908768, 21908787, 21908788, 21908769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264891, 33657023, 65274620, 33657109, 18108370, 35689585, 264638, 60170394, 87188518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4890661 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]	ATPase-associated		
3155	87762384 (6308, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED		29331828, 264509, 264805, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264583, 264486
3156	87737448 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45821.1 AC00801 - (AC008017) N-acetylglucosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	transferase Contains protein domain (PF00652) - struct Similarity to lectin domain of ricin beta-chain, 3 copies.		56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35689052, 52644045, 285007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21908769, 35689517, 265020, 265022, 264692, 18108370, 35688423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 264259, 29331826, 35689052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108386, 52645129, 35688423, 52644332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306064 gb AAD41895.1 AF15677 - (AF156776) ASB-3 protein [Homo sapiens]	kinase Contains protein domain (PF00023) - struct Ank repeat		264488, 263974
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50887.1 - (A1243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED		56182575, 22278998, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21908788, 265020, 264691, 264692, 33657109, 18108374, 35688423, 264555, 60170394, 22279000
3160	80221068 (6318, 6320)	Novel Protein sim. GBank gi3930525 (AF084447) - sex-determination protein homolog Fem1a [Mus musculus]	struct Contains protein domain (PF00023) - struct Ank repeat		18108351, 264555, 264556, 264557, 264558, 264559



3161	8607411 (8321, 8322)				264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 52644045, 265017, 285018, 264448, 264288, 21806764, 21806767, 285020, 18108374, 264636, 264566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer



22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleen[TP])		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: I:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

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<211> 331

<212> PRT

<213> Homo sapiens

<400> 3222

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Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met	Arg	Cys
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Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr	Arg	Ala
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Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro	Gly	Thr
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Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val	Thr	Cys
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Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly	Asp	Val
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Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg	Arg	Pro
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Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro	Ile	Arg
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Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln	Ser	Thr
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<210> 3224

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3224

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Val Ile Pro Gly Ala Glu Pro Leu Ile Cys Ala Ser Ser Leu Leu Ala
      50           55           60
Thr Ala Pro Cys Leu Tyr Leu Ala Leu Val Leu Ala Pro Thr Thr Leu
      65           70           75           80
Leu Ala Ser Tyr Val Phe Leu Gly Leu Gly Glu Leu Leu Leu Ser Cys
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Asn Trp Ala Val Val Ala Asp Ile Leu Leu Ser Val Val Val Pro Arg
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Cys Arg Gly Thr Ala Glu Ala Leu Gln Ile Thr Val Gly His Ile Leu
      115          120          125
Gly Asp Ala Gly Ser Pro Tyr Leu Thr Gly Leu Ile Ser Ser Val Leu
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Arg Pro Gly Ala Leu Thr Pro Leu Gln Arg Phe Arg Ser Leu Gln Gln
      145          150          155          160
Ser Phe Leu Cys Cys Ala Phe Val Ile Ala Leu Gly Gly Gly Cys Phe
      165          170          175
Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr Arg Ala Trp Gln
      180          185          190
Pro Val Thr Gly Thr Pro Asp Ser Asn Asp Val Asp Ser Asn Asp Leu
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Glu Arg Gln Gly Leu Leu Ser Gly Ala Gly Ala Ser Thr Glu Glu Pro
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&lt;210&gt; 3225

&lt;211&gt; 506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3225

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 Leu Val Pro Cys His Arg Gly Thr Gly Pro Ala Val Val Trp Pro Ala  
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 Met Glu Pro Pro Ser Ala Ala Lys Asn Asn His Thr Ala Phe Glu Val  
 85 90 95  
 Ser His Pro Arg Cys Arg Trp Gly Cys Met Lys Leu His Glu His Gly  
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&lt;210&gt; 3228

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3228

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Val	Gln	Val	Gly	Asp	Ser	Leu	Arg	Ala	Ser	Thr	Ile	Arg	Lys	Val	Gln
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Thr	Glu	Ser	Ser	Thr	Gly	Ser	Val	Gly	Ser	Asn	Arg	Val	Arg	Thr	Thr
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Leu	Thr	Leu	Cys	Val	Glu	Ala	Ile	Asp	Phe	Asp	Ser	Gln	Ala	Cys	Gln

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    100                                      105                                      110  
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 Cys Asp Pro Ala Trp Ser Ala Asp Val Ala Ala Val Met Gln Glu  
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 Gly Leu Ala His Ile Cys Leu Val Thr Pro Ser Met Thr Leu Thr Arg  
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 Ala Lys Val Glu Val Asn Ile Pro Arg Lys Arg Lys Gly Asn Cys Ser  
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&lt;210&gt; 3229

&lt;211&gt; 1008

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3229

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<212> PRT

<213> Homo sapiens

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Lys	Tyr	Leu	Leu	Leu	Thr	Tyr	Tyr	Asp	Ile	Asn	Lys	Arg	Asp	Arg	Lys
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Val	His	Leu	Leu	Val	Ser	Arg	Arg	Cys	Glu	Leu	Asn	Leu	Cys	Asp	Arg
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Glu	Asp	Arg	Thr	Pro	Leu	Ile	Lys	Ala	Val	Gln	Leu	Arg	Gln	Glu	Ala
			100					105					110		
Cys	Ala	Thr	Leu	Leu	Leu	Gln	Asn	Gly	Ala	Asp	Pro	Asn	Ile	Thr	Asp
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Val	Phe	Gly	Arg	Thr	Ala	Leu	His	Tyr	Ala	Val	Tyr	Asn	Glu	Asp	Thr
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Ser	Met	Ile	Glu	Lys	Leu	Leu	Ser	His	Gly	Thr	Asn	Ile	Glu	Glu	Cys

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Ser	Lys	Asn	Glu	Tyr	Gln	Pro	Leu	Leu	Leu	Ala	Val	Ser	Arg	Arg	Lys
Val	Lys	Met	Val	Glu	Phe	Leu	Leu	Lys	Lys	Lys	Ala	Asn	Val	Asn	Ala
Ile	Asp	Tyr	Leu	Gly	Arg	Ser	Ala	Leu	Ile	Leu	Ala	Val	Thr	Leu	Gly
Glu	Lys	Asp	Ile	Val	Ile	Leu	Leu	Gln	His	Asn	Ile	Asp	Val	Phe	
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&lt;210&gt; 3231

&lt;211&gt; 1367

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3231

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 actgactaca ttttttggtg tttttttttt tcccccttcc gttctgaata atgggtttta  
 1260  
 gcgggtccta gtctgctggc attgagctgg ggctgggtca ccaaaccctt cccaaaagga  
 1320  
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 1367

<210> 3232

<211> 251

<212> PRT

<213> Homo sapiens

<400> 3232

Met	Ser	Asp	Ile	Gly	Asp	Trp	Phe	Arg	Ser	Ile	Pro	Ala	Ile	Thr	Arg
1				5					10					15	
Tyr	Trp	Phe	Ala	Ala	Thr	Val	Ala	Val	Pro	Leu	Val	Gly	Lys	Leu	Gly
			20					25					30		
Leu	Ile	Ser	Pro	Ala	Tyr	Leu	Phe	Leu	Trp	Pro	Glu	Ala	Phe	Leu	Tyr
		35					40					45			
Arg	Phe	Gln	Ile	Trp	Arg	Pro	Ile	Thr	Ala	Thr	Phe	Tyr	Phe	Pro	Val
	50					55					60				
Gly	Pro	Gly	Thr	Gly	Phe	Leu	Tyr	Leu	Val	Asn	Leu	Tyr	Phe	Leu	Tyr
65					70					75				80	
Gln	Tyr	Ser	Thr	Arg	Leu	Glu	Thr	Gly	Ala	Phe	Asp	Gly	Arg	Pro	Ala
			85						90				95		
Asp	Tyr	Leu	Phe	Met	Leu	Leu	Phe	Asn	Trp	Ile	Cys	Ile	Val	Ile	Thr
			100					105					110		
Gly	Leu	Ala	Met	Asp	Met	Gln	Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	
		115					120					125			
Val	Leu	Tyr	Val	Trp	Ala	Gln	Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe
	130					135						140			
Trp	Phe	Gly	Thr	Arg	Phe	Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu
145					150					155				160	
Gly	Phe	Asn	Tyr	Ile	Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly
			165					170					175		
Asn	Leu	Val	Gly	His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met
		180					185					190			
Asp	Leu	Gly	Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg
		195					200					205			
Trp	Leu	Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro
	210					215						220			
Ala	Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
225					230					235				240	
Asn	Trp	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Asp	Gln					
			245						250						

<210> 3233

<211> 975

<212> DNA

<213> Homo sapiens

<400> 3233  
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 accgttgttt accttgtggc ttcccatctg ttctttgtta tgtttgtatg gtccatttgg  
 120  
 atgacaattt tcacatctcc cgcttcccc tccaaagagt tctacttgtc caattctgaa  
 180  
 aaggaacggt atgaaaaaga attcagccaa gaaagacaac aagaaatttt gagaagagca  
 240  
 gcaagagcgt tacctatcta taccacatca gcttcaaaaa ctatcagata ttgtgaaaaa  
 300  
 tgtcagctga ttaaacctga tcgggcgcac cactgctcag cctgtgactc atgtattctt  
 360  
 aagatggatc atccctgtcc ttgggtgaat aactgtgtgg gatcttctaa ttacaaattc  
 420  
 ttctgtgtgt ttttattgta ttccctatta tattgccttt tcgtggccgc acagtttttag  
 480  
 agtacttaaa aaatttttga cgaaagaacc gaccaaacc cgggccaaaa ttccacgtac  
 540  
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 600  
 cactgctggc tttaaacagc attgtccaca gctccgtctg cagggtcagg gcatggcctc  
 660  
 tctccgtgtt cctgtgaaga gccttcattg gaatcatccc gggacataca gcttgaatgt  
 720  
 gctgtctggc tagccctcc acaagtccgt cactctgcac aaggaatccg agagctcatc  
 780  
 aaggatcagc acggtctggg gccaggtgg ggtggaacac gcacggtcca caagcaattc  
 840  
 tgtctttctc aaggcttttt cttgtgcagt atgaaatcct tcatatttca tatgaagtat  
 900  
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 960  
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 975

<210> 3234

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3234  
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 20 25 30  
 Val Met Phe Val Trp Ser Tyr Trp Met Thr Ile Phe Thr Ser Pro Ala  
 35 40 45  
 Ser Pro Ser Lys Glu Phe Tyr Leu Ser Asn Ser Glu Lys Glu Arg Tyr  
 50 55 60  
 Glu Lys Glu Phe Ser Gln Glu Arg Gln Gln Glu Ile Leu Arg Arg Ala  
 65 70 75 80  
 Ala Arg Ala Leu Pro Ile Tyr Thr Thr Ser Ala Ser Lys Thr Ile Arg

				85					90					95		
Tyr	Cys	Glu	Lys	Cys	Gln	Leu	Ile	Lys	Pro	Asp	Arg	Ala	His	His	Cys	
			100					105					110			
Ser	Ala	Cys	Asp	Ser	Cys	Ile	Leu	Lys	Met	Asp	His	Pro	Cys	Pro	Trp	
		115					120					125				
Val	Asn	Asn	Cys	Val	Gly	Phe	Ser	Asn	Tyr	Lys	Phe	Phe	Leu	Leu	Phe	
	130				135						140					
Leu	Leu	Tyr	Ser	Leu	Leu	Tyr	Cys	Leu	Phe	Val	Ala	Ala	Gln	Phe		
145					150					155						

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<400> 3235
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120
gcagtacaag ttagtatgaa gcatgagatt gaacttgcca tgaagttgct ggagaaagat
180
atccatgaga aacaagatac tctgataggc cttcgacaac aactagagga agttaaaagca
240
attaacatag agatgtatca aaagttgcag ggttctgaag atggcttgaa agaaaaaaat
300
gaaataattg cccgactaga agaaaaaacc aataaaatta ctgcagccat gaggcagctg
360
gaacaaagat tgcagcaagc agagaaggcg caaatggaag ctgaagatga ggatgagaaa
420
tatctacaag aatgtctcag taaatctgat agtctgcaga aacaaatctc ccaaaaggag
480
aaacagctgg tgcaactgga. aactgacttg aagattgaga aggaatggag gcagactttg
540
caggaagatc t
551
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<400> 3236															
Xaa	Glu	Thr	Glu	Leu	Gln	Thr	Tyr	Lys	His	Ser	Arg	Gln	Gly	Leu	Asp
1				5				10						15	
Glu	Met	Tyr	Asn	Glu	Ala	Arg	Arg	Gln	Leu	Arg	Asp	Glu	Ser	Gln	Leu
			20					25					30		
Arg	Gln	Asp	Val	Glu	Asn	Glu	Leu	Ala	Val	Gln	Val	Ser	Met	Lys	His
		35					40					45			
Glu	Ile	Glu	Leu	Ala	Met	Lys	Leu	Leu	Glu	Lys	Asp	Ile	His	Glu	Lys
	50					55					60				
Gln	Asp	Thr	Leu	Ile	Gly	Leu	Arg	Gln	Gln	Leu	Glu	Glu	Val	Lys	Ala
65				70						75				80	
Ile	Asn	Ile	Glu	Met	Tyr	Gln	Lys	Leu	Gln	Gly	Ser	Glu	Asp	Gly	Leu

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<400> 3237
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120
gatgaggacc gttgggaagt acggggggac cgcaaggccc ggaagcccct ggtggagaag
180
aagcgacgcg cgcgatcaa cgagagtctt caggagttgc ggctgctgct ggcgggcgcc
240
gagggtgcagg ccaagctgga gaacgccgaa gtgctggagc tgacggtgcg gcgggtccag
300
ggtgtgctgc ggggccgggc gcgcgagcgc gaggcagctgc aggcggaagc gaggcagcgc
360
ttcgctgccg gctacatcca gtgcatgcac gagggtgcaca cgttcgtgtc cacgtgccag
420
gccatcgacg ctaccgtcgc tgccgagctc ctgaaccatc tgctcgagtc catgccgctg
480
cgtgagggca gcagcttcca ggatctgctg ggggacgccc tggcgggggc acctagagcc
540
cctggacgga gtggctggcc tgcggggggc gtcctgggat cccaatacc cagccccccg
600
ggtcctgggg acgacctgtg ctccgacctg gaggaggccc ctgaggctga actgagtcag
660
gctcctgctg agggggcccg cttggtgccc gcagccctgg gcagcctgac cacagcccaa
720
attgcccgga gtgtctggag gccttggtga ccaatgccag ccagagtcct gcgggggtgg
780
gccccgccc ccttggaatc cctccctcct ccagggggtt cagatgtggt ggggtagggc
840
cctggaagtc tcccaggtct tcctccctc ctctgatgga tggcttgagc ggcagcccct
900
ggtaaccagc ccagtcaggc ccagccccg tttcttaaga aacttttagg gaccctgcag
960
ctctggagtg ggtggagggg gggagctacg ggcaggagga agaattttgt agagctgcca
1020

```



gcgctctccc aggttcaccc acccaggctt caccagccct gtgcgggctc tgggggcaga  
 1080  
 ggtggcagaa atggtgctgg gcactagtgt tccaggcagc cctgggctaa acaaaagctt  
 1140  
 gaacttgcca cttcagcggg gagatgagag gcagggtgcac tcagctgcac tgcccagagc  
 1200  
 tgtgatgctc tgtacatctt gttttagca cacttgagtt tgtgtattcc attgacatca  
 1260  
 aatgtgacaa ttttactaaa taaagaattt tggagttagt tacccttgaa aaaaaagtcg  
 1320  
 acg  
 1323

<210> 3238

<211> 249

<212> PRT

<213> Homo sapiens

<400> 3238

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1			5						10					15	
Gly	Ala	Gly	Leu	Arg	Ala	Leu	Trp	Thr	Met	Ala	Pro	Pro	Ala	Ala	Pro
			20					25					30		
Gly	Arg	Asp	Arg	Val	Gly	Arg	Glu	Asp	Glu	Asp	Arg	Trp	Glu	Val	Arg
		35				40						45			
Gly	Asp	Arg	Lys	Ala	Arg	Lys	Pro	Leu	Val	Glu	Lys	Lys	Arg	Arg	Ala
	50					55					60				
Arg	Ile	Asn	Glu	Ser	Leu	Gln	Glu	Leu	Arg	Leu	Leu	Leu	Ala	Gly	Ala
65					70					75				80	
Glu	Val	Gln	Ala	Lys	Leu	Glu	Asn	Ala	Glu	Val	Leu	Glu	Leu	Thr	Val
			85					90						95	
Arg	Arg	Val	Gln	Gly	Val	Leu	Arg	Gly	Arg	Ala	Arg	Glu	Arg	Glu	Gln
		100						105					110		
Leu	Gln	Ala	Glu	Ala	Ser	Glu	Arg	Phe	Ala	Ala	Gly	Tyr	Ile	Gln	Cys
		115					120					125			
Met	His	Glu	Val	His	Thr	Phe	Val	Ser	Thr	Cys	Gln	Ala	Ile	Asp	Ala
	130					135					140				
Thr	Val	Ala	Ala	Glu	Leu	Leu	Asn	His	Leu	Leu	Glu	Ser	Met	Pro	Leu
145					150					155				160	
Arg	Glu	Gly	Ser	Ser	Phe	Gln	Asp	Leu	Leu	Gly	Asp	Ala	Leu	Ala	Gly
			165					170						175	
Pro	Pro	Arg	Ala	Pro	Gly	Arg	Ser	Gly	Trp	Pro	Ala	Gly	Gly	Ala	Pro
		180						185					190		
Gly	Ser	Pro	Ile	Pro	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Asp	Leu	Cys	Ser
		195					200					205			
Asp	Leu	Glu	Glu	Ala	Pro	Glu	Ala	Glu	Leu	Ser	Gln	Ala	Pro	Ala	Glu
	210					215					220				
Gly	Pro	Asp	Leu	Val	Pro	Ala	Ala	Leu	Gly	Ser	Leu	Thr	Thr	Ala	Gln
225					230					235				240	
Ile	Ala	Arg	Ser	Val	Trp	Arg	Pro	Trp							
				245											

<210> 3239

<211> 432

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3239

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aaaaccaaag attctcctgg agttttctct aaactgggtg ttctcctgag gagagtgaca
60
agaaacttgg tgagaaataa gctggcagtg attacgcgtc tccttcagaa tctgatcatg
120
ggtttgttcc tccttttctt cgttctgcgg gtccgaagca atgtgctaaa gggtgctatc
180
caggaccgcg taggtctcct ttaccagttt gtgggcgcca ccccgtaac aggcattgctg
240
aacgctgtga atctgtttcc cgtgctgcga gctgtcagcg accaggagag tcaggacggc
300
ctctaccaga agtggcagat gatgctggcc tatgcactgc acgtcctccc cttcagcgtt
360
gttgccacca tgattttcag cagtgtgtgc tactggacgc tgggcttaca tcctgaggtt
420
gcccgattgg gt
432

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&lt;210&gt; 3240

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3240

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Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu Gly Val Leu Leu
1      5      10      15
Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu Ala Val Ile Thr
20     25     30
Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu Leu Phe Phe Val
35     40     45
Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile Gln Asp Arg Val
50     55     60
Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr Thr Gly Met Leu
65     70     75     80
Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val Ser Asp Gln Glu
85     90     95
Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met Leu Ala Tyr Ala
100    105    110
Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met Ile Phe Ser Ser
115    120    125
Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val Ala Arg Leu Gly
130    135    140

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&lt;210&gt; 3241

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3241

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gtggaatttt tttagacaaa gtctcaaaaa acaacaaaac aaacaaaagg taagataaat
60

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acgaaataca aaataagagg caggaagagc ccaaagcatc agaaatgtgc cagttataat  
 120  
 gggccaaaat cccctcttgt gtctccagaa gtatttgaaa aatacgttag gatctgcctc  
 180  
 acagacatgc tcccaggaca ctgcacagca aggaggtacg gcgggcccag ccagccaagg  
 240  
 cagaggagga catcactgcc acagcagggg gcctgactgg cagcaaaagg gacgactccg  
 300  
 gcgaaaagtc agcaggaaac aggacagggg ctggaccaat ggccctccctc agccccacac  
 360  
 cccacccagg caggagcggg gcctggcccc gggcaggcgg gtgggagagc tcactgagtg  
 420  
 ggcagcaggg catggcccct gatgctgcag gtacccaggc tgcagctgca gaaacctcag  
 480  
 tgggaaccca gg  
 492

&lt;210&gt; 3242

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3242

Met	Gly	Gln	Asn	Pro	Leu	Leu	Cys	Leu	Gln	Lys	Tyr	Leu	Lys	Asn	Thr
1			5						10					15	
Leu	Gly	Ser	Ala	Ser	Gln	Thr	Cys	Ser	Gln	Asp	Thr	Arg	Gln	Gln	Gly
		20					25					30			
Gly	Thr	Ala	Gly	Pro	Ala	Ser	Gln	Gly	Arg	Gly	Gly	His	His	Cys	His
		35				40					45				
Ser	Arg	Gly	Pro	Asp	Trp	Gln	Gln	Lys	Gly	Arg	Leu	Arg	Arg	Lys	Val
	50				55					60					
Ser	Arg	Lys	Gln	Asp	Arg	Gly	Trp	Thr	Asn	Gly	Leu	Pro	Gln	Pro	His
65				70					75					80	
Thr	Pro	Pro	Arg	Gln	Glu	Arg	Cys	Leu	Ala	Arg	Gly	Arg	Arg	Val	Gly
			85					90						95	
Glu	Leu	Thr	Glu	Trp	Ala	Ala	Gly	His	Gly	Pro					
			100					105							

&lt;210&gt; 3243

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3243

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 ttccccaccc tttggtctgg ggcaaggagt acttacggag tgacaaaagg aaaagtctgc  
 120  
 tttgaggcaa aggtaaccca gaatctccca atgaaagaag gctgcacaga ggtctctctc  
 180  
 cttcgagttg ggtggtctgt tgatttttcc cgtccacagc ttggtgaaga tgaattctct  
 240  
 tacggtttcg atggacgagg actcaaggca gaaaatggac aatttgagga atttgccag  
 300

acttttgggg agaatgatgt tattggctgc ttgctaatt ttgagactga agaagtagaa  
 360  
 ctttccttct ccaagaatgg agaagacctt ggtgtggcat tctggatcag caaggattcc  
 420  
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 480  
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 540  
 gtgcctgttg aggagcgtgt acgcactgca gtccctccca agaccataga ggaatgtgag  
 600  
 gtgattctga tgggtgggact acccgatctt ggaaagaccc agtgggcact gaaatatgca  
 660  
 aaagaaaacc ctgagaaaag atacaatgtc ctgggagctg agactgtgct caatcaaatg  
 720  
 aggatgaagg gtctcgagga gccagagatg gacccccaaa gccgagacct tttagttag  
 780  
 caagcctccc agtgccttag taagctggtc cagattgctt cccggacaaa gaggaacttt  
 840  
 attcttgatc agtgtaatgt gtacaattct ggccaacggc ggaagctatt gctgttcaag  
 900  
 accttctctc ggaaagtggg ggtggttgtc cctaagtagg aaga  
 944

&lt;210&gt; 3244

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3244

Asp	Leu	His	Phe	Gln	Val	Ser	Lys	Asp	Arg	Tyr	Gly	Gly	Gln	Pro	Leu
1				5					10					15	
Phe	Ser	Glu	Lys	Phe	Pro	Thr	Leu	Trp	Ser	Gly	Ala	Arg	Ser	Thr	Tyr
			20					25					30		
Gly	Val	Thr	Lys	Gly	Lys	Val	Cys	Phe	Glu	Ala	Lys	Val	Thr	Gln	Asn
		35					40					45			
Leu	Pro	Met	Lys	Glu	Gly	Cys	Thr	Glu	Val	Ser	Leu	Leu	Arg	Val	Gly
		50				55					60				
Trp	Ser	Val	Asp	Phe	Ser	Arg	Pro	Gln	Leu	Gly	Glu	Asp	Glu	Phe	Ser
65					70					75				80	
Tyr	Gly	Phe	Asp	Gly	Arg	Gly	Leu	Lys	Ala	Glu	Asn	Gly	Gln	Phe	Glu
			85						90					95	
Glu	Phe	Gly	Gln	Thr	Phe	Gly	Glu	Asn	Asp	Val	Ile	Gly	Cys	Phe	Ala
			100					105					110		
Asn	Phe	Glu	Thr	Glu	Glu	Val	Glu	Leu	Ser	Phe	Ser	Lys	Asn	Gly	Glu
		115					120					125			
Asp	Leu	Gly	Val	Ala	Phe	Trp	Ile	Ser	Lys	Asp	Ser	Leu	Ala	Asp	Arg
		130				135					140				
Ala	Leu	Leu	Pro	His	Val	Leu	Cys	Lys	Asn	Cys	Val	Val	Glu	Leu	Asn
145					150					155				160	
Phe	Gly	Gln	Lys	Glu	Glu	Pro	Phe	Phe	Pro	Pro	Pro	Glu	Glu	Phe	Val
			165					170						175	
Phe	Ile	His	Ala	Val	Pro	Val	Glu	Glu	Arg	Val	Arg	Thr	Ala	Val	Pro
			180					185					190		
Pro	Lys	Thr	Ile	Glu	Glu	Cys	Glu	Val	Ile	Leu	Met	Val	Gly	Leu	Pro

195	200	205
Gly Ser Gly Lys Thr Gln Trp Ala Leu Lys Tyr Ala Lys Glu Asn Pro		
210	215	220
Glu Lys Arg Tyr Asn Val Leu Gly Ala Glu Thr Val Leu Asn Gln Met		
225	230	235
Arg Met Lys Gly Leu Glu Glu Pro Glu Met Asp Pro Lys Ser Arg Asp		240
245	250	255
Leu Leu Val Gln Gln Ala Ser Gln Cys Leu Ser Lys Leu Val Gln Ile		
260	265	270
Ala Ser Arg Thr Lys Arg Asn Phe Ile Leu Asp Gln Cys Asn Val Tyr		
275	280	285
Asn Ser Gly Gln Arg Arg Lys Leu Leu Leu Phe Lys Thr Phe Ser Arg		
290	295	300
Lys Val Val Val Val Val Pro Asn Glu Glu		
305	310	

&lt;210&gt; 3245

&lt;211&gt; 980

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3245

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 120  
 ccaaccagc agggcctctg agagacaagg tacatcccat gattctagca caggaagaag  
 180  
 acgacgtcct gggagaggaa gcacaaggca gcccgcacga tatcatcaga ataggtgtgg  
 240  
 cggggcgccc tgctcctggc agactacatc ctgttccgac aggacctctt ccgaggatgt  
 300  
 acagcgctgg agctcggggc cggcacgggg ctcgctagca tcatcgcagc caccatggca  
 360  
 cggaccgttt attgtacaga tgtcggtgca gatcttttgt ccatgtgcca gcgaaacatt  
 420  
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 720  
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 780  
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<213> Homo sapiens

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<212> DNA

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<400> 3248

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&lt;211&gt; 4487

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3249

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<211> 849

<212> PRT

<213> Homo sapiens

<400> 3250

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&lt;210&gt; 3251

&lt;211&gt; 2595

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3251

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 <212> PRT  
 <213> Homo sapiens

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 Gln Gln His Gln Ile His Arg Ser Cys Thr Val Asn Ile Met Phe Gly  
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 195 200 205  
 Leu Gly Cys Leu Ala Glu Asp Thr Ala Lys Leu Pro Thr Ala Pro Glu  
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 Arg Asp Lys Glu Phe Tyr Arg Pro Ile Pro Asn Pro Asn Pro Lys Leu  
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 Ser Ala Asp Phe Pro Cys Leu Val Asp Pro Lys His Gln Pro Ala Ala  
 130 135 140  
 Glu Met Ala Lys Gly Tyr Leu Leu Leu Pro Gly Cys Pro Cys Leu His  
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 Pro Phe Tyr Gln  
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<210> 3255  
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 <212> DNA  
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<400> 3255



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<211> 169

<212> PRT

<213> Homo sapiens

<400> 3256

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		20						25				30			
Gly	Arg	Asn	Glu	Ala	Gly	Glu	Arg	His	Gly	Arg	Gly	Arg	Ala	Arg	Leu
		35					40				45				
Pro	Asn	Gly	Asp	Thr	Tyr	Glu	Gly	Ser	Tyr	Glu	Phe	Gly	Lys	Arg	His
	50					55				60					
Gly	Gln	Gly	Ile	Tyr	Lys	Phe	Lys	Asn	Gly	Ala	Arg	Tyr	Ile	Gly	Glu
65					70				75					80	
Tyr	Val	Arg	Asn	Lys	Lys	His	Gly	Gln	Gly	Thr	Phe	Ile	Tyr	Pro	Asp
			85					90						95	
Gly	Ser	Arg	Tyr	Glu	Gly	Glu	Trp	Ala	Asn	Asp	Leu	Arg	His	Gly	His
		100						105					110		
Gly	Val	Tyr	Tyr	Tyr	Ile	Asn	Asn	Asp	Thr	Tyr	Thr	Gly	Glu	Trp	Phe
		115				120						125			
Ala	His	Gln	Arg	His	Gly	Gln	Gly	Thr	Tyr	Leu	Tyr	Ala	Glu	Thr	Gly
	130				135						140				
Ser	Lys	Tyr	Val	Gly	Thr	Trp	Val	Asn	Gly	Gln	Glu	Gly	Thr	Ala	
145					150				155					160	
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165

&lt;210&gt; 3257

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3257

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368

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&lt;210&gt; 3258

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3258

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35     40     45
Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr Tyr Ala Ser Glu Ser
50     55     60
Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val Pro Arg Ala Arg Arg
65     70     75     80
Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp Arg Ser Met His Lys
85     90     95
Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu Glu Met Lys Ala
100    105    110
Arg Ser Ser Ser Tyr Ala Asp Pro Trp Arg
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&lt;210&gt; 3259

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3259

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<210> 3260

<211> 197

<212> PRT

<213> Homo sapiens

<400> 3260

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		20					25					30			
Gly	Ser	Glu	Val	Asp	Arg	Val	Ile	Leu	Lys	Ala	Asn	Glu	Thr	Phe	Ala
	35					40					45				
Phe	Val	Gly	Asn	Val	Thr	His	Tyr	Ala	Gln	Val	Trp	Leu	Asn	Ile	Ser
	50				55				60						
Ala	Glu	Ile	Arg	Ser	Phe	Leu	Glu	Gln	Gly	Arg	Leu	Gln	Gln	His	Leu
65				70				75						80	
Arg	Trp	Leu	Gln	Gln	Tyr	Val	Ala	Glu	Leu	Arg	Leu	His	Pro	Glu	Ala
		85					90					95			
Leu	Asn	Leu	Ser	Leu	Asp	Glu	Leu	Pro	Pro	Ala	Leu	Arg	Gln	Asp	Asn
	100						105				110				
Phe	Ser	Leu	Pro	Ser	Gly	Met	Ala	Leu	Leu	Gln	Gln	Leu	Asp	Thr	Ile
	115					120					125				
Asp	Asn	Ala	Ala	Cys	Gly	Trp	Ile	Gln	Phe	Met	Ser	Lys	Val	Ser	Val
130					135					140					
Asp	Ile	Phe	Lys	Gly	Phe	Pro	Asp	Glu	Glu	Ser	Ile	Val	Asn	Tyr	Thr
145			150					155						160	
Leu	Asn	Gln	Ala	Tyr	Gln	Asp	Asn	Val	Thr	Val	Phe	Ala	Ser	Val	Ile
		165					170						175		
Phe	Gln	Thr	Arg	Lys	Asp	Gly	Ser	Ser	Arg	Leu	Thr	Cys	Thr	Thr	Arg

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185

190

&lt;210&gt; 3261

&lt;211&gt; 1323

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3261

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<212> PRT  
<213> Homo sapiens

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<211> 308

<212> PRT

<213> Homo sapiens

<400> 3264

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Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser	Thr	Glu	Pro	Ala	Arg	Lys	Pro
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Pro	Val	Lys	Val	Glu	Arg	Thr	Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met
				85					90					95	
Asp	Arg	Lys	Val	Glu	Lys	Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu
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Gln	Lys	Leu	His	Ser	Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro
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	130				135						140				
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Lys	Lys	Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala
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Ala	Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile
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Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	Ala
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Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	Pro	Gln
	210					215					220				
Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	Pro	Val	Asn
225					230					235				240	
Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	Asp	Lys	Glu	His
				245					250					255	
Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	Cys	Gly	Ser	Ser	Glu
			260					265					270		
Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	Asp	Leu	Asp	Arg	Pro	Gly

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<211> 524

<212> DNA

<213> Homo sapiens

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 gtcattgaaa agacagaatc atggccaaga atcattatga gattcaggaa aaggaaaaac  
 300  
 ttcaagaaga aaagaagtaa gttagagaaa gtaccgctgg gccctgttgc acggtgctgg  
 360  
 ttgccaggc gcatgcgac ggagggtgtg gggcacgtgg gtctcgggac aggaagccca  
 420  
 ggcaggtctc aacctggctg ccaactgccca cttgccaccc tcatactaga gggagcacc  
 480  
 agagggtcca gcctcgctcc ccttctctc cagctccac gcgt  
 524

<210> 3266

<211> 82

<212> PRT

<213> Homo sapiens

<400> 3266  
 Met Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ser Lys Leu  
 1                      5                      10                      15  
 Glu Lys Val Pro Leu Gly Pro Val Ala Arg Cys Trp Leu Pro Arg Arg  
 20                      25                      30  
 Met Arg Thr Glu Gly Val Gly His Val Gly Leu Gly Thr Gly Ser Pro  
 35                      40                      45  
 Gly Arg Ser Gln Pro Gly Cys His Cys Pro Leu Ala Thr Leu Ile Leu  
 50                      55                      60  
 Glu Gly Ala Pro Arg Gly Ser Ser Leu Ala Pro Leu Leu Leu His Ala  
 65                      70                      75                      80  
 Pro Arg

<210> 3267

<211> 393

<212> DNA

<213> Homo sapiens

&lt;400&gt; 3267

gtcgaatatg catgcagagt acagggttta gaacatgaca tggaagagat caatgctcga  
60  
tggaatacat tgaataaaaa ggtcgcacaa agaattgcac agctacagga agctttgttg  
120  
cattgtggga agtttcaaga tgccttggag ccattgctca gctgggtggc agataccgag  
180  
gagctcatag ccaatcagaa acctccatct gctgagtata aagtgggtgaa agcacagatc  
240  
caagaacaga agttgctcca gcggctccta gatgatcgaa aggccacagt agacatgctt  
300  
caagcagaag gaggcagaat agcccagtca gcagagctgg ctgatagaga gaaaatcact  
360  
ggacagctgg agagtcttga aagtagatgg act  
393

&lt;210&gt; 3268

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3268

Val	Glu	Tyr	Ala	Cys	Arg	Val	Gln	Gly	Leu	Glu	His	Asp	Met	Glu	Glu
1				5				10					15		
Ile	Asn	Ala	Arg	Trp	Asn	Thr	Leu	Asn	Lys	Lys	Val	Ala	Gln	Arg	Ile
			20					25					30		
Ala	Gln	Leu	Gln	Glu	Ala	Leu	Leu	His	Cys	Gly	Lys	Phe	Gln	Asp	Ala
		35				40						45			
Leu	Glu	Pro	Leu	Leu	Ser	Trp	Leu	Ala	Asp	Thr	Glu	Glu	Leu	Ile	Ala
		50				55				60					
Asn	Gln	Lys	Pro	Pro	Ser	Ala	Glu	Tyr	Lys	Val	Val	Lys	Ala	Gln	Ile
65					70					75				80	
Gln	Glu	Gln	Lys	Leu	Leu	Gln	Arg	Leu	Leu	Asp	Asp	Arg	Lys	Ala	Thr
				85				90					95		
Val	Asp	Met	Leu	Gln	Ala	Glu	Gly	Gly	Arg	Ile	Ala	Gln	Ser	Ala	Glu
			100				105					110			
Leu	Ala	Asp	Arg	Glu	Lys	Ile	Thr	Gly	Gln	Leu	Glu	Ser	Leu	Glu	Ser
		115					120					125			
Arg	Trp	Thr													
		130													

&lt;210&gt; 3269

&lt;211&gt; 1423

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3269

ctgtatcaaa aataatagta actttttgaa tatacacaaat ttatctagaa tctattttcc  
60  
tttgaagctg taactttatg agcgattatt tactaccttt gagaaatgtg ttttagtata  
120  
aaatatagga tgtggaagcg aaaaaatattc tgggtagcaa gtgaggtgta ctcaaaaata  
180



agcaaaagtc acgtgggtct gattttatac cctcgctgga aagcttggtc tcagacacac  
 240  
 tgttactgca agtgtgtgtg aggggggaaac tctcacacac tttgcagttg aggacagggc  
 300  
 tagactttga ggtggaccct ggctcccagg gctgtgtact cccagcccgt gtttctcttt  
 360  
 tgctcagact gaacaagtgg aacgaaatta cattaaagaa aagaaggcag cagtgaagaa  
 420  
 atttgaagac aagaagggtg agctgaaaga gaacctgatt gctgagctag aagaaaagaa  
 480  
 gaaaatgatt gaaaacgaaa tgctgacaat ggaactgaat ggagattcta tggaggtgaa  
 540  
 acctatcatg accagaaagt tgcggaggcg accaaatgat cccgtcccca tcccagacaa  
 600  
 gaggaggaaa cctgctccag cccagctaaa ctatttggtta acagatgaac agatcatgga  
 660  
 ggatctgaga acattaaata agcttaagtc acccaagaga ccagcatctc catcctctcc  
 720  
 tgagcacttg cctgcaacac ccgcggaatc tccagcacag agatttgagg cgcggataga  
 780  
 agatggcaaa ctgtattatg acaaaagatg gtaccacaag agccaggcca tctatctgga  
 840  
 gtcaaaggac aaccagaaac tgagctgctg gatcagttct gtaggagcca atgagatctg  
 900  
 ggtgaggaag acaagtgaca gcaccaagat gaggatctac ctgggtcagc ttcagcgcg  
 960  
 gctcttcgtg atccgccggc gctcagctgc ttgactttct acagtgtctt tctcttgacc  
 1020  
 ctttttctgg agtgggtttt atttttgttt tgtttcgttt tctccttaat agaaaaatgt  
 1080  
 taacttactg ggaatagcta ctcagccttg gaaatggaga gcactgcagt gaattcttta  
 1140  
 gggcactttt gtggccgat gcttccaact ttgtcagtct tttctgcctc aacttcttcc  
 1200  
 agacatcagt caccatgaga ctgttttact ttcaggcgta ttgggggggtt tgatttactt  
 1260  
 tccttttatt tctttatttt ttgcttatac ttgtttttga aaacctctc tgagtttgaa  
 1320  
 gggacagcta tttttattga ttatctttaa gtctctctac catggagaag agcaggaagg  
 1380  
 gatacactct ccagtgcatt ttcatgtttt gaatcggatt agt  
 1423

<210> 3270

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3270

Met	Ile	Glu	Asn	Glu	Met	Leu	Thr	Met	Glu	Leu	Asn	Gly	Asp	Ser	Met
1			5					10						15	
Glu	Val	Lys	Pro	Ile	Met	Thr	Arg	Lys	Leu	Arg	Arg	Arg	Pro	Asn	Asp
			20					25					30		
Pro	Val	Pro	Ile	Pro	Asp	Lys	Arg	Arg	Lys	Pro	Ala	Pro	Ala	Gln	Leu

```

      35              40              45
Asn Tyr Leu Leu Thr Asp Glu Gln Ile Met Glu Asp Leu Arg Thr Leu
      50              55              60
Asn Lys Leu Lys Ser Pro Lys Arg Pro Ala Ser Pro Ser Ser Pro Glu
65              70              75              80
His Leu Pro Ala Thr Pro Ala Glu Ser Pro Ala Gln Arg Phe Glu Ala
      85              90              95
Arg Ile Glu Asp Gly Lys Leu Tyr Tyr Asp Lys Arg Trp Tyr His Lys
      100             105             110
Ser Gln Ala Ile Tyr Leu Glu Ser Lys Asp Asn Gln Lys Leu Ser Cys
      115             120             125
Val Ile Ser Ser Val Gly Ala Asn Glu Ile Trp Val Arg Lys Thr Ser
      130             135             140
Asp Ser Thr Lys Met Arg Ile Tyr Leu Gly Gln Leu Gln Arg Gly Leu
145             150             155             160
Phe Val Ile Arg Arg Arg Ser Ala Ala
      165

```

<210> 3271  
 <211> 464  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3271
tcatgagcag ggcccaattc tggcttctct gtggtcgcca tccatgtgct gggcgtcact
60
gaaggcactg gggatacagc cgagcacaag atggacagag atccctggcc cctcggagca
120
ggcagtctgt ggctctggcc cctccagttc cttgtcacca ggagataggc aatgcagctg
180
atgagaaggg ccccggcagc aagagatcca atgatggtgg ccgccaggat cccagcgttg
240
gtgggcaggt gtgtactggg cagctcctta ttcttttcag ctacctggac ctcagtcttg
300
gccttcatag tccattcaga gttgatggta atggctactt ggtaggtgcc actgtctgta
360
ggctgggagc ggcgcagcag catggaacca ttggggaagc ccacgatgtc tcgctgtccc
420
atggcactgc catccctctg aggcggttgt atccccaggg atgt
464

```

<210> 3272  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

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<400> 3272
Met Gly Gln Arg Asp Ile Val Gly Phe Pro Asn Gly Ser Met Leu Leu
1      5      10      15
Arg Arg Ala Gln Pro Thr Asp Ser Gly Thr Tyr Gln Val Ala Ile Thr
      20      25      30
Ile Asn Ser Glu Trp Thr Met Lys Ala Lys Thr Glu Val Gln Val Ala
      35      40      45
Glu Lys Asn Lys Glu Leu Pro Ser Thr His Leu Pro Thr Asn Ala Gly

```

```

      50              55              60
Ile Leu Ala Ala Thr Ile Ile Gly Ser Leu Ala Ala Gly Ala Leu Leu
65              70              75              80
Ile Ser Cys Ile Ala Tyr Leu Leu Val Thr Arg Asn Trp Arg Gly Gln
      85              90              95
Ser His Arg Leu Pro Ala Pro Arg Gly Gln Gly Ser Leu Ser Ile Leu
      100              105              110
Cys Ser Ala Val Ser Pro Val Pro Ser Val Thr Pro Ser Thr Trp Met
      115              120              125
Ala Thr Thr Glu Lys Pro Glu Leu Gly Pro Ala His
      130              135              140

```

<210> 3273  
 <211> 387  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3273
ngcgcgccag ggatggaaaa ctttattctg tatgaggaga tcggaagagg aagcaagact
60
gttggtctata aagggcgacg gaaggggaaca atcaattttg tagccattct ttgtactgat
120
aagtgcagaa ggcctgaaat aaccaactgg gtccgtctca cccgtgaaat aaaacacaag
180
aatattgtaa cttttcatga atggtatgaa acaagcaacc acctctggct agtggtggaa
240
ctccgcacag gtggttcctt aaaaacagtt attgctcaag atgaaaacct cccagaagat
300
gttggtgagag aatttggaat tgacctgatt agtggattac atcatcttca taaacttggc
360
attctctttg tgacatttct cctagga
387

```

<210> 3274  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

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<400> 3274
Xaa Ala Pro Gly Met Glu Asn Phe Ile Leu Tyr Glu Glu Ile Gly Arg
1      5      10      15
Gly Ser Lys Thr Val Val Tyr Lys Gly Arg Arg Lys Gly Thr Ile Asn
      20      25      30
Phe Val Ala Ile Leu Cys Thr Asp Lys Cys Arg Arg Pro Glu Ile Thr
      35      40      45
Asn Trp Val Arg Leu Thr Arg Glu Ile Lys His Lys Asn Ile Val Thr
      50      55      60
Phe His Glu Trp Tyr Glu Thr Ser Asn His Leu Trp Leu Val Val Glu
65      70      75      80
Leu Arg Thr Gly Gly Ser Leu Lys Thr Val Ile Ala Gln Asp Glu Asn
      85      90      95
Leu Pro Glu Asp Val Val Arg Glu Phe Gly Ile Asp Leu Ile Ser Gly
      100      105      110
Leu His His Leu His Lys Leu Gly Ile Leu Phe Val Thr Phe Leu Leu

```

115                                      120                                      125  
 Gly  
  
 <210> 3275  
 <211> 1266  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 3275  
 ttttttttaa tcagttaaga ttcttgttga cacaaattgt tttacatcaa ctgttgttat  
 60  
 agaacacatg aaaggaatac atggggaaga aataaagtag aaccaagag ttcttttaag  
 120  
 ttttctttta tagagacatg aataacagat acactgaagt ataaacaaaa attggcctga  
 180  
 agcgtccggt ggccggctta gttaggagct atggctaaac atcatcctga tttgatcttt  
 240  
 tgccgcaagc aggctggtgt tgccatcgga agactgtgtg aaaaatgtga tggcaagtgt  
 300  
 gtgatttgtg actcctatgt gcgtccctgc actctggtgc gcatatgtga tgagtgtaac  
 360  
 tatggatctt accaggggag ctgtgtgatc tgtggaggac ctgggggtctc tgatgcctat  
 420  
 tattgtaagg agtgcaccat ccaggagaag gacagagatg gctgccccaa gattgtcaat  
 480  
 ctggggagct ctaagacaga cctcttctat gaacgcaaaa aatacggctt caagaagagg  
 540  
 tgattggtgg gtggccctt cctcccccca acatcagtct gctgcagctg ccagaaaaca  
 600  
 tgcctactac taccagcaga aaggagcag agcccagagc atcaccagga gtgcctgcta  
 660  
 gtgtactggc agcttgccac cccctcctct cccttcaccc agacacgtgg tagggatgga  
 720  
 aaaggattct tcacagagca ctctggcaca ccatatcgga gaaaaattga tagattagtt  
 780  
 aatggttttt cttgaattcg agaagcatag atctgttctc catattggta tgttctccct  
 840  
 caaccaagat cttctaaaaa gaaataatat tttagtcttc tgcttgagga actgactgtg  
 900  
 aagcgacgcc cagtgaaaaa catgatcttg cagcagctct ggtggcagct gtccttgagg  
 960  
 aacctttggt gtgtggtggg aagctatcag aacaagaaat gtaggcattt cccgtttttt  
 1020  
 ttgggggggg ggtggggggg cagggtcttg ccctcttgaa aggcatttac ttgtttaaca  
 1080  
 cttgtccagc tacagtgggg tacagtagct ggctattcac aggcattcat atagcccact  
 1140  
 agtctcatat tattttcctt ttgagaaatt ggaaactctt tctgttgcta ttatattaat  
 1200  
 aaagtgggtg tttattttct ggtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
 1260  
 aaaaaa  
 1266

<210> 3276  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 3276  
 Met Ala Lys His His Pro Asp Leu Ile Phe Cys Arg Lys Gln Ala Gly  
 1 5 10 15  
 Val Ala Ile Gly Arg Leu Cys Glu Lys Cys Asp Gly Lys Cys Val Ile  
 20 25 30  
 Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu  
 35 40 45  
 Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro  
 50 55 60  
 Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys  
 65 70 75 80  
 Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr  
 85 90 95  
 Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg  
 100 105 110

<210> 3277  
 <211> 1435  
 <212> DNA  
 <213> Homo sapiens

<400> 3277  
 ncttcgtct ccgagaacaa caacaacagc aacaagaaaa caacaataaa aaaaataagg  
 60  
 ctgcgtggga ggcagaaaga gctaattgagg ccacgcttgt ccctcggcca cgtcccacc  
 120  
 cagattccg tctccttaaa atgttcattg gtaagtgcgt ggcagaagcg gctcaagcgc  
 180  
 actcgtgcgt cattgtgtgc agggccgagg gagcgggtgca aggcgcgcgc gtgacgtcag  
 240  
 gacgccgcgg tcaggacgtc gaagccaaag aagaccagag ccagccgggt ggcacagcgg  
 300  
 tgctcgtggc gtgttgctga tcgcctgggt ggttggtggc gtgtccctgc agcgaaggat  
 360  
 cctgggtggc agtgaaaaag cagtctggct cccgaggtcc accccttata cccaaggctc  
 420  
 cagatggcgg ccaacgtggg tgatcaacgt agcacagatt ggtcttctca gtacagcatg  
 480  
 gtggctgggg caggccgaga gaatggcatg gagacgccga tgcacgagaa cccggagtgg  
 540  
 gagaaggccc gtcaggccct ggccagcatc agcaagtcag gagctgccgg cggctctgcc  
 600  
 aagtccagca gcaatgggct tgtggccagt gcaagtacgt gtcccaggca gaagcctcag  
 660  
 ctttcagca gcagcagtag taccagtggg accagcagta caactatgcc tacccttaca  
 720  
 gctactacta tccatgagc atgtaccaga gctatggctc ccctccag tatgggatgg  
 780

ccggctccta tggctagcca caccacagca gccatccgca ccccaacacc aagggactct  
 840  
 gaaccagccc ccagtccccg gcatggatga gagcatgtcc taccaggctc cccctcagca  
 900  
 gctgccgtcg gctcagcccc ctcagccctc aaatccccc catggggctc acacgctgaa  
 960  
 cagtggccct cagcctggga cagctccagc cacacagcan ncagccaggc ggggcccgcc  
 1020  
 acggggccagg cctatgggccc acacacctac accgaacctg ccaagcccaa gaagggccaa  
 1080  
 cagctgtgga accgcatgaa acccgcccct gggactggag gttcaagtcc aacatccaga  
 1140  
 agcgaccctt tgetgttacc acccagagct ttggctccaa cgcagagggc cagcacagtg  
 1200  
 gttttggccc ccagcccaac cctgagaaag ttcagaacca cagcgggtcc tctgcccggg  
 1260  
 ggaacctgtc tgggaagccc gatgactggc cccaggacat gaaagagtat gtggagcgct  
 1320  
 gcttcaccgc ctgtgagtcg gaggaggaca aggaccgcac ggaaaagctg ctcaaggagg  
 1380  
 tgctgcaggc ggggctgcag gacggctcgg cctataccat tgactggagc cgggg  
 1435

&lt;210&gt; 3278

&lt;211&gt; 104

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3278

Met	Ala	Ala	Asn	Val	Gly	Asp	Gln	Arg	Ser	Thr	Asp	Trp	Ser	Ser	Gln
1				5				10					15		
Tyr	Ser	Met	Val	Ala	Gly	Ala	Gly	Arg	Glu	Asn	Gly	Met	Glu	Thr	Pro
			20					25					30		
Met	His	Glu	Asn	Pro	Glu	Trp	Glu	Lys	Ala	Arg	Gln	Ala	Leu	Ala	Ser
			35				40					45			
Ile	Ser	Lys	Ser	Gly	Ala	Ala	Gly	Gly	Ser	Ala	Lys	Ser	Ser	Ser	Asn
			50				55				60				
Gly	Pro	Val	Ala	Ser	Ala	Ser	Thr	Cys	Pro	Arg	Gln	Lys	Pro	Gln	Leu
65					70					75				80	
Cys	Ser	Ser	Ser	Ser	Thr	Thr	Ser	Gly	Thr	Ser	Ser	Thr	Thr	Met	Pro
				85				90						95	
Thr	Pro	Thr	Ala	Thr	Thr	Ile	Pro								
							100								

&lt;210&gt; 3279

&lt;211&gt; 1130

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3279

nngcgcgccc accgcgccc atccatgttc gacaccacac cccactctgg ccggagcacg  
 60  
 ccaagcagct ccccatcgct ccggaaacgg ctgcagctcc tgccccaag ccggcccca  
 120

cctgagccag aaccaggcac catggtggag aagggatcag atagctcctc agagaagggt  
 180  
 ggggtgcctg ggacccccag caccagagc ctaggcagcc ggaacttcac ccgcaacagc  
 240  
 aagaagatgc agagctggta cagtatgctg agccccactt ataagcagcg taatgaggac  
 300  
 ttccggaaac tggtcagcaa actccccgaa gcagaacgcc tcattgtgga ttactcctgc  
 360  
 gccctgcagc gtgagatcct gctccagggc cgctctacc tctctgagaa ctggatctgc  
 420  
 ttctacagca acatcttccg ctgggagacc acgatctcca tccagctgaa ggaagtgaca  
 480  
 tgtctgaaga aggaaaagac ggccaagctg atccccaacg ccatccagat ctgcacggag  
 540  
 agcgagaagc atttcttcac ttcctttggg gcccgtagacc gctgcttctt cctcatcttc  
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 780  
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 840  
 cgtggccatg tcacgccccaa cttttcccga gccagcagcg acgcagacca tggggcagag  
 900  
 gaggacaagg aggagcaggt agacagccag ccagacgcct cctccagcca gacagtgacc  
 960  
 ccggtggctg aacccccgag cacagagccc acccagcctg acgggcccac caccctgggc  
 1020  
 cccttggatc tgctgcccag tgaggagcta ttgacagaca caagtaactc ctcttcaccc  
 1080  
 actggggagg aagcggactt ggctgccctg cttcccagacc tctccggccg  
 1130

<210> 3280

<211> 376

<212> PRT

<213> Homo sapiens

<400> 3280

Xaa	Arg	Ala	His	Arg	Ala	Ala	Ser	Met	Phe	Asp	Thr	Thr	Pro	His	Ser
1				5					10					15	
Gly	Arg	Ser	Thr	Pro	Ser	Ser	Ser	Pro	Ser	Leu	Arg	Lys	Arg	Leu	Gln
			20					25					30		
Leu	Leu	Pro	Pro	Ser	Arg	Pro	Pro	Pro	Glu	Pro	Glu	Pro	Gly	Thr	Met
			35				40					45			
Val	Glu	Lys	Gly	Ser	Asp	Ser	Ser	Ser	Glu	Lys	Gly	Gly	Val	Pro	Gly
		50				55					60				
Thr	Pro	Ser	Thr	Gln	Ser	Leu	Gly	Ser	Arg	Asn	Phe	Ile	Arg	Asn	Ser
65					70				75					80	
Lys	Lys	Met	Gln	Ser	Trp	Tyr	Ser	Met	Leu	Ser	Pro	Thr	Tyr	Lys	Gln
			85					90						95	
Arg	Asn	Glu	Asp	Phe	Arg	Lys	Leu	Phe	Ser	Lys	Leu	Pro	Glu	Ala	Glu

```

      100      105      110
Arg Leu Ile Val Asp Tyr Ser Cys Ala Leu Gln Arg Glu Ile Leu Leu
      115      120      125
Gln Gly Arg Leu Tyr Leu Ser Glu Asn Trp Ile Cys Phe Tyr Ser Asn
      130      135      140
Ile Phe Arg Trp Glu Thr Thr Ile Ser Ile Gln Leu Lys Glu Val Thr
      145      150      155      160
Cys Leu Lys Lys Glu Lys Thr Ala Lys Leu Ile Pro Asn Ala Ile Gln
      165      170      175
Ile Cys Thr Glu Ser Glu Lys His Phe Phe Thr Ser Phe Gly Ala Arg
      180      185      190
Asp Arg Cys Phe Leu Leu Ile Phe Arg Leu Trp Gln Asn Ala Leu Leu
      195      200      205
Glu Lys Thr Leu Ser Pro Arg Glu Leu Trp His Leu Val His Gln Cys
      210      215      220
Tyr Gly Ser Glu Leu Gly Leu Thr Ser Glu Asp Glu Asp Tyr Val Ser
      225      230      235      240
Pro Leu Gln Leu Asn Gly Leu Gly Thr Pro Lys Glu Val Gly Asp Val
      245      250      255
Ile Ala Leu Ser Asp Ile Thr Ser Ser Gly Ala Ala Asp Arg Ser Gln
      260      265      270
Glu Pro Ser Pro Val Gly Ser Arg Arg Gly His Val Thr Pro Asn Leu
      275      280      285
Ser Arg Ala Ser Ser Asp Ala Asp His Gly Ala Glu Glu Asp Lys Glu
      290      295      300
Glu Gln Val Asp Ser Gln Pro Asp Ala Ser Ser Ser Gln Thr Val Thr
      305      310      315      320
Pro Val Ala Glu Pro Pro Ser Thr Glu Pro Thr Gln Pro Asp Gly Pro
      325      330      335
Thr Thr Leu Gly Pro Leu Asp Leu Leu Pro Ser Glu Glu Leu Leu Thr
      340      345      350
Asp Thr Ser Asn Ser Ser Ser Thr Gly Glu Glu Ala Asp Leu Ala
      355      360      365
Ala Leu Leu Pro Asp Leu Ser Gly
      370      375

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&lt;210&gt; 3281

&lt;211&gt; 842

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3281

```

gaattctgcc ttgccgtgtg cctcattggc caaaggaaag caacagagtc tgcagccagg
60
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120
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 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 3282  
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<210> 3284  
 <211> 1012  
 <212> PRT  
 <213> Homo sapiens

<400> 3284

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Ala Phe Thr Arg Xaa His Val Cys Ala Glu Asn Leu Pro Pro Val Leu
          35           40           45
Met Glu His Lys Ala Thr Thr Ile Gln Lys His Val Arg Gly Trp Met
          50           55           60
Ala Arg Arg His Phe Gln Arg Leu Arg Asp Ala Ala Ile Val Ile Gln
          65           70           75           80
Cys Ala Phe Arg Met Leu Lys Ala Arg Arg Glu Leu Lys Ala Leu Arg
          85           90           95
Ile Glu Ala Arg Ser Ala Glu His Leu Lys Arg Leu Asn Val Gly Met
          100          105          110
Glu Asn Lys Val Val Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys
          115          120          125
Glu Phe Lys Thr Leu Ser Glu Gln Leu Ser Val Thr Thr Ser Thr Tyr
          130          135          140
Thr Met Glu Val Glu Arg Leu Lys Lys Glu Leu Val His Tyr Gln Gln
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Ser Pro Gly Glu Asp Thr Ser Leu Arg Leu Gln Glu Glu Val Glu Ser
          165          170          175
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          180          185          190
Asp Ala His Ser Arg Glu Lys Asp Glu Leu Arg Lys Arg Val Ala Asp
          195          200          205
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Tyr Gln Asn Leu Val Lys Glu Tyr Ser Gln Leu Glu Gln Arg Tyr Asp
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Arg Asn Pro Ser Asn Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro
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Ser Ile Ser Thr Ser Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln
          305          310          315          320
Val Glu Glu Ile Gly Leu Glu Lys Ala Ala Met Asp Met Thr Val Phe
          325          330          335
Leu Lys Leu Gln Lys Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys
          340          345          350
Leu Gln Val Gln Leu Glu Lys Arg Glu Gln Gln Asp Ser Lys Lys Val
          355          360          365
Gln Ala Glu Pro Pro Gln Thr Asp Ile Asp Leu Asp Pro Asn Ala Asp

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Glu Glu Val Leu Ile Leu Arg Thr Gln Ile Val Ser Ala Asp Gln Arg		
450	455	460
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465	470	475
Trp Pro Asn Ser Glu Arg His Val Asp Gln Glu Asp Ala Ile Glu Ala		
485	490	495
Tyr His Gly Val Cys Gln Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln		
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Ala Gln Ser Leu Glu His Glu Glu Glu Val Glu His Leu Lys Ala Gln		
515	520	525
Leu Glu Ala Leu Lys Glu Glu Met Asp Lys Gln Gln Gln Thr Phe Cys		
530	535	540
Gln Thr Leu Leu Leu Ser Pro Glu Ala Gln Val Glu Phe Gly Val Gln		
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Gln Glu Ile Ser Arg Leu Thr Asn Glu Asn Leu Asp Leu Lys Glu Leu		
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Val Glu Lys Leu Glu Lys Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys		
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Ile Tyr Met Lys Lys Ala Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala		
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Gln Ser Glu Arg Lys Arg His Glu Leu Asn Arg Gln Val Thr Val Gln		
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Arg Lys Glu Lys Asp Phe Gln Gly Met Leu Glu Tyr His Lys Glu Asp		
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Glu Ala Leu Leu Ile Arg Asn Leu Val Thr Asp Leu Lys Pro Gln Met		
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Leu Ser Gly Thr Val Pro Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys		
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Ile Arg His Ala Asp Tyr Thr Asn Asp Asp Leu Lys Val His Ser Leu		
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Leu Thr Ser Thr Ile Asn Gly Ile Lys Lys Val Leu Lys Lys His Asn		
690	695	700
Asp Asp Phe Glu Met Thr Ser Phe Trp Leu Ser Asn Thr Cys Arg Leu		
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Leu His Cys Leu Lys Gln Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln		
725	730	735
Asn Thr Ala Lys Gln Asn Glu His Cys Leu Lys Asn Phe Asp Leu Thr		
740	745	750
Glu Tyr Arg Gln Val Leu Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln		
755	760	765
Leu Ile Lys Ile Ala Glu Gly Val Leu Gln Pro Met Ile Val Ser Ala		
770	775	780
Met Leu Glu Asn Glu Ser Ile Gln Gly Leu Ser Gly Val Lys Pro Thr		
785	790	795
Gly Tyr Arg Lys Arg Ser Ser Ser Met Ala Asp Gly Asp Asn Ser Tyr		

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 820 825 830  
 Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln  
 835 840 845  
 Leu Phe Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg  
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 Lys Asp Val Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile  
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 Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg Asn Leu His Gln Ser Gly  
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 Pro Leu Asn Glu Phe Glu Glu Arg Val Thr Val Ala Phe Ile Arg Thr  
 945 950 955 960  
 Ile Gln Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu  
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 Asp Ala Lys His Met Phe Pro Val Leu Phe Pro Phe Asn Pro Ser Ser  
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&lt;210&gt; 3285

&lt;211&gt; 1518

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3285

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<210> 3286

<211> 142

<212> PRT

<213> Homo sapiens

<400> 3286

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		20						25					30		
Lys	Asn	Asn	Asp	Asn	Thr	Arg	Pro	Ala	Pro	Pro	Pro	Lys	Ser	Cys	Cys
		35					40					45			
Cys	Glu	Leu	Arg	Leu	Gln	Lys	Arg	Thr	His	Thr	Val	Ala	Asp	Lys	Thr
	50					55					60				
Gln	Ala	Arg	Arg	Met	Phe	Glu	Ser	Gln	Ser	Ala	Leu	Ser	Leu	Val	Pro
65					70					75					80
Val	Thr	Ser	Tyr	Val	Gln	Leu	Pro	Gly	Pro	Ile	Pro	Tyr	Ser	Asp	Cys
				85					90					95	
Arg	Leu	Arg	Thr	Glu	Asp	Ala	Pro	Leu	Leu	Ser	Leu	His	Phe	Asp	Leu
			100					105					110		
Leu	Phe	Pro	Leu	Lys	Thr	Arg	Arg	Pro	Ala	Phe	Pro	Lys	Thr	Ala	Trp

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<210> 3287

<211> 921

<212> DNA

<213> Homo sapiens

<400> 3287

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<210> 3288

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3288

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 Ser Cys Ser Phe Ser Phe Gly Leu Ser Lys Tyr Pro Gly Pro Pro Cys



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      35          40          45
Ile Pro Leu Pro Phe Ser Cys Gly Cys Gly Ala Ser Leu Asn Arg Ser
  50          55          60
Thr Phe Leu Phe Pro Ser Thr Arg Asp Arg Glu Ser Leu Lys Gly Ser
  65          70          75          80
Gly Ala Pro Ser Ala His Leu Asp Gly Ala Gly Asp Ala Gln Arg Arg
      85          90          95
Phe Arg Ala Leu Tyr Phe Gln Leu Gln His Ser Gln Val Phe Thr Ala
      100          105          110
Gln Gly Asp Gly Ala Arg Val Thr Arg Asn Pro Gly Glu Gly Arg Ser
      115          120          125
Phe Pro Arg Arg Gly Ala Thr Ser Phe Pro Asp Trp Ala Tyr Ala Gly
      130          135          140
Gly Arg Gln Leu
145

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&lt;210&gt; 3289

&lt;211&gt; 554

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3289

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540
ataagctgca attg
554

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&lt;210&gt; 3290

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3290

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      20          25          30
Gly Ser Leu Thr Gln Cys Arg Arg Ala Trp Val Pro Pro Trp Thr Gln

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<400> 3291
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<210> 3292

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3292

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		20					25					30			
Trp	Ser	Ala	Thr	Pro	Gly	Pro	Pro	Trp	Ala	Pro	Ser	Pro	Ala	Thr	Pro
	35					40					45				
Ala	Val	Arg	Leu	Pro	Ala	Pro	Ser	Pro	Thr	Ile	Ala	Ala	Ser	Val	Pro
	50				55				60						
Pro	His	Trp	Leu	Phe	Thr	Trp	Leu	Ala	Val	Ser	Val	Ser	Gln	Pro	Gly
65			70					75					80		
Ser	Glu	Ser	Xaa	Arg	Arg	Pro	Leu	Pro	Pro	Pro	Gln	Leu	Pro	Pro	Pro
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<210> 3293

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 3293

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2362

<210> 3294

<211> 353

<212> PRT

<213> Homo sapiens

<400> 3294

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      20           25           30
Thr Ser Leu Pro Pro Gly Pro Pro Ala Gly Arg Arg His Leu Pro Leu
      35           40           45
Ser Arg Arg Arg Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala
      50           55           60
Val Phe Val Ile Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser
      65           70           75           80
Ser Asn Ser Ala Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg
      85           90           95
Ser Arg Arg Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr
      100          105          110
Val Pro Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys
      115          120          125
Val Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
      130          135          140
Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr
      145          150          155          160
Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val
      165          170          175
Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val
      180          185          190
Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys
      195          200          205
Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly
      210          215          220
Leu Val Phe Pro Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met
      225          230          235          240
Arg Gln Phe Asp Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu
      245          250          255
Lys Ser His Ser Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala
      260          265          270
Val Glu Leu Cys Asp His Val His Val Tyr Gly Met Val Pro Pro Asn
      275          280          285
Tyr Cys Ser Gln Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr
      290          295          300
Glu Pro Lys Gly Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His
      305          310          315          320
Ser Arg Lys Gly Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe
      325          330          335
Ser Ser Trp Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp
      340          345          350
Thr

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&lt;210&gt; 3295

&lt;211&gt; 690

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3295

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 690

&lt;210&gt; 3296

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3296

Met	Gly	Asn	Trp	Lys	Asn	Lys	Pro	Ser	Arg	Ile	Val	Gly	Arg	Lys	Thr
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Leu	Trp	Glu	Arg	Pro	Gly	Cys	Cys	Ile	Arg	His	Arg	Ile	Thr	Trp	Glu
			20					25					30		
Pro	Arg	His	Met	Gly	Pro	Ala	Leu	Arg	Ser	Leu	Gln	Val	Lys	Lys	Gly
		35					40					45			
Thr	Glu	His	Ala	Asp	Pro	Leu	Pro	Phe	Pro	Ser	Val	Ser	Leu	Ser	Gly
		50				55					60				
Phe	Thr	Val	Gly	Thr	Leu	Ser	Glu	Thr	Ser	Thr	Gly	Gly	Pro	Ala	Thr
65					70					75				80	
Pro	Thr	Trp	Lys	Glu	Cys	Pro	Ile	Cys	Lys	Glu	Arg	Phe	Pro	Ala	Glu
			85					90					95		
Ser	Asp	Lys	Asp	Ala	Leu	Glu	Asp	His	Met	Asp	Gly	His	Phe	Phe	Phe
			100					105					110		
Ser	Thr	Gln	Gly	Pro	Leu	His	Leu								

115

120

&lt;210&gt; 3297

&lt;211&gt; 3176

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3297

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<210> 3298

<211> 251

<212> PRT

<213> Homo sapiens

<400> 3298

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			20					25					30		
Cys	Leu	Trp	Val	Ser	Phe	Cys	Val	Cys	Val	Cys	Ile	Cys	Val	Cys	Val
		35					40					45			
Xaa	Leu	Cys	Ala	Cys	Met	Cys	Leu	Asp	Val	Cys	Phe	Cys	Met	Cys	Leu
	50					55					60				
Cys	Val	Cys	Leu	Tyr	Val	Cys	Ile	Cys	Val	Tyr	Val	Cys	Val	Cys	His
65					70					75					80
Phe	Val	Cys	Phe	Trp	Val	Cys	Leu	Ser	Ala	Cys	Leu	Cys	Ile	Pro	Val
			85						90					95	
Ser	Pro	Cys	Val	Cys	Leu	Cys	Val	Cys	Ile	Cys	Xaa	Cys	Leu	Cys	Met
			100					105					110		
Cys	Val	Arg	Gly	Cys	Val	Ser	Val	Cys	Val	Cys	Val	Cys	Ile	Glu	Arg
		115					120					125			
Glu	Gly	Glu	Arg	Lys	Gly	Ala	Thr	Asp	Gly	Ser	Ala	Trp	Lys	Val	Tyr
	130					135					140				
Pro	His	Ser	Gln	Pro	Trp	Glu	Glu	Ser	Val	Asn	Pro	Pro	Thr	Gly	Gln
145					150					155					160
Asp	Gln	Leu	Trp	Trp	Cys	Leu	Ala	Asp	Ser	Gly	Asn	Val	Thr	Phe	His
			165					170						175	
Leu	Arg	Met	Gly	Leu	His	Phe	Leu	Gly	Lys	Glu	Cys	Arg	Ser	Trp	Ser
		180					185					190			
Leu	Lys	Glu	Cys	Phe	Phe	Phe	Pro	Phe	Val	Ile	Glu	Arg	Ala	Gln	Pro
		195					200					205			
Cys	Val	His	Trp	Leu	Thr	Val	Thr	Asn	Leu	Arg	Val	Gly	Asp	Ser	His
	210					215					220				
Arg	Glu	Glu	Thr	Glu	Gly	Thr	Ala	Asp	Ser	Glu	Gln	Glu	Ser	Gly	Gly
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Thr	Ser	Leu	Pro	Leu	Gly	Pro	Asn	Pro	Gln	Leu					
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<210> 3299

<211> 1387

<212> DNA

<213> Homo sapiens

<400> 3299

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&lt;210&gt; 3300

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3300

Met Ser Arg Cys Glu Thr Cys Gly Thr Glu Glu Ala Lys Tyr Arg Cys

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Pro Arg Cys Met Arg Tyr Ser Cys Ser Leu Pro Cys Val Lys Lys His
      20           25           30
Lys Ala Glu Leu Thr Cys Asn Gly Val Arg Asp Lys Thr Ala Tyr Ile
      35           40           45
Ser Ile Gln Gln Phe Thr Glu Met Asn Leu Leu Ser Asp Tyr Arg Phe
      50           55           60
Leu Glu Asp Val Ala Arg Thr Ala Asp His Ile Ser Arg Asp Ala Phe
      65           70           75           80
Leu Lys Arg Pro Ile Ser Asn Lys Tyr Met Tyr Phe Met Lys Asn Arg
      85           90           95
Ala Arg Ser Lys Gly Ile Asn Leu Lys Leu Leu Pro Asn Gly Phe Thr
      100          105          110
Lys Arg Lys Glu Asn Ser Thr Phe Phe Asp Lys Lys Lys Gln Gln Phe
      115          120          125
Cys Trp His Val Lys Leu Gln Phe Pro Gln Ser Gln Ala Glu Tyr Ile
      130          135          140
Glu Lys Arg Val Pro Asp Asp Lys Thr Ile Asn Glu Ile Leu Lys Pro
      145          150          155          160
Tyr Ile Asp Pro Glu Lys Ser Asp Pro Val Ile Arg Gln Arg Leu Lys
      165          170          175
Ala Tyr Ile Arg Ser Gln Thr Gly Val Gln Ile Leu Met Lys Ile Glu
      180          185          190
Tyr Met Gln Gln Asn Leu Val Arg Tyr Tyr Glu Leu Asp Pro Tyr Lys
      195          200          205
Ser Leu Leu Asp Asn Leu Arg Asn Lys Val Ile
      210          215

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&lt;210&gt; 3301

&lt;211&gt; 2109

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3301

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1980  
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2109

&lt;210&gt; 3302

<211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 3302

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 20           25           30
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
 35           40           45
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
 50           55           60
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
 65           70           75           80
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
 85           90           95
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
 100          105          110
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala
 115          120          125
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
 130          135          140
Ala Ser Met Glu Ser Pro Xaa Val Asn Ala Phe Pro Ala Gln Asn Asn
 145          150          155          160
Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
 165          170          175
Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly His Pro
 180          185          190
Gly Ser Thr Gln Leu Met Ala Leu Pro Ile Thr Gly Pro Gly Ser Pro
 195          200          205
Pro Gly Trp Ala Thr Leu Gln Ile Gln Pro Gln Thr Thr Ser Val Ser
 210          215          220
Ala Val Leu Gln Thr Gln Ala Gly Arg Gln Gly Ser Cys Lys Gln Pro
 225          230          235          240
Gly Gly Asp Lys Glu Lys Ser Leu Leu Gly Ser Leu Ser Phe Pro Gly
 245          250          255
His Val Ala Asn Ser Ala Ile Pro Ser Ser Arg Ala Ser Ala Ser Gly
 260          265          270
Lys Asn Phe Pro Phe Pro Val Ser His Pro Ser Val Ala Gly Ala Ser
 275          280          285
His Gln Gly Arg Arg Gly Leu Ser Leu Leu Cys Phe Gly Glu Gly Ala
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Lys Tyr Tyr

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<210> 3303  
 <211> 699  
 <212> DNA  
 <213> Homo sapiens

<400> 3303

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 420  
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 699

&lt;210&gt; 3304

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3304

Pro Arg Lys Arg Asp Phe Thr Asn Glu Ala Pro Pro Ala Pro Leu Pro  
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 Asp Ala Ser Ala Ser Pro Leu Ser Pro His Arg Arg Ala Lys Ser Leu  
 20 25 30  
 Asp Arg Arg Ser Thr Glu Pro Ser Val Thr Pro Asp Leu Leu Asn Phe  
 35 40 45  
 Lys Lys Gly Trp Leu Thr Lys Gln Tyr Glu Asp Gly Gln Trp Lys Lys  
 50 55 60  
 His Trp Phe Val Leu Ala Asp Gln Ser Leu Arg Tyr Tyr Arg Asp Ser  
 65 70 75 80  
 Val Ala Glu Glu Ala Ala Asp Leu Asp Gly Glu Ile Asp Leu Ser Ala  
 85 90 95  
 Cys Tyr Asp Val Thr Glu Tyr Pro Val Gln Arg Asn Tyr Gly Phe Gln  
 100 105 110  
 Ile His Thr Lys Glu Gly Glu Phe Thr Leu Ser Ala Met Thr Ser Gly  
 115 120 125  
 Ile Arg Arg Asn Trp Ile Gln Thr Ile Met Lys His Val His Pro Thr  
 130 135 140  
 Thr Ala Pro Asp Val Thr Ser Ser Leu Pro Glu Glu Lys Asn Lys Ser  
 145 150 155 160  
 Ser Cys Ser Phe Glu Thr Cys Pro Arg Ser Thr Glu Lys Gln Glu Ala  
 165 170 175  
 Glu Leu Gly Glu Pro Asp Pro Glu Gln Lys Arg Ser Arg Ala Arg Glu

180 185 190  
 Arg Arg Arg Glu Gly Arg Ser Lys Thr Phe Asp Trp Ala Glu Phe Arg  
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 Ala Asp Thr His Glu Pro Leu Arg Pro  
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<210> 3305  
 <211> 2717  
 <212> DNA  
 <213> Homo sapiens

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2520  
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2580  
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&lt;210&gt; 3306



<211> 319  
 <212> PRT  
 <213> Homo sapiens

<400> 3306  
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 Ile Ser Leu Val Met Lys Thr Pro Arg Val Ala Lys Asn Glu Ala Leu  
 35 40 45  
 Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln Gly Thr Val Arg  
 50 55 60  
 Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln Ser Leu Ser Phe  
 65 70 75 80  
 Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe Ser Met Ala Pro  
 85 90 95  
 Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln His Lys Gly Arg  
 100 105 110  
 Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly Gln Ala Val Arg  
 115 120 125  
 Lys Gly Ala Thr Leu Xaa Ala Cys Thr Thr Gly His Gly Xaa Arg Asp  
 130 135 140  
 Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu Gly Thr Tyr  
 145 150 155 160  
 Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln Ile Ile Gln  
 165 170 175  
 Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu Ala Asn Glu  
 180 185 190  
 Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr Tyr Pro Leu  
 195 200 205  
 Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly Ser Pro Ala  
 210 215 220  
 Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Val Ala Gly  
 225 230 235 240  
 Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly Leu Cys Arg  
 245 250 255  
 Cys His Leu His Leu Pro Gly His Thr His Leu Ser Gly Gly Ala Pro  
 260 265 270  
 Trp Gly Gln His Pro Gly Cys Pro Thr Arg Ala Glu Asn Ser Leu Gly  
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<210> 3307  
 <211> 352  
 <212> DNA  
 <213> Homo sapiens

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 180  
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 240  
 agcttctcag ggcctgtgtc cggctggttg gtccctgtgc tgcccaaacc aggtgtccac  
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<210> 3308

<211> 110

<212> PRT

<213> Homo sapiens

<400> 3308

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Ser	Leu	His	Pro	Asp	Pro	Gly	Ala	Ser	Leu	Pro	Cys	Pro	Val	Leu	Ile
			20					25					30		
Pro	Arg	Trp	Glu	Pro	Cys	Leu	Gly	Gln	Gly	Gly	Arg	Val	Asp	Gly	Ser
		35					40					45			
Trp	Asp	Cys	Asp	Ile	Gly	Arg	Arg	Gly	Arg	Ser	Pro	Ala	Leu	Ser	Ser
	50					55					60				
Ala	Gly	Trp	Ala	Gly	Ile	His	Leu	Ala	Ala	Ser	Gln	Gly	Leu	Cys	Pro
65					70					75				80	
Ala	Gly	Trp	Ser	Leu	Cys	Cys	Pro	Asn	Gln	Val	Ser	Thr	Phe	Pro	Ala
			85					90					95		
Pro	Met	Arg	Arg	Glu	Gly	Gly	Arg	Trp	Trp	Leu	Gly	Trp	Arg		
			100					105					110		

<210> 3309

<211> 737

<212> DNA

<213> Homo sapiens

<400> 3309

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 180  
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 240  
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 300  
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 480

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<210> 3310

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3310

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		20					25						30		
Ala	Gln	Leu	Glu	Glu	Gln	Phe	Tyr	Leu	Gln	Ala	Leu	Lys	Leu	Pro	Asn
		35				40					45				
Gln	Thr	His	Pro	Asp	Val	Pro	Val	Gly	Asp	Glu	Ser	Gln	Ala	Arg	Val
	50				55					60					
Leu	His	Met	Val	Gly	Asp	Lys	Pro	Val	Phe	Ser	Phe	Gln	Pro	Arg	Gly
65				70					75					80	
His	Leu	Glu	Ile	Gly	Glu	Lys	Leu	Asp	Ile	Ile	Arg	Gln	Lys	Arg	Leu
			85					90					95		
Ser	His	Val	Ser	Gly	His	Arg	Ser	Tyr	Leu	Arg	Gly	Ala	Gly	Ala	
		100					105					110			
Leu	Leu	Gln	His	Gly	Leu	Val	Asn	Phe	Thr	Phe	Asn	Lys	Leu	Leu	Arg
		115				120					125				
Arg	Gly	Phe	Thr	Pro	Met	Thr	Val	Pro	Asp	Leu	Leu	Arg	Gly	Ala	Val
		130				135					140				
Phe	Glu	Gly	Cys	Gly	Met	Thr	Pro	Asn	Ala	Asn	Pro	Ser	Gln	Ile	Tyr
145				150					155					160	
Asn	Ile	Asp	Pro	Ala	Arg	Phe	Lys	Asp	Leu	Asn	Leu	Ala	Gly	Thr	Ala
			165					170					175		
Glu	Val	Gly	Leu	Ala	Gly	Tyr	Phe	Met	Asp	His	Thr	Val	Ala	Phe	Arg
		180				185						190			
Asp	Leu	Pro	Val	Arg	Met	Val	Cys	Ser	Ser	Thr	Cys	Tyr	Arg	Ala	Glu
		195				200					205				
Thr	Asn														
	210														

<210> 3311

<211> 486

<212> DNA

<213> Homo sapiens

<400> 3311

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 360  
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 420  
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 480  
 gtcgac  
 486

&lt;210&gt; 3312

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3312

Met	Ser	Ser	Cys	Ser	Asn	Val	Cys	Gly	Ser	Arg	Gln	Ala	Gln	Ala	Ala
1				5					10					15	
Ala	Glu	Gly	Gly	Tyr	Gln	Arg	Tyr	Gly	Val	Arg	Ser	Tyr	Leu	His	Gln
			20					25					30		
Phe	Tyr	Glu	Asp	Cys	Thr	Ala	Ser	Ile	Trp	Glu	Tyr	Glu	Asp	Asp	Phe
		35					40					45			
Gln	Ile	Gln	Arg	Ser	Pro	Asn	Arg	Trp	Ser	Ser	Val	Phe	Trp	Lys	Val
		50				55					60				
Gly	Leu	Ile	Ser	Gly	Thr	Val	Phe	Val	Ile	Leu	Gly	Leu	Thr	Val	Leu
65				70					75				80		
Ala	Val	Gly	Phe	Leu	Val	Pro	Pro	Lys	Ile	Glu	Ala	Phe	Gly	Glu	Ala
			85					90					95		
Asp	Phe	Val	Val	Val	Asp										
			100												

&lt;210&gt; 3313

&lt;211&gt; 1791

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3313

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 60  
 ccgaggaggg ggagatcgac tactcggccg aggaaggcga gaaccgcggg gaagcgacgc  
 120  
 cccggggcgg gtcgagttgg cggcggcggc ggccgantgc gttctcgtca gccggaaggg  
 180  
 ctgcgaagtc atcataaagt ttctgtttca cccgtcgtcc atgttcgagg actctgtgaa  
 240  
 tctgtggtgg aagcagacct cgtggaagcg ctggaaaaat ttgggacaat atgctatgtg  
 300

atgatgatgc catttaaacy acaggctcta gtggaatttg aaaacataga tagtgccaaa  
360  
gaatgtgtga catttgctgc agatgaaccc gtgtacattg ctgggtcaaca ggcttttttc  
420  
aactattcta caagcaaaag gatcactcgg ccaggaaata ctgatgatcc atcaggaggc  
480  
aacaagttc ttctgctctc aattcagaat ccgctttatc caattacagt ggatgtttta  
540  
tatactgtat gcaaccctgt tggcaaagtg caacgtattg ttatattcaa gagaaatggg  
600  
atacaagcaa tgggtgagtt tgaatcagtc ctttgtgccc agaaagctaa agcagcactc  
660  
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720  
cgtctaaaatg ttattaggaa tgacaatgac agttgggact aactaaacc atatttggga  
780  
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1320  
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1380  
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1440  
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1680  
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1740  
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1791

&lt;210&gt; 3314

&lt;211&gt; 537

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3314

Xaa Leu Gly Arg Arg Thr Arg Arg Thr Gly Ser Thr Arg Ala Arg Pro  
 1 5 10 15  
 Ser Val Ser Arg Pro Arg Arg Gly Arg Ser Thr Thr Arg Pro Arg Lys  
 20 25 30  
 Ala Arg Thr Ala Val Lys Arg Arg Pro Gly Ala Gly Arg Val Gly Gly  
 35 40 45  
 Gly Gly Gly Arg Xaa Arg Ser Arg Gln Pro Glu Gly Leu Arg Ser His  
 50 55 60  
 His Lys Val Ser Val Ser Pro Val Val His Val Arg Gly Leu Cys Glu  
 65 70 75 80  
 Ser Val Val Glu Ala Asp Leu Val Glu Ala Leu Glu Lys Phe Gly Thr  
 85 90 95  
 Ile Cys Tyr Val Met Met Met Pro Phe Lys Arg Gln Ala Leu Val Glu  
 100 105 110  
 Phe Glu Asn Ile Asp Ser Ala Lys Glu Cys Val Thr Phe Ala Ala Asp  
 115 120 125  
 Glu Pro Val Tyr Ile Ala Gly Gln Gln Ala Phe Phe Asn Tyr Ser Thr  
 130 135 140  
 Ser Lys Arg Ile Thr Arg Pro Gly Asn Thr Asp Asp Pro Ser Gly Gly  
 145 150 155 160  
 Asn Lys Val Leu Leu Ser Ile Gln Asn Pro Leu Tyr Pro Ile Thr  
 165 170 175  
 Val Asp Val Leu Tyr Thr Val Cys Asn Pro Val Gly Lys Val Gln Arg  
 180 185 190  
 Ile Val Ile Phe Lys Arg Asn Gly Ile Gln Ala Met Val Glu Phe Glu  
 195 200 205  
 Ser Val Leu Cys Ala Gln Lys Ala Lys Ala Ala Leu Asn Gly Ala Asp  
 210 215 220  
 Ile Tyr Ala Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Arg Pro Thr  
 225 230 235 240  
 Arg Leu Asn Val Ile Arg Asn Asp Asn Asp Ser Trp Asp Tyr Thr Lys  
 245 250 255  
 Pro Tyr Leu Gly Arg Arg Asp Arg Gly Lys Gly Arg Gln Arg Gln Ala  
 260 265 270  
 Ile Leu Gly Glu His Pro Ser Ser Phe Arg His Asp Gly Tyr Gly Ser  
 275 280 285  
 His Gly Pro Leu Leu Pro Leu Pro Ser Arg Tyr Arg Met Gly Ser Arg  
 290 295 300  
 Asp Thr Pro Glu Leu Val Ala Tyr Pro Leu Pro Gln Ala Ser Ser Ser  
 305 310 315 320  
 Tyr Met His Gly Gly Asn Pro Ser Gly Ser Val Val Met Val Ser Gly  
 325 330 335  
 Leu His Gln Leu Lys Met Asn Cys Ser Arg Val Phe Asn Leu Phe Cys  
 340 345 350  
 Leu Tyr Gly Asn Ile Glu Lys Val Lys Phe Met Lys Thr Ile Pro Gly  
 355 360 365  
 Thr Ala Leu Val Glu Met Gly Asp Glu Tyr Ala Val Glu Arg Ala Val  
 370 375 380  
 Thr His Leu Asn Asn Val Lys Leu Phe Gly Lys Arg Leu Asn Val Cys  
 385 390 395 400  
 Val Ser Lys Gln His Ser Val Val Pro Ser Gln Ile Phe Glu Leu Glu

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<400> 3315
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120
gaagggttcaa ttcacagagc acttcatatc taccagggtg atatcaaaat atatgttcc
180
aaaacatccc tgagttcacc accttgggcca gaagttgttc tgccagaccc agttgaggag
240
accagacacc atgcagaggt cgtgaagaag gtgaatgaga tgatcgtcac ggggcagtat
300
ggcaggctct ttgccgtggt gcactttgcc agccgccagt ggaagggtgac ctctgaagac
360
ctgatcttaa ttggaaatga actagacctt gcgtgtggag agagaattcg actggagaag
420
gtcctgctgg ttggggcaga caacttcacg ctgcttggca agccactcct cggaaaggat
480
cttgttcgag tagaagccac agtcattgaa aagacagaat catggccaag aatcattatg
540
agattcagga aaaggaaaaa cttcaagaag aaaagaatcg tcacgacccc gcagactgtc
600
ctccggataa acagcattga gattgctccg tgtttgttgt gattaccgag ttaatactta
660
caaaaggata aaaataaaact cctgcttccc aaggagacca ggtttctgtg ttctggttta
720
aagccgtgca tgcctgttgt agatagttta actggagcag catgtctgtg agcaccaggc
780
ccccgagcca gagaaaaacag gaactggggg agaatgacaa gcatggccct cccaggggctg
840
gataaatagt attcttggca gccctccacc ccatgtggcg gcggcagggc ccagggggagt
900

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934,

<210> 3316

<211> 187

<212> PRT

<213> Homo sapiens

<400> 3316

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Asp Leu Arg Gly Pro Glu Gln Pro Pro Phe Gly Leu Leu Leu Glu Gly
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Ser Ile His Arg Ala Leu His Ile Tyr Gln Gly Asn Ile Lys Ile Tyr
 20           25           30
Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Glu Val Val Leu
 35           40           45
Pro Asp Pro Val Glu Glu Thr Arg His His Ala Glu Val Val Lys Lys
 50           55           60
Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly Arg Leu Phe Ala Val
 65           70           75           80
Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser Glu Asp Leu Ile
 85           90           95
Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu Arg Ile Arg Leu
 100          105          110
Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr Leu Leu Gly Lys
 115          120          125
Pro Leu Leu Gly Lys Asp Leu Val Arg Val Glu Ala Thr Val Ile Glu
 130          135          140
Lys Thr Glu Ser Trp Pro Arg Ile Ile Met Arg Phe Arg Lys Arg Lys
 145          150          155          160
Asn Phe Lys Lys Lys Arg Ile Val Thr Thr Pro Gln Thr Val Leu Arg
 165          170          175
Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu Leu
 180          185

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<210> 3317

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 3317

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120
aaaagaagct gagaaaaaaa gatgccaaaga ctggaagcat cgaagatggg gagccctttc
180
caagtgtctac gttatgaagc tgccaaatta agaacactga gcaaatgtaa ttctcccgtg
240
gttgggaaag attatatatta ttttcttctt actttttaat gtctagatcc agaataaag
300
aagtttttag aaacctactg tgtggaggaa gagaagacca gtgccaaccc tgagactctg
360
ctggggggaga tggaggcgaa gacaagagag ctcatgctga gaagaaccac acctcttttg
420

```



gaatatatta aaaatagaaa attagaaaag cagagaattc gagaagagaa gcgagaagaa  
 480  
 cggaggagga gagagttaga aaagaaacgt ttgcgggaag aggaaaaaag aagaagaaga  
 540  
 gaagaagaaa gatgcaaaaa aaaagagaca gataaacaga agaaaattgc agagaaagaa  
 600  
 gtaaggatta agcttcttaa gaaaccagaa aagggagagg aaccaaccac agagaaacca  
 660  
 aaagaaagag gagaggagat tgatactgga ggtggcaagc aggaatcctg tgcccccggt  
 720  
 gcagtcgtaa aagccaggcc catggaaggc tcgctggagg agccccagga gacgtcacac  
 780  
 agcggcagtg ataaagagca cagggatgtg gagagatctc aagaacaaga atctgaagca  
 840  
 caaagatacc atgtggatga cggcaggagg cacagagctc accacgagcc tgaacggctt  
 900  
 tccagaagga gtgaggatga gcagagatgg gggaaaggac ctggccaaga cagagggaag  
 960  
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 1020  
 aggtgtgacg acagtccagc acccagaaaa gagcgactgg caaacaaggt ttttattaaa  
 1080  
 cccaaaaaga aaaatgtgtc tggctgtctt aaggtccagg ctgcatgctg accatgtcac  
 1140  
 cccacttggt ccttgtgtct tggggaacgc agtgctttga gcattttcaa gagcagtttt  
 1200  
 tcttgaaagt cagatcccag agtgagacta gtcacatct tttctcagat aatcaaatta  
 1260  
 tttttcacca ggaaaaagaa agattttatt tagtataaaa ctagcacgtt tatatgattc  
 1320  
 acttgagaat aagattatta aatttacctt tgagacagga aggaaagttt taatgatatt  
 1380  
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 1440  
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 1500  
 cttagccaag caaacaactt ttttttttca ggagctaatt tttgttcagg ttgcattttc  
 1560  
 ccagcgagc actacagatg gcatcacctt tctgacagca ccaggcccca ccctggcctc  
 1620  
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 1665

&lt;210&gt; 3318

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3318

Met	Glu	Ala	Lys	Thr	Arg	Glu	Leu	Ile	Ala	Arg	Arg	Thr	Thr	Pro	Leu
1				5					10					15	
Leu	Glu	Tyr	Ile	Lys	Asn	Arg	Lys	Leu	Glu	Lys	Gln	Arg	Ile	Arg	Glu
			20					25				30			
Glu	Lys	Arg	Glu	Glu	Arg	Arg	Arg	Arg	Glu	Leu	Glu	Lys	Lys	Arg	Leu

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      35              40              45
Arg Glu Glu Glu Lys Arg Arg Arg Arg Glu Glu Glu Arg Cys Lys Lys
      50              55              60
Lys Glu Thr Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile
65              70              75              80
Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys
      85              90              95
Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu
      100             105             110
Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser
      115             120             125
Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His
      130             135             140
Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr
145             150             155             160
His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg
      165             170             175
Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly
      180             185             190
Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu
      195             200             205
Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala
210             215             220
Pro Arg Lys Glu Arg Leu Ala Asn Lys Val Phe Ile Lys Pro Lys Lys
225             230             235             240
Lys Asn Val Ser Gly Cys Leu Lys Val Gln Ala Ala Cys
      245             250

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&lt;210&gt; 3319

&lt;211&gt; 1541

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3319

```

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120
ctctgctcc gccgaggac agccggatcg cccctctgct tcccgcaact gccctgatca
180
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240
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300
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360
tatgtgcggt ggatgatgta ctggattgtt tttgactct tcatggcagc agagatcgtt
420
acagacattt ttatctctg gtccctttc tactatgaga tcaagatggc cttcgtgctg
480
tggtgctct caccctacac caagggcgcc agcctgcttt accgcaagtt tgtccaccgc
540
tcctgtccc gccatgagaa ggagatcgac gcgtacatcg tgcaggccaa ggagcgcagc
600

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 720  
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 1440  
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 1500  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a  
 1541

<210> 3320

<211> 256

<212> PRT

<213> Homo sapiens

<400> 3320

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Cys	Pro	Ala	Tyr	Ala	Ser	Tyr	Lys	Ala	Val	Lys	Thr	Lys	Asn	Ile	Arg
			20					25					30		
Glu	Tyr	Val	Arg	Trp	Met	Met	Tyr	Trp	Ile	Val	Phe	Ala	Leu	Phe	Met
		35					40					45			
Ala	Ala	Glu	Ile	Val	Thr	Asp	Ile	Phe	Ile	Ser	Trp	Phe	Pro	Phe	Tyr
	50					55				60					
Tyr	Glu	Ile	Lys	Met	Ala	Phe	Val	Leu	Trp	Leu	Ser	Pro	Tyr	Thr	
65				70				75					80		
Lys	Gly	Ala	Ser	Leu	Leu	Tyr	Arg	Lys	Phe	Val	His	Pro	Ser	Leu	Ser
			85					90					95		
Arg	His	Glu	Lys	Glu	Ile	Asp	Ala	Tyr	Ile	Val	Gln	Ala	Lys	Glu	Arg
			100					105					110		
Ser	Tyr	Glu	Thr	Val	Leu	Ser	Phe	Gly	Lys	Arg	Gly	Leu	Asn	Ile	Ala

115	120	125
Ala Ser Ala Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala		
130	135	140
Gly Arg Leu Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Ser Asp		
145	150	155
Ala Pro Ala Pro Ala Tyr His Asp Pro Leu Tyr Leu Glu Asp Gln Val		
165	170	175
Ser His Arg Arg Pro Pro Ile Gly Tyr Arg Ala Gly Gly Leu Gln Asp		
180	185	190
Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Thr Glu Ala Val Pro Arg		
195	200	205
Ala Pro Ala Arg Pro Arg Glu Lys Pro Leu Ile Arg Ser Gln Ser Leu		
210	215	220
Arg Val Val Lys Arg Lys Pro Pro Val Arg Glu Gly Thr Ser Arg Ser		
225	230	235
Leu Lys Val Arg Thr Arg Lys Lys Thr Val Pro Ser Asp Val Asp Ser		
245	250	255

&lt;210&gt; 3321

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3321

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240
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300
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360
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420
gcaggattgc ttccaatacc gaccccaaat cctttgacta ctcttggtgt ttcacttagc
480
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540
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600
gtttatgttg gaaatctgaa ttcccagaca acgacagctg atcaactact tgaatttttt
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720
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780
cgagtacgag aagctcagtc atttatctca gcagctattg aaccagagtc tggaaagagc
840
aatgaaagaa aaggcggtcg atctcgttcc catactcgct caaaatccag gtctagctca
900

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 1020  
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 1080  
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 1140  
 agggaaaagg aacgtgaaaa agaaaaggaa cggggtaaaa acaaagaccg ggacaaggaa  
 1200  
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 1260  
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 1320  
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 1380  
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 1440  
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<210> 3322

<211> 454

<212> PRT

<213> Homo sapiens

<400> 3322

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Val	Cys	Tyr	Val	Lys	Phe	Arg	Asp	Pro	Ser	Ser	Val	Gly	Val	Ala	Gln
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Ala	Pro	Ala	Pro	Thr	Met	Thr	Ser	Leu	Met	Pro	Gly	Ala	Gly	Leu	Leu
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Pro	Ile	Pro	Thr	Pro	Asn	Pro	Leu	Thr	Thr	Leu	Gly	Val	Ser	Leu	Ser
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Ser	Leu	Gly	Ala	Ile	Pro	Ala	Ala	Ala	Leu	Asp	Pro	Asn	Ile	Ala	Thr
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Leu	Gly	Glu	Ile	Pro	Gln	Pro	Pro	Leu	Met	Gly	Asn	Val	Asp	Pro	Ser
			180					185					190		
Lys	Ile	Asp	Glu	Ile	Arg	Arg	Thr	Val	Tyr	Val	Gly	Asn	Leu	Asn	Ser

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Glu Val Met Lys Arg Val Arg Glu Ala Gln Ser Phe Ile Ser Ala Ala
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Ile Glu Pro Glu Ser Gly Lys Ser Asn Glu Arg Lys Gly Gly Arg Ser
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Arg Ser His Thr Arg Ser Lys Ser Arg Ser Ser Ser Lys Ser His Ser
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Lys Arg Ser Lys Ser Arg Glu Arg Arg Lys Ser Arg Ser Arg Ser His
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Ser Arg Asp Lys Arg Lys Asp Thr Arg Glu Lys Ile Lys Glu Lys Glu
      355              360              365
Arg Val Lys Glu Lys Asp Arg Glu Lys Glu Arg Glu Arg Glu Lys Glu
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Arg Glu Lys Glu Lys Glu Arg Gly Lys Asn Lys Asp Arg Asp Lys Glu
385              390              395              400
Arg Glu Lys Asp Arg Glu Lys Asp Lys Glu Lys Asp Arg Glu Arg Glu
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Arg Glu Lys Glu His Glu Lys Asp Arg Asp Lys Glu Lys Glu Lys Glu
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Glu Lys Lys Lys Glu Gly
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&lt;210&gt; 3323

&lt;211&gt; 949

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3323

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&lt;210&gt; 3324

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3324

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Pro	Asp	Glu	Gly	Gln	Glu	Glu	Leu	Glu	Glu	Val	Gln	Ala	Glu	Leu	Lys
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Lys	Lys	Asp	Glu	Glu	Val	Ser	His	Gly	Thr	Val	Asp	Leu	Asp	Gln	Lys
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&lt;210&gt; 3325

&lt;211&gt; 5055

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3325

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720  
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5055

&lt;210&gt; 3326

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3326

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&lt;210&gt; 3327

&lt;211&gt; 2263

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3327

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<210> 3328

<211> 521

<212> PRT

<213> Homo sapiens

<400> 3328

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His	Trp	Ser	Asp	Ser	Arg	Tyr	Glu	His	Val	Met	Lys	Leu	Arg	Gln	Ala
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Asp	Ala	Asp	Asn	Leu	Ile	Leu	Asn	Pro	Asp	Thr	Leu	Ser	Leu	Leu	Ile
65				70					75					80	
Ala	Glu	Asn	Lys	Thr	Val	Val	Ala	Pro	Met	Leu	Asp	Ser	Arg	Ala	Ala
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Val	Gln	Met	Tyr	Val	Cys	Asn	Lys	Glu	Glu	Tyr	Gly	Phe	Leu	Pro	Val
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Glu	Val	Phe	Met	Ile	Asn	Leu	Arg	Arg	Arg	Gln	Asp	Arg	Arg	Glu	Arg
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 405 410 415  
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 Val Ser Glu Tyr Lys Ala His Phe Ser Leu Arg Asn Leu His Ala Phe  
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 Ser Val Glu Pro Leu Leu Ile Tyr Pro Thr His Tyr Thr Gly Asp Asp  
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 Gly Tyr Val Ser Asp Thr Glu Thr Ser Val Val Trp Asn Asn Glu His  
 465 470 475 480  
 Val Lys Thr Asp Trp Asp Arg Ala Lys Ser Gln Lys Met Arg Glu Gln  
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&lt;210&gt; 3329

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3329

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<211> 235

<212> PRT

<213> Homo sapiens

<400> 3330

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Pro	Val	Pro	Thr	Leu	Ala	Phe	Thr	His	Val	Ala	Arg	Ala	Gln	Ala	Gly
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Met	Tyr	His	Cys	Leu	Ala	Glu	Leu	Pro	Thr	Gly	Ala	Ala	Ala	Ser	Ala
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Pro	Val	Met	Leu	Arg	Val	Leu	Tyr	Pro	Pro	Lys	Thr	Pro	Thr	Met	Met
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Val	Phe	Val	Glu	Pro	Glu	Gly	Gly	Leu	Arg	Gly	Ile	Leu	Asp	Cys	Arg
		100						105					110		
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		115					120				125				
Leu	Val	Ala	Ser	Ser	Gln	Pro	Gln	Gly	Ala	Pro	Ala	Glu	Pro	His	Ile
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His	Val	Leu	Ala	Ser	Pro	Asn	Ala	Leu	Arg	Val	Asp	Ile	Glu	Ala	Leu
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			165					170					175		
Gly	Ser	Ala	Ser	Thr	Ser	Thr	Tyr	Phe	Gly	Val	Arg	Ala	Leu	His	Arg
		180					185						190		
Leu	His	Gln	Phe	Gln	Gln	Leu	Leu	Trp	Val	Leu	Gly	Leu	Leu	Val	Gly
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Leu	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Ala	Cys	Tyr	Thr	Trp	Arg	Arg
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<211> 1644

<212> DNA

<213> Homo sapiens

<400> 3331

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<210> 3332  
<211> 128  
<212> PRT  
<213> Homo sapiens

<400> 3332  
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Ile Lys Ile Pro Gly Cys Arg Lys Gln Gly Leu Val His Arg Thr His  
35 40 45  
Met Ser Ser Cys Arg Val Asp Lys Pro Ser Glu Ile Val Asp Val Gly  
50 55 60  
Asp Lys Val Trp Val Lys Leu Ile Gly Arg Glu Met Lys Asn Asp Arg  
65 70 75 80  
Ile Lys Val Ser Leu Ser Met Lys Val Val Asn Gln Gly Thr Gly Lys  
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<212> DNA  
<213> Homo sapiens

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<210> 3334

<211> 672

<212> PRT

<213> Homo sapiens

<400> 3334

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Ile	Tyr	Glu	Ala	Gly	Ala	Gly	Asp	Arg	Met	Ala	Gly	Ala	Pro	Met
			20				25					30		
Ala	Ala	Val	Gln	Pro	Ala	Glu	Val	Thr	Val	Glu	Val	Gly	Glu	Asp
		35				40					45			
His	Met	His	His	Val	Arg	Asp	Arg	Glu	Met	Pro	Glu	Ala	Leu	Glu
	50				55					60				Phe
Asn	Leu	Ser	Ala	Asn	Pro	Glu	Ser	Ser	Thr	Ile	Phe	Gln	Arg	Asn
65				70						75				80
Gln	Thr	Glu	Ala	Leu	Glu	Phe	Asn	Pro	Ser	Ala	Asn	Pro	Glu	Ala
			85					90					95	
Thr	Ile	Phe	Gln	Arg	Asn	Ser	Gln	Thr	Asp	Val	Val	Glu	Ile	Arg
		100					105					110		
Ser	Asn	Cys	Thr	Asn	His	Val	Ser	Ala	Val	Arg	Phe	Ser	Gln	Gln
	115					120					125			
Ser	Leu	Cys	Ser	Thr	Ile	Phe	Leu	Asp	Asp	Ser	Thr	Ala	Ile	Gln
	130				135					140				His
Tyr	Leu	Thr	Met	Thr	Ile	Ser	Val	Thr	Leu	Glu	Ile	Pro	His	His
145				150					155					160
Ile	Thr	Gln	Arg	Asp	Ala	Asp	Arg	Thr	Leu	Ser	Ile	Pro	Asp	Glu
		165					170					175		
Leu	His	Ser	Phe	Ala	Val	Ser	Thr	Val	His	Ile	Met	Lys	Lys	Arg
		180					185					190		
Gly	Gly	Gly	Ser	Leu	Asn	Asn	Tyr	Ser	Ser	Ser	Ile	Pro	Ser	Thr
	195					200					205			Pro
Ser	Thr	Ser	Gln	Glu	Asp	Pro	Gln	Phe	Ser	Val	Pro	Pro	Thr	Ala
	210					215					220			Asn
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Thr	Ser	Glu	Lys	Gly	Ser	His	Pro	Asp	Lys	Glu	Arg	Lys	Ala	Pro
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		260				265						270		Gln
Gly	Met	Leu	Leu	Lys	Arg	Ser	Gly	Lys	Trp	Leu	Lys	Thr	Trp	Lys
	275					280					285			Lys
Lys	Tyr	Val	Thr	Leu	Cys	Ser	Asn	Gly	Met	Leu	Thr	Tyr	Tyr	Ser
	290				295				300					Ser
Leu	Gly	Asp	Tyr	Met	Lys	Asn	Ile	His	Lys	Lys	Glu	Ile	Asp	Leu
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Thr	Ser	Thr	Ile	Lys	Val	Pro	Gly	Lys	Trp	Pro	Ser	Leu	Ala	Thr
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Ser Thr Thr Ser Pro Lys Leu Asn Pro Pro Pro Ser Pro His Ala Asn
          370          375          380
Lys Lys Lys His Leu Lys Lys Lys Ser Thr Asn Asn Phe Met Ile Val
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Ser Ala Thr Gly Gln Thr Trp His Phe Glu Ala Thr Thr Tyr Glu Glu
          405          410          415
Arg Asp Ala Trp Val Gln Ala Ile Gln Ser Gln Ile Leu Ala Ser Leu
          420          425          430
Gln Ser Cys Glu Ser Ser Lys Ser Lys Ser Gln Leu Thr Ser Gln Ser
          435          440          445
Glu Ala Met Ala Leu Gln Ser Ile Gln Asn Met Arg Gly Asn Ala His
          450          455          460
Cys Val Asp Cys Glu Thr Gln Asn Pro Lys Trp Ala Ser Leu Asn Leu
          465          470          475          480
Gly Val Leu Met Cys Ile Glu Cys Ser Gly Ile His Arg Ser Leu Gly
          485          490          495
Thr Arg Leu Ser Arg Val Arg Ser Leu Glu Leu Asp Asp Trp Pro Val
          500          505          510
Glu Leu Arg Lys Val Met Ser Ser Ile Gly Asn Glu Leu Ala Asn Ser
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Ile Trp Glu Glu Ser Ser Gln Gly Arg Thr Lys Pro Ser Val Asp Ser
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Thr Arg Glu Glu Lys Glu Arg Trp Ile Arg Ser Lys Tyr Glu Glu Lys
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Leu Phe Leu Ala Pro Leu Pro Cys Thr Glu Leu Ser Leu Gly Gln Gln
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Leu Leu Arg Ala Thr Ala Asp Glu Asp Leu Gln Thr Ala Ile Leu Leu
          580          585          590
Leu Ala His Gly Ser Arg Glu Glu Val Asn Glu Thr Cys Gly Glu Gly
          595          600          605
Asp Gly Cys Thr Ala Leu His Leu Ala Cys Arg Lys Gly Asn Val Val
          610          615          620
Leu Ala Gln Leu Leu Ile Trp Tyr Gly Val Asp Val Met Ala Arg Asp
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Ala His Gly Asn Thr Ala Leu Thr Tyr Ala Arg Gln Ala Ser Ser Gln
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Glu Cys Ile Asn Val Leu Leu Gln Tyr Gly Cys Pro Asp Lys Cys Val
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&lt;210&gt; 3335

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3335

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120

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<210> 3336

<211> 59

<212> PRT

<213> Homo sapiens

<400> 3336

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			20					25					30		
Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly	Gln	Tyr	Tyr	Cys	Ser	Pro	Cys
			35				40					45			
His	Trp	Asn	Ala	Leu	Ala	Val	Ile	Pro	Ala	Arg					
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<210> 3337

<211> 679

<212> DNA

<213> Homo sapiens

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<210> 3338

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3338

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		20						25					30		
Lys	Glu	Val	Arg	Trp	Gly	Ser	Leu	Ser	Leu	Ala	Ser	Lys	Asp	Thr	Asp
	35					40						45			
Arg	Val	Arg	Glu	Arg	Asp	Arg	Glu	Arg	His	Arg	Asp	Arg	Gln	Arg	Pro
	50				55					60					
Lys	Gln	Lys	Arg	Gln	Thr	Ala	Lys	Thr	Lys	Gln	Asn	Gln	Cys	Lys	Leu
65				70						75				80	
Glu	Lys	Lys	Ile	Lys	Leu	Asn	Ile	Arg	Ala	Gly	Lys	Ser	His	Leu	Leu
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Arg	Ile	Thr	Pro	Val	Tyr										
					100										

<210> 3339

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 3339

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&lt;210&gt; 3340

&lt;211&gt; 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3340

Met	Ser	Thr	Leu	Ala	Ser	Lys	Lys	Thr	Thr	Val	Thr	Arg	Ser	Ser	Asn
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Ser	Val	Asn	Ile	Phe	Leu	Tyr	Gln	Asn	Cys	Tyr	Tyr	Ala	Ala	Phe	Ile
		20					25					30			
Trp	Ala	Gly	Phe	Ile	Ile	Leu	His	Cys	Glu	Ile	Ala	Leu	Gln	Cys	Ile
		35				40					45				
Thr	Thr	Ala	Arg	Arg	Thr	Tyr	Ile	Tyr	Ile	Tyr	Ile	Lys	Asn	Ile	Ser
	50				55				60						
Asp	Ser	Cys	Ile	Gln	Met	Ser	Lys	Val	Phe	Val	Ala	Thr	Tyr	Tyr	Ile
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Ala	Tyr	Thr	Gln	Asn	His										
			85												

&lt;210&gt; 3341

&lt;211&gt; 1132

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3341

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 120

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 180  
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 240  
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 1132

&lt;210&gt; 3342

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3342

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 20 25 30  
 Gly Pro Phe Ile Leu Gly Pro Arg Leu Gly Asn Ser Pro Val Pro Ser  
 35 40 45  
 Ile Val Gln Cys Leu Ala Arg Lys Asp Gly Thr Asp Asp Phe Tyr Gln  
 50 55 60  
 Leu Lys Ile Leu Thr Leu Glu Glu Arg Gly Asp Gln Gly Ile Glu Ser  
 65 70 75 80  
 Gln Glu Glu Arg Gln Gly Lys Met Leu Leu His Thr Glu Tyr Ser Leu  
 85 90 95  
 Leu Ser Leu Leu His Thr Gln Asp Gly Val Val His His His Gly Leu



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      100      105      110
Phe Gln Asp Arg Thr Cys Glu Ile Val Glu Asp Thr Glu Ser Ser Arg
      115      120      125
Met Val Lys Lys Met Lys Lys Arg Ile Cys Leu Val Leu Asp Cys Leu
      130      135      140
Cys Ala His Asp Phe Ser Asp Lys Thr Ala Asp Leu Ile Asn Leu Gln
145      150      155      160
His Tyr Val Ile Lys Glu Lys Arg Leu Ser Glu Arg Glu Thr Val Val
      165      170      175
Ile Phe Tyr Asp Val Val Arg Val Val Glu Ala Leu His Gln Lys Asn
      180      185      190
Ile Val His Arg Asp Leu Lys Leu Gly Asn Met Val Leu Asn Lys Arg
      195      200      205
Thr His Arg Ile Thr Ile Thr Asn Phe Cys Leu Gly Lys His Leu Val
      210      215      220
Ser Glu Gly Asp Leu Leu Lys Asp Gln Arg Gly Ser Pro Ala Tyr Ile
225      230      235      240
Ser Pro Asp Val Leu Ser Gly Arg Pro Tyr Arg Gly Lys Pro Ser Asp
      245      250      255
Met Trp Ala Leu Gly Val Val Leu Phe Thr Met Leu Tyr Gly Gln Phe
      260      265      270
Pro Phe Tyr Asp Ser Ile Pro Gln Glu Leu Phe Arg Lys Ile Lys Ala
      275      280      285
Ala Glu Tyr Thr Ile Pro Glu Asp Gly Arg Val Ser Glu Asn Thr Val
      290      295      300
Cys Leu Ile Arg
305

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&lt;210&gt; 3343

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3343

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420
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594

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<210> 3344  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
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 35 40 45  
 Ser Ala Asp Leu Glu Ile Ile Asn Ala Thr Thr Gly Arg Arg Ser Cys  
 50 55 60  
 Gly Gly Pro Ser Arg Leu Cys Lys His Val Leu Ser Ala Arg Trp Ala  
 65 70 75 80  
 Arg Leu Tyr Gly Arg Leu Ser Thr Arg Thr Pro Ser Pro Gly Asp Thr  
 85 90 95  
 Pro Ser Met Tyr Cys Glu Ala Lys Leu Gly Ala His Thr Tyr Gln Ser  
 100 105 110  
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 Trp Val Arg Lys Pro Pro Glu Gln Gln Gln Phe Leu Leu Thr Leu  
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 <212> DNA  
 <213> Homo sapiens

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<210> 3346

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3346

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			20					25					30		
Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35					40				45				
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
	50					55					60				
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
65					70					75					80
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
			85					90						95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
		100						105					110		
Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
		115				120						125			
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
	130					135					140				
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
145					150					155					160
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
			165					170						175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
		180					185						190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
		195					200					205			
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
	210					215					220				
Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly

225		230		235		240
Gln Tyr Tyr Cys Ser His Cys His Trp Asn Asp Leu Ala Val Ile Pro						
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Glu Ala Gly Val Cys Ser Arg						
	260					

&lt;210&gt; 3347

&lt;211&gt; 2267

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3347

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1260

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 <212> PRT  
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<400> 3348  
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 Gln Val Ala Trp Tyr Asn Glu Leu Leu Pro Pro Ala Phe His Leu Pro  
 35 40 45  
 Leu Pro Gly Pro Thr Leu Ala Phe Leu Val Leu Ser Thr Pro Ala Met  
 50 55 60  
 Phe Asp Arg Ala Leu Lys Pro Phe Leu Gln Ser Cys His Leu Arg Met  
 65 70 75 80  
 Leu Thr Asp Pro Val Asp Gln Cys Val Ala Tyr His Leu Gly Arg Val  
 85 90 95  
 Gly Glu Ser Leu Pro Glu Leu Gln Ile Glu Ile Ile Ala Asp Tyr Glu  
 100 105 110

Val His Pro Asn Arg Arg Pro Lys Ile Leu Ala Gln Thr Ala Ala His  
           115                          120                          125  
 Val Ala Gly Ala Ala Tyr Tyr Tyr Gln Arg Gln Asp Val Glu Ala Asp  
           130                          135                          140  
 Pro Trp Gly Asn Gln Arg Ile Ser Gly Val Cys Ile His Pro Arg Phe  
           145                          150                          155                          160  
 Gly Gly Trp Phe Ala Ile Arg Gly Val Val Leu Leu Pro Gly Ile Glu  
                           165                          170                          175  
 Val Pro Asp Leu Pro Pro Arg Lys Pro His Asp Cys Val Pro Thr Arg  
                           180                          185                          190  
 Ala Asp Arg Ile Ala Leu Leu Glu Gly Phe Asn Phe His Trp Arg Asp  
                           195                          200                          205  
 Trp Thr Tyr Arg Asp Ala Val Thr Pro Gln Glu Arg Tyr Ser Glu Glu  
           210                          215                          220  
 Gln Lys Ala Tyr Phe Ser Thr Pro Pro Ala Gln Arg Leu Ala Leu Leu  
           225                          230                          235                          240  
 Gly Leu Ala Gln Pro Ser Glu Lys Pro Ser Ser Pro Ser Pro Asp Leu  
                           245                          250                          255  
 Pro Phe Thr Thr Pro Ala Pro Lys Lys Pro Gly Asn Pro Ser Arg Ala  
                           260                          265                          270  
 Arg Ser Trp Leu Ser Pro Arg Val Ser Pro Pro Ala Ser Pro Gly Pro  
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&lt;210&gt; 3349

&lt;211&gt; 1132

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3349

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 300  
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 aagaacaatg tcaaattgga gctgaaccct gaaatagttg cccgccactt cttaagaat  
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960  
tgtttagctt ctccctccat tggagtttat tgggacaaac aggagagcca gccattgtct  
1020  
ccagtacttg cctcattctc atcatccaaa ctgaacattt gtatcccaag cagaaataaa  
1080  
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1132

<210> 3350

<211> 174

<212> PRT

<213> Homo sapiens

<400> 3350

Gly	Pro	Gly	Arg	Gly	Ala	Ser	Ser	Gln	Ala	Asp	Val	Gly	Val	Arg	Gly
1			5					10						15	
Asp	Leu	Val	Ser	Val	Lys	Lys	Ser	Leu	Gly	Arg	Asn	Arg	Leu	Leu	Pro
		20						25					30		
Gln	Gly	Leu	Ala	Val	Tyr	Ala	Ser	Pro	Glu	Asn	Lys	Lys	Leu	Phe	Glu
		35					40					45			
Glu	Glu	Lys	Leu	Leu	Arg	Gln	Glu	Gly	Lys	Leu	Glu	Lys	Ile	Gln	Thr
		50				55					60				
Lys	Ala	Gly	Glu	Ala	Thr	Val	Lys	Phe	Leu	Lys	Ser	Cys	Arg	Leu	Glu
65					70					75				80	
Val	Gly	Met	Lys	Asn	Val	Lys	Trp	Glu	Leu	Asn	Pro	Glu	Ile	Val	
			85					90					95		
Ala	Arg	His	Phe	Phe	Lys	Asn	Leu	Gly	Val	Val	Val	Ala	Pro	His	Thr
			100					105					110		
Leu	Lys	Leu	Pro	Ala	Glu	Pro	Ile	Thr	Arg	Trp	Gly	Glu	Tyr	Trp	Cys
		115					120					125			
Glu	Val	Thr	Val	Asn	Gly	Leu	Asp	Thr	Val	Arg	Val	Pro	Met	Ser	Val
		130				135					140				
Val	Asn	Phe	Glu	Lys	Pro	Lys	Thr	Lys	Arg	Tyr	Lys	Tyr	Trp	Leu	Ala
145				150					155					160	
Gln	Gln	Ala	Ala	Lys	Ala	Met	Ala	Pro	Thr	Ser	Pro	Gln	Ile		
			165						170						

<210> 3351

<211> 1422

<212> DNA

<213> Homo sapiens

<400> 3351

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cttgaggaat actccatacc tgagtagaca gccatgtggc catcgagct actaattttc  
120

atgatgctct tagctccaat aattcatggt ggcaagcaca gtgaacgaca tcttgcctc  
180  
gctgctgcgc cgcgatgcgc tgagcgccgc caaggagggtg ttgtaccacc tggacatcta  
240  
cttcagcagc cagctgcaga gcgcgccgct gcccatcgtg gacaagggcc ccgtggagct  
300  
gctggaggag ttcgtgttcc aggtgcccga ggagcgcagc gcgcagccca agagactgaa  
360  
ttcccttcag gagcttcaac ttcttgaaat catgtgcaat tatttccagg agcaaaccga  
420  
ggactctgtt cggcagatta ttttttcac ccttttcagc cctcaaggga acaaagccga  
480  
tgacagccgg atgagcttgt tgggaaaact ggtctccatg gcggtggctg tgtgtcgaat  
540  
cccgggtgtg gagtgtgctg cctcctggct tcagcggacg cccgtgggtt actgtgtgag  
600  
gttagccaag gccctttag atgactactg ctgtttggtg ccgggatcca ttcagacgct  
660  
gaagcagata ttcagtgccg gcccgagatt ctgctgccag ttcacacct ccgttacccg  
720  
gctctatgac ctgtcatcag atgacctcat tccacctatg gacttgcttg aaatgattgt  
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840  
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960  
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1020  
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1080  
gaagaatctg tatgggcgcc tggggctgat cctcttcgac cacatggtcc cgctggtaga  
1140  
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1200  
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1260  
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1320  
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1380  
ccacatccac acgccccgc tgggctacgg ggctgtcccc cc  
1422

&lt;210&gt; 3352

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3352

Met	Trp	Pro	Ser	Gln	Leu	Leu	Ile	Phe	Met	Met	Leu	Leu	Ala	Pro	Ile
1				5			10				15				
Ile	His	Gly	Gly	Lys	His	Ser	Glu	Arg	His	Pro	Ala	Leu	Ala	Ala	Ala



```

                20                25                30
Pro Arg Cys Ala Glu Arg Arg Gln Gly Gly Val Val Pro Pro Gly His
                35                40                45
Leu Leu Gln Gln Pro Ala Ala Glu Arg Ala Ala Ala His Arg Gly Gln
                50                55                60
Gly Pro Arg Gly Ala Ala Gly Gly Val Arg Val Pro Gly Ala Gln Gly
65                70                75                80
Ala Gln Arg Ala Ala Gln Glu Thr Glu Phe Pro Ser Gly Ala Ser Thr
                85                90                95
Ser

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&lt;210&gt; 3353

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3353

```

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60
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120
ggctccctac ctgacctcac caacctgcac ttccccccac cactgcccac cccctggac
180
cctgaagaga cagcctaccc tagcctgagt gggggcaaca gtacctcaa ttgacctac
240
accatgactc acctgggcat cagcaggggc atgggccttg gccaggcta tgatgcacca
300
gggcgtcccc ctggatacca gtaaactgtc cactgaccag cggttacccc cataccata
360
cagttcccca agtttggtnt ctgcttacct agccccacac cccaaagttt taacagcagc
420

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&lt;210&gt; 3354

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3354

```

Xaa Lys Leu Ser Ser Ser Ser Arg Pro Arg Ser Cys Glu Val Pro
1                5                10                15
Gly Ile Asn Ile Phe Pro Ser Pro Asp Gln Pro Ala Asn Val Pro Val
                20                25                30
Leu Pro Pro Ala Met Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn
                35                40                45
Leu His Phe Pro Pro Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Thr
                50                55                60
Ala Tyr Pro Ser Leu Ser Gly Gly Asn Ser Thr Ser Asn Leu Thr His
65                70                75                80
Thr Met Thr His Leu Gly Ile Ser Arg Gly Met Gly Leu Gly Pro Gly
                85                90                95
Tyr Asp Ala Pro Gly Arg Pro Pro Gly Tyr Gln
                100                105

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<210> 3355  
 <211> 474  
 <212> DNA  
 <213> Homo sapiens

<400> 3355  
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 120  
 gacaagagtc atgcttttct ccccatcatt ccaaaccacc agagaggtca gctagaagac  
 180  
 agactgaaca accaggcgcg taccatagct ttccttcttg aacaagcctt ccgcatcaag  
 240  
 gaggacatct ctgcttgctt gcaggggacc catggctttc gaaaagagga atcgctcgcc  
 300  
 aggaagttac tggaaagcca catccagacc atcaccagca tcgtcaaaaa actcagccaa  
 360  
 aatattgaga ttttagaaga ccaaataaga gctcgagatc aggcggccac aggaactaac  
 420  
 tttgcagtac acgagataaa catcaaacac ctacaaggag ttgggagatc tttc  
 474

<210> 3356  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<400> 3356  
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 20 25 30  
 Asp Arg Leu Asn Asn Gln Ala Arg Thr Ile Ala Phe Leu Leu Glu Gln  
 35 40 45  
 Ala Phe Arg Ile Lys Glu Asp Ile Ser Ala Cys Leu Gln Gly Thr His  
 50 55 60  
 Gly Phe Arg Lys Glu Glu Ser Leu Ala Arg Lys Leu Leu Glu Ser His  
 65 70 75 80  
 Ile Gln Thr Ile Thr Ser Ile Val Lys Lys Leu Ser Gln Asn Ile Glu  
 85 90 95  
 Ile Leu Glu Asp Gln Ile Arg Ala Arg Asp Gln Ala Ala Thr Gly Thr  
 100 105 110  
 Asn Phe Ala Val His Glu Ile Asn Ile Lys His Leu Gln Gly Val Gly  
 115 120 125  
 Arg Ser Phe  
 130

<210> 3357  
 <211> 2268  
 <212> DNA  
 <213> Homo sapiens

<400> 3357

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agcagccatt atggatttgg atgtgctctt tatacccatg tctctaattg cagatggagg  
120  
agggcctata aaaataattc cttcttgctt acaaagttca gcaaattcca tgttttctga  
180  
aagaaaaccg catcctggat ggatagcctg tgcagcagag gtcttggcca cttgaatgat  
240  
tttctccata gataggtagc tctgctggga ggaacgggtt tggcgtgtgg gacgcagctg  
300  
cctctgtact ggggagtcac ggagtggcgg ggctccaggg acatggcggc ggctctgcg  
360  
gtgtcgggtgc tgctgggtggc ggcgagagg aaccgggtggc atcgtctccc gagcctgctc  
420  
ctgccgccga ggacatgggt gtggaggcaa agaaccatga agtacacaac agccacagga  
480  
agaaacatta ccaaggctcct cattgcaaac agaggagaaa ttgcctgcag ggtgatgcgc  
540  
acagccaaaa aactgggtgt acagactgtg gcggtttata gtgaggctga cagaaattcc  
600  
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660  
tacctatcta tggagaaaat cattcaagtg gccaaagacct ctgctgcaca ggctatccat  
720  
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780  
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840  
aaatccataa tggctgctgc tggagtacct gttgtggagg gttatcatgg tgaggaccaa  
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960  
gtccgggggtg gaggaggaaa aggaatgagg attgttagat cagaacaaga atttcaagaa  
1020  
cagttagagt cagcacggag agaagctaag aagtctttca atgatgatgc tatgctgac  
1080  
gagaagtttg tagacacacc gaggcagtga gaagtccagg tgtttggtga tcaccatggc  
1140  
aatgctgtgt acttgtttga aagagactgt agtgtgcaga ggcgacatca gaagatcatt  
1200  
gaggaggccc cagcgcctgg tattaatct gaagtaagaa aaaagctggg agaagctgca  
1260  
gtcagagctg ctaaagctgt aaattatgtt ggagcagga ctgtggagtt tattatggac  
1320  
tcaaaacata atttctgttt catggagatg aatacaaggc tgcaagtgga acatcctgtt  
1380  
actgagatga tcacaggaac tgacttgggtg gagtggcagc ttagaattgc agcaggagag  
1440  
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1500  
tatgcagaag atcctagcaa taacttcatt cctgtggcag gccattagt gcacctctct  
1560  
actcctcgag cagacccttc caccaggatt gaaactggag tacggcaagg agacgaagtt  
1620

tccgtgcatt atgaccccat gattgcgaag ctggctcgtgt gggcagcaga tcgccaggcg  
 1680  
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 1740  
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 1860  
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 1920  
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 1980  
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 2040  
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 2100  
 ttccagacca ctacaataaa atgtagccat agctgtaacg tataaccatg atgggtctta  
 2160  
 tagcatgcag attgaagata aaactttcca agtccttggt aatctttaca gcgagggaga  
 2220  
 ctgcacttac ctgaaatggt ctgttaatgg agttgctagt aaagcgaa  
 2268

&lt;210&gt; 3358

&lt;211&gt; 493

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3358

Gln	Thr	Val	Ala	Val	Tyr	Ser	Glu	Ala	Asp	Arg	Asn	Ser	Met	His	Val
1			5					10						15	
Asp	Met	Ala	Asp	Glu	Ala	Tyr	Ser	Ile	Gly	Pro	Ala	Pro	Ser	Gln	Gln
		20						25					30		
Ser	Tyr	Leu	Ser	Met	Glu	Lys	Ile	Ile	Gln	Val	Ala	Lys	Thr	Ser	Ala
		35					40					45			
Ala	Gln	Ala	Ile	His	Pro	Gly	Cys	Gly	Phe	Leu	Ser	Glu	Asn	Met	Glu
	50					55				60					
Phe	Ala	Glu	Leu	Cys	Lys	Gln	Glu	Gly	Ile	Ile	Phe	Ile	Gly	Pro	Pro
65					70				75					80	
Pro	Ser	Ala	Ile	Arg	Asp	Met	Gly	Ile	Lys	Ser	Thr	Ser	Lys	Ser	Ile
			85					90					95		
Met	Ala	Ala	Ala	Gly	Val	Pro	Val	Val	Glu	Gly	Tyr	His	Gly	Glu	Asp
			100					105					110		
Gln	Ser	Asp	Gln	Cys	Leu	Lys	Glu	His	Ala	Arg	Arg	Ile	Gly	Tyr	Pro
		115					120					125			
Val	Met	Ile	Lys	Ala	Val	Arg	Gly	Gly	Gly	Gly	Lys	Gly	Met	Arg	Ile
	130					135					140				
Val	Arg	Ser	Glu	Gln	Glu	Phe	Gln	Glu	Gln	Leu	Glu	Ser	Ala	Arg	Arg
145				150						155				160	
Glu	Ala	Lys	Lys	Ser	Phe	Asn	Asp	Asp	Ala	Met	Leu	Ile	Glu	Lys	Phe
			165						170					175	
Val	Asp	Thr	Pro	Arg	His	Val	Glu	Val	Gln	Val	Phe	Gly	Asp	His	His
			180					185					190		
Gly	Asn	Ala	Val	Tyr	Leu	Phe	Glu	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg

```

      195              200              205
His Gln Lys Ile Ile Glu Glu Ala Pro Ala Pro Gly Ile Lys Ser Glu
  210              215              220
Val Arg Lys Lys Leu Gly Glu Ala Ala Val Arg Ala Ala Lys Ala Val
  225              230              235              240
Asn Tyr Val Gly Ala Gly Thr Val Glu Phe Ile Met Asp Ser Lys His
      245              250              255
Asn Phe Cys Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro
      260              265              270
Val Thr Glu Met Ile Thr Gly Thr Asp Leu Val Glu Trp Gln Leu Arg
      275              280              285
Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser Gln Glu Glu Ile Thr Leu
      290              295              300
Gln Gly His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asp Pro Ser Asn
  305              310              315              320
Asn Phe Met Pro Val Ala Gly Pro Leu Val His Leu Ser Thr Pro Arg
      325              330              335
Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly Val Arg Gln Gly Asp Glu
      340              345              350
Val Ser Val His Tyr Asp Pro Met Ile Ala Lys Leu Val Val Trp Ala
      355              360              365
Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu Arg Tyr Ser Leu Arg Gln
      370              375              380
Tyr Asn Ile Val Gly Leu His Thr Asn Ile Asp Phe Leu Leu Asn Leu
  385              390              395              400
Ser Gly His Pro Glu Phe Glu Ala Gly Asn Val His Thr Asp Phe Ile
      405              410              415
Pro Gln His His Lys Gln Leu Leu Leu Ser Arg Lys Ala Ala Ala Lys
      420              425              430
Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu Ile Leu Lys Glu Lys Ala
      435              440              445
Met Thr Asp Thr Phe Thr Leu Gln Ala His Asp Gln Phe Ser Pro Phe
      450              455              460
Ser Ser Ser Ser Gly Arg Arg Leu Asn Ile Ser Tyr Thr Arg Asn Met
  465              470              475              480
Thr Leu Lys Asp Gly Lys Asn Ser Phe Arg Leu Leu Gly
      485              490

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&lt;210&gt; 3359

&lt;211&gt; 652

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3359

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60
gcctatacct actgtagctt ctccacgtat ggaccctaaa ggctactgct gctactacgg
120
ggctagacag ttactgtctc agctctagga tgtgcgttct tccactagaa gctcttctga
180
gggaggtaat taaaaaacag tggaatggaa aaacagtgc ttagtcatcc tgtaatatgc
240
tccttgtaaa caatgtatac attcctgcta ggtgccatat tcattgcttt aagctcaagt
300

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 360  
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 420  
 gttataaaga aagatcatca aagtagaaat ttgaaatatg ctctctggaa ggaattctct  
 480  
 gatttcacga agtggcccat tctgccttt ctttatttcc tggataactt gattgtcttc  
 540  
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 600  
 acaacagctc ttctattcag gatagtgcgt aagaggcgct taaactggat cc  
 652

<210> 3360

<211> 149

<212> PRT

<213> Homo sapiens

<400> 3360

Met	Glu	Lys	Gln	Cys	Cys	Ser	His	Pro	Val	Ile	Cys	Ser	Leu	Ser	Thr
1				5					10					15	
Met	Tyr	Thr	Phe	Leu	Leu	Gly	Ala	Ile	Phe	Ile	Ala	Leu	Ser	Ser	Ser
			20				25						30		
Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn	Lys	Tyr	Asp
		35					40					45			
Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu	Val	Lys	Leu	Val
		50				55					60				
Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys	Lys	Asp	His	Gln	Ser
65					70					75				80	
Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu	Phe	Ser	Asp	Phe	Met	Lys
			85					90					95		
Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe	Leu	Asp	Asn	Leu	Ile	Val	Phe
			100					105					110		
Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro	Ala	Met	Ala	Val	Ile	Phe	Ser	Asn
		115					120					125			
Phe	Ser	Ile	Ile	Thr	Thr	Ala	Leu	Leu	Phe	Arg	Ile	Val	Leu	Lys	Arg
		130				135					140				
Arg	Leu	Asn	Trp	Ile											
145															

<210> 3361

<211> 1040

<212> DNA

<213> Homo sapiens

<400> 3361

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 120  
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gtctttgatt atacatcagc atcaccagct ccctcaccac caatgcgacc atgggagatg  
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 420  
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 600  
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 660  
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 720  
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 780  
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 aatgaagtgg aactcttagg agaacatctt ccaggagccc acccccagca ccccatctg  
 1020  
 ttaataaata tctcaactcc  
 1040

&lt;210&gt; 3362

&lt;211&gt; 252

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3362

Met	Arg	Pro	Trp	Glu	Met	Thr	Ser	Asn	Arg	Gln	Pro	Pro	Ser	Val	Arg
1				5					10					15	
Pro	Ser	Gln	His	Phe	Ser	Gly	Glu	Arg	Cys	Asn	Thr	Pro	Ala	Arg	
			20					25				30			
Asn	Arg	Arg	Ser	Pro	Pro	Val	Arg	Arg	Gln	Arg	Gly	Arg	Arg	Asp	Arg
			35					40				45			
Leu	Ser	Arg	His	Asn	Ser	Ile	Ser	Gln	Asp	Glu	Asn	Tyr	His	His	Leu
			50					55				60			
Pro	Tyr	Ala	Gln	Gln	Gln	Ala	Ile	Glu	Glu	Pro	Arg	Ala	Phe	His	Pro
65					70					75				80	
Pro	Asn	Val	Ser	Pro	Arg	Leu	Leu	His	Pro	Ala	Ala	His	Pro	Pro	Gln
				85					90					95	
Gln	Asn	Ala	Val	Met	Val	Asp	Ile	His	Asp	Gln	Leu	His	Gln	Gly	Thr
			100					105					110		
Val	Pro	Val	Ser	Tyr	Thr	Val	Thr	Thr	Val	Ala	Pro	His	Gly	Ile	Pro
			115					120					125		
Leu	Cys	Thr	Gly	Gln	His	Ile	Pro	Ala	Cys	Ser	Thr	Gln	Gln	Val	Pro
			130				135					140			
Gly	Cys	Ser	Val	Val	Phe	Ser	Gly	Gln	His	Leu	Pro	Val	Cys	Ser	Val

```

145             150             155             160
Pro Pro Pro Met Leu Gln Ala Cys Ser Val Gln His Leu Pro Val Pro
             165             170             175
Tyr Ala Ala Phe Pro Pro Leu Ile Ser Ser Asp Pro Phe Leu Ile His
             180             185             190
Pro Pro His Leu Ser Pro His His Pro Pro His Leu Pro Pro Pro Gly
             195             200             205
Gln Phe Val Pro Phe Gln Thr Gln Gln Ser Arg Ser Pro Leu Gln Arg
             210             215             220
Ile Glu Asn Glu Val Glu Leu Leu Gly Glu His Leu Pro Gly Ala His
225             230             235             240
Pro Gln His Pro His Leu Leu Ile Asn Ile Ser Thr
             245             250

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&lt;210&gt; 3363

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3363

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60
ggccagcatg atcagggacc ccgtcatgcc catgattttt tgggtggcat tggcgaccga
120
gtagctcagg agtgtctccg gagccactg gagaagcccc ccaacggcct cctcttcccc
180
cagcacgggg actatcagta cggccgcaac aacatctaaa cagaccactt ccaatacage
240
cggcagagct acccaaactc gtacagtttg aaccgctatg atgtgtagag tccaaaggac
300
aggaccagac tgttggtgac tccttccccg gccccacag cagtatcaga aacttctgac
360
aatcagtga tgtacaaccc agccgagggg acggtgcata actctccatc agaagccctg
420
gggttctctg cccccgtga gccgcaggag gatgcgttgc ctgcagtgca gacggccgtg
480
agctctgggc aaacctaaac agagaccagt gtcccatgct ctttcttctt ggagcctgtc
540
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600
ttccccaagc agtgtagctc agagcacttg tgtctgcatt ccagataaca ttcaggacct
660
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718

```

&lt;210&gt; 3364

&lt;211&gt; 163

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3364

```

Met Gly His Trp Ser Leu Phe Arg Phe Ala Gln Ser Ser Arg Pro Ser
1             5             10             15
Ala Leu Gln Ala Thr His Pro Pro Ala Ala His Gly Gly Pro Gly Thr

```



	20		25		30										
Pro	Gly	Leu	Leu	Met	Glu	Ser	Tyr	Ala	Pro	Ser	Pro	Arg	Leu	Gly	Cys
	35		40		45										
Thr	Phe	Thr	Asp	Cys	Gln	Lys	Phe	Leu	Ile	Leu	Leu	Trp	Gly	Pro	Gly
	50		55		60										
Lys	Glu	Ser	Pro	Thr	Val	Trp	Ser	Cys	Pro	Leu	Asp	Ser	Thr	His	His
	65		70		75									80	
Ser	Gly	Ser	Asn	Cys	Thr	Ser	Leu	Gly	Ser	Ser	Ala	Gly	Cys	Ile	Gly
			85		90								95		
Ser	Gly	Leu	Phe	Arg	Cys	Cys	Cys	Gly	Arg	Thr	Asp	Ser	Pro	Arg	Ala
			100		105								110		
Gly	Gly	Arg	Gly	Gly	Arg	Trp	Gly	Ala	Ser	Pro	Val	Gly	Ser	Gly	Asp
		115			120								125		
Thr	Pro	Glu	Leu	Leu	Gly	Arg	Gln	Cys	His	Pro	Lys	Asn	His	Gly	His
		130			135								140		
Asp	Gly	Val	Pro	Asp	His	Ala	Gly	Gln	Pro	Ile	Pro	His	His	Gln	Arg
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Ser	Trp	Ala													

<210> 3365

<211> 2389

<212> DNA

<213> Homo sapiens

<400> 3365

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120  
tcgggtggca gcgccggcg caacgcagg gtcacggcga cggcggcggc ggctgacggc  
180  
tggaagggtta ggcttccctc accgctcgtc ctcttctctc gctccgctcg gtgtcaggcg  
240  
cggcggcggc gcggcggcg gacttcgtcc ctcttctctc tccccccac accggagcgg  
300  
gcactcttcg cttcggcatc ccccgaccct tcaccccgag gactgggcgc ctcttccggc  
360  
gcagctgagg gagcgggggc cggctctctg ctcggttggtc gagcctccat gtcggataat  
420  
cagaactgga actcgtcggg ctccggaggag gatccagaga cggagtcttg gccgcctgtg  
480  
gagcgtcgcg gggctctcag taagtggaca aactacatc atgggtggca ggatcgttg  
540  
gtagttttga aaaataatgc tctgagttac taaaatctg aagatgaaac agagtatggc  
600  
tgcagaggat ccatctgtct tagcaaggct gtcacacac ctacgattt tgatgaatgt  
660  
cgatttgata ttagtgtaaa tgatagtgtt tggatcttc gtgctcagga tccagatcat  
720  
agacagcaat ggatagatgc cattgaacag cacaagactg aatctggata tggatctgaa  
780  
tccagcttgc gtcgacatgg ctcaatggtg tccctggtgt ctggagcaag tggctactct  
840

gcaacatcca cctcttcatt caagaaaggc cacagtttac gtgagaagtt ggctgaaatg  
900  
gaaacattta gagacatctt atgtagacaa gttgacacgc tacagaagta ctttgatgcc  
960  
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1020  
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1080  
gaaaagttat ttccacatgt gacaccaaaa ggaattaatg gtatagactt taaaggggaa  
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1320  
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1380  
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1440  
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1620  
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1680  
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1740  
aaagctaccc atgcagttaa aggcgtcaca ggacatgaag tctgcaatta tttctggaat  
1800  
gttgacgttc gcaatgactg ggaaacaact atagaaaact ttcattgtggg gaaacatta  
1860  
gctgataatg caatcatcat ttatcaaaca cacaagaggg tgtggcctgc ttctcagcga  
1920  
gacgtattat atctttctgt cattcgaaag ataccagcct tgactgaaaa tgaccctgaa  
1980  
acttgatag tttgtaattt ttctgtggat catgacagtg ctctctctaa caaccgatgt  
2040  
gtccgtgcc aataaatgt tgctatgatt tgtcaaactt tggtaagccc accagagggg  
2100  
aaccaggaaa ttagcaggga caacattcta tgcaagatta catatgtagc taatgtgaac  
2160  
cctggaggat gggcaccagc ctcatgttta agggcagtgg caaagcgaga gtatcctaaa  
2220  
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2280  
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2389

&lt;210&gt; 3366

&lt;211&gt; 624

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3366

```

Met Ser Asp Asn Gln Asn Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
 1          5          10          15
Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
 20          25          30
Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
 35          40          45
Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
 50          55          60
Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
 65          70          75          80
Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
 85          90          95
Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100          105          110
Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115          120          125
Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130          135          140
Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145          150          155          160
Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165          170          175
Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
180          185          190
Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
195          200          205
Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
210          215          220
Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225          230          235          240
Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
245          250          255
Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
260          265          270
Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
275          280          285
Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
290          295          300
Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305          310          315          320
Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
325          330          335
Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
340          345          350
Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
355          360          365
Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
370          375          380
Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met

```

```

385          390          395          400
Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
          405          410          415
Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
          420          425          430
Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
          435          440          445
Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
          450          455          460
Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
          465          470          475          480
Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
          485          490          495
Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
          500          505          510
Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
          515          520          525
Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
          530          535          540
Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
          545          550          555          560
Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
          565          570          575
Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
          580          585          590
Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
          595          600          605
Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
          610          615          620

```

&lt;210&gt; 3367

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3367

```

acgcgtgcag gagaggagag gccaggagat agggagggca gtttgtggat tgaaatgacc
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gagaattacg ccacagaggt gttggaggct ggcacgtgg catctcagga gcacggaggg
120
tgccttcccc acttcaggcc tcttagtgtc aaggatgtga gaggcaaggg ctgctgggag
180
agtattttac ggactgaagg aggcgtgccg cctgccctgc cctcctactg gtggaggaag
240
gaggtgctgg gagccccaca actcagggcc ccccgacgcc cagtaaggcc actgtacacc
300
cctcctgacc cagaccataa ccagcctccg attgtgcttt tgaccctgtt tccttcaggc
360
accagg
366

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&lt;210&gt; 3368

&lt;211&gt; 104

&lt;212&gt; PRT

<213> Homo sapiens

<400> 3368

```

Met Thr Glu Asn Tyr Ala Thr Glu Val Leu Glu Ala Gly Ile Val Ala
 1           5           10           15
Ser Gln Glu His Gly Gly Cys Leu Pro His Phe Arg Pro Leu Ser Val
          20          25          30
Lys Asp Val Arg Gly Lys Gly Cys Trp Glu Ser Ile Leu Arg Thr Glu
          35          40          45
Gly Gly Val Pro Pro Ala Leu Pro Ser Tyr Trp Trp Arg Lys Glu Val
          50          55          60
Leu Gly Ala Pro Gln Leu Arg Ala Pro Arg Arg Pro Val Arg Pro Leu
65          70          75          80
Tyr Thr Pro Pro Asp Pro Asp His Asn Gln Pro Pro Ile Val Leu Leu
          85          90          95
Thr Leu Phe Pro Ser Gly Thr Arg
          100

```

<210> 3369

<211> 1405

<212> DNA

<213> Homo sapiens

<400> 3369

```

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gataaggagc agaaaaatca ggaaaactgt ggtgcaaaga agaataaaaa gaagaggaaa
120
aaggttttat ataatgccaa taaaaatgat gattatgaca acgaggagat cttaacctat
180
gaggaaatgt cactttatca tcagccagca aataggaaga gacctatcat cttgattggt
240
ccacagaact gtggccagaa tgaattgctg cagaggctca tgaacaaaga aaaggaccgc
300
tttgcatctg cagttcctca tacaaccgag agtaggcgag accaagaagt agccggtaga
360
gattaccact ttgtttcgcg gcaagcattc gaggcagaca tagcagctgg aaagttcatt
420
gagcatgggtg aatttgagaa gaatttgtat ggaactagca tagattctgt acggcaagtg
480
atcaactctg gcaaaatatg tcttttaagt cttcgtacac agtcattgaa gactctccgg
540
aattcagatt tgaaccata tattatcttc attgcacccc cttcacaaga aagacttcgg
600
gcattattgg ccaaagaagg caagaatcca aagcctgaag agttgagaga aatcattgag
660
aagacaagag agatggagca gaacaatggc cactactttg atacggcaat tgtgaattcc
720
gatcttgata aagcctatca ggaattgctt aggttaatta acaaacttga tactgaacct
780
cagtgggtac catccacttg gctgaggtga aagaaacatc cattctgtgg catgttgga
840
ttgatctggc aaaaactgcc aataggagga ctgcccagca ctgcagcaag attgaggata
900

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 960  
 gacagttccc ttaggcagtt tgtgcatggc atcctttatt ctctatacat ggcttttagcg  
 1020  
 gttcttgccct cattttggga ttctaaatgg aagctttcaa cagagcattc cattttgtcc  
 1080  
 tgttaaaacc ttttgttttc acctaaaccc tttctgctta gttgtatctc tgtgaaaaac  
 1140  
 ttgtatacac aagcgtccat gtctcacaca aatattgatg tgattattct taagtgttaa  
 1200  
 atcattaaca cttaaagac ttcatggga atattgagca gagggactgt gcttctatgc  
 1260  
 actgggcaag gcagtatttg cttaggaaac taatttagtc atcagagata ctttcctaaa  
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 1380  
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 1405

<210> 3370

<211> 269

<212> PRT

<213> Homo sapiens

<400> 3370

Leu	Val	Pro	Gly	Lys	Ser	Phe	Gln	Gln	Gln	Arg	Glu	Ala	Met	Lys	Gln
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Thr	Ile	Glu	Glu	Asp	Lys	Glu	Gln	Lys	Asn	Gln	Glu	Asn	Cys	Gly	Ala
			20					25					30		
Lys	Lys	Asn	Lys	Lys	Lys	Arg	Lys	Lys	Val	Leu	Tyr	Asn	Ala	Asn	Lys
		35					40					45			
Asn	Asp	Asp	Tyr	Asp	Asn	Glu	Glu	Ile	Leu	Thr	Tyr	Glu	Glu	Met	Ser
	50				55						60				
Leu	Tyr	His	Gln	Pro	Ala	Asn	Arg	Lys	Arg	Pro	Ile	Ile	Leu	Ile	Gly
65					70				75					80	
Pro	Gln	Asn	Cys	Gly	Gln	Asn	Glu	Leu	Arg	Gln	Arg	Leu	Met	Asn	Lys
			85					90					95		
Glu	Lys	Asp	Arg	Phe	Ala	Ser	Ala	Val	Pro	His	Thr	Thr	Arg	Ser	Arg
			100					105					110		
Arg	Asp	Gln	Glu	Val	Ala	Gly	Arg	Asp	Tyr	His	Phe	Val	Ser	Arg	Gln
		115					120					125			
Ala	Phe	Glu	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Phe	Ile	Glu	His	Gly	Glu
		130				135					140				
Phe	Glu	Lys	Asn	Leu	Tyr	Gly	Thr	Ser	Ile	Asp	Ser	Val	Arg	Gln	Val
145				150					155					160	
Ile	Asn	Ser	Gly	Lys	Ile	Cys	Leu	Leu	Ser	Leu	Arg	Thr	Gln	Ser	Leu
			165					170					175		
Lys	Thr	Leu	Arg	Asn	Ser	Asp	Leu	Lys	Pro	Tyr	Ile	Ile	Phe	Ile	Ala
			180				185						190		
Pro	Pro	Ser	Gln	Glu	Arg	Leu	Arg	Ala	Leu	Leu	Ala	Lys	Glu	Gly	Lys
		195				200						205			
Asn	Pro	Lys	Pro	Glu	Glu	Leu	Arg	Glu	Ile	Ile	Glu	Lys	Thr	Arg	Glu
	210					215					220				
Met	Glu	Gln	Asn	Asn	Gly	His	Tyr	Phe	Asp	Thr	Ala	Ile	Val	Asn	Ser

<400> 3372

Gly	Thr	Ala	Val	Arg	Val	Val	Leu	Val	Pro	Ala	Phe	Ala	Leu	Ala	Lys
1				5					10					15	
Glu	Ala	Pro	Arg	Glu	His	Leu	Asp	His	Gln	Ala	Ala	His	Gln	Pro	Phe
			20					25					30		
Pro	Arg	Pro	Arg	Phe	Arg	Gln	Glu	Thr	Gly	His	Pro	Ser	Leu	Gln	Arg
		35					40					45			
Asp	Phe	Pro	Arg	Ser	Phe	Leu	Leu	Asp	Leu	Pro	Asn	Phe	Pro	Asp	Leu

```

      50              55              60
Ser Lys Ala Asp Ile Asn Gly Gln Asn Pro Asn Ile Gln Val Thr Ile
65              70              75              80
Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His Pro
      85              90              95
Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala Trp
      100             105             110
Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln Asp
      115             120             125
Tyr Lys Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro Pro
      130             135             140
Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr Lys
      145             150             155             160
Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser Leu
      165             170             175
Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg Thr
      180             185             190
Arg Ser Cys Gly Tyr Ala
      195

```

&lt;210&gt; 3373

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3373

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120
gtgttctggt gcgggccagc gcctgaccgg tgcggggcggc ctcaggagag gagagcttgc
180
tcagtgcgtc acgtatgcag ggctcaggct gggggccggc tccagagcct ggtcacattc
240
ccaagcttca ttctcttcac ctgtgaattg caggcttccc tgggtgtgccc tgcacatgag
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480
agcgcacatcgg tggctctcac gacgtacacc cagaagcacc cgtccatcga ggacgggcct
540
ccgtttgtgg agccgctgct taacttcac tggttcctgc tgctggctgt ggacgggtgc
600
gtcttgggat cctgcagggg gagggggctg tgaatgtgcg ggttgtgtgt agacgtgggtg
660
tggatagctg tgtgggtgtg tgtgcaagt tagccatggt gtgggtagcc gtgtgggtat
720
atgcat
726

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&lt;210&gt; 3374



<211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 3374  
 Met Ser Glu Ala Gly Ala Cys Ala Gly Arg Ser Cys Val Leu Gln Pro  
 1 5 10 15  
 Phe His His Gln His Val Leu Ile Ser Arg Phe Leu Cys Leu Lys Asn  
 20 25 30  
 Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro  
 35 40 45  
 Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile  
 50 55 60  
 Trp Phe Leu Leu Leu Ala Val Asp Gly Cys Val Leu Gly Ser Cys Arg  
 65 70 75 80  
 Gly Arg Gly Leu

<210> 3375  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<400> 3375  
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 60  
 gcacatgtgc ccacacactc agcactcaca ccccgctctg caggctcagc cccactcctg  
 120  
 agccacctgc ctgggctttg ggggcccagc cggcatgggg agccccaggc tccagctggc  
 180  
 ctgccttggc tctgaaatct aggccaggat gcagagcccc cagtgcggcc agtggagccc  
 240  
 ctggtactgt gcgcagcccc cacctggcag ccccttttcc tgtcaaagcc cctcccagcg  
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 360  
 cttgcccagc atccccggcc tgcattctcac cag  
 393

<210> 3376  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 3376  
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 Ala His Thr Leu Ser Thr His Thr Pro Ser Cys Arg Leu Ser Pro Thr  
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 35 40 45  
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<210> 3377

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<210> 3378

<211> 970

<212> PRT

<213> Homo sapiens

<400> 3378

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Gln Asn Leu Cys Asn Ser Tyr Gln Ser Arg Ala Asp Ser Arg Ala Lys
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Ala Ser Glu Glu Ser Leu Arg Thr Ser Glu Arg Lys Leu Arg Glu Thr
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Glu Glu Lys Leu Gln Lys Leu Arg Thr Asn Ile Val Ala Leu Leu Gln
      930              935              940
Lys Val Gln Glu Asp Ile Asp Ile Asn Thr Asp Asp Glu Leu Asp Ala
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Tyr Ile Glu Asp Leu Ile Thr Lys Gly Asp
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&lt;210&gt; 3379

&lt;211&gt; 898

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3379

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&lt;210&gt; 3380

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3380

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&lt;210&gt; 3381

&lt;211&gt; 1379

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3381

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<210> 3382

<211> 279

<212> PRT

<213> Homo sapiens

<400> 3382

Xaa	Pro	Leu	Val	Ser	Val	Asn	Met	Glu	Ala	Glu	Glu	Ser	Glu	Lys	Ala
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Ala	Thr	Glu	Gln	Glu	Pro	Leu	Glu	Gly	Thr	Glu	Gln	Thr	Leu	Asp	Ala
			20					25					30		
Glu	Glu	Glu	Gln	Glu	Glu	Ser	Glu	Glu	Ala	Ala	Cys	Gly	Ser	Lys	Lys
			35				40					45			
Arg	Val	Val	Pro	Gly	Ile	Val	Tyr	Leu	Gly	His	Ile	Pro	Pro	Arg	Phe
	50					55					60				
Arg	Pro	Leu	His	Val	Arg	Asn	Leu	Leu	Ser	Ala	Tyr	Gly	Glu	Val	Gly
65				70						75				80	
Arg	Val	Phe	Phe	Gln	Ala	Glu	Asp	Arg	Phe	Val	Arg	Arg	Lys	Lys	Lys
				85					90					95	
Ala	Ala	Ala	Ala	Ala	Gly	Gly	Lys	Lys	Arg	Ser	Tyr	Thr	Lys	Asp	Tyr
			100				105						110		
Thr	Glu	Gly	Trp	Val	Glu	Phe	Arg	Asp	Lys	Arg	Ile	Ala	Lys	Arg	Val
		115					120					125			
Ala	Ala	Ser	Leu	His	Asn	Thr	Pro	Met	Gly	Ala	Arg	Arg	Arg	Ser	Pro
	130					135					140				
Phe	Arg	Tyr	Asp	Leu	Trp	Asn	Leu	Lys	Tyr	Leu	His	Arg	Phe	Thr	Trp
145				150						155				160	
Ser	His	Leu	Ser	Glu	His	Leu	Ala	Phe	Glu	Arg	Gln	Val	Arg	Arg	Gln
			165					170						175	
Arg	Leu	Arg	Ala	Glu	Val	Ala	Gln	Ala	Lys	Arg	Glu	Thr	Asp	Phe	Tyr
		180					185						190		
Leu	Gln	Ser	Val	Glu	Arg	Gly	Gln	Arg	Phe	Leu	Ala	Ala	Asp	Gly	Asp
	195					200					205				
Pro	Ala	Arg	Pro	Asp	Gly	Ser	Trp	Thr	Phe	Ala	Gln	Arg	Pro	Thr	Glu

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      210              215              220
Gln Glu Leu Arg Ala Arg Lys Ala Ala Arg Pro Gly Gly Arg Glu Arg
225              230              235              240
Ala Arg Leu Ala Thr Ala Gln Asp Lys Ala Arg Ser Asn Lys Gly Leu
      245              250              255
Leu Ala Arg Ile Phe Gly Ala Pro Pro Pro Ser Glu Ser Met Glu Gly
      260              265              270
Pro Ser Leu Val Arg Asp Ser
      275

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<210> 3383
<211> 309
<212> DNA
<213> Homo sapiens

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<400> 3383
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60
gtgttgcttg cacacaaatt ttgtagctgg agtgagtatt gttgttattt gtgttatagg
120
aaatgctcac ttcttaacct cttttgtcct ggagcataga attactgcaa atgctcaccc
180
ctgggagctg tcctgcccc gatctccac acaaacactc cagcatgaaa gagcgagact
240
caatctcaaa aaaaaaagt ttcgggcacc tgaacaggaa ctggtttcca tcatcaactc
300
agaaagccc
309

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<210> 3384
<211> 94
<212> PRT
<213> Homo sapiens

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<400> 3384
Met Leu Ala His His Gly Ser Arg Glu Lys Cys Gln Cys Cys Leu His
1              5              10              15
Thr Asn Phe Val Ala Gly Val Ser Ile Val Val Ile Cys Val Ile Gly
      20              25              30
Asn Ala His Phe Leu Thr Ser Phe Val Leu Glu His Arg Ile Thr Ala
      35              40              45
Asn Ala His Pro Trp Glu Leu Ser Cys Pro Arg Ser Pro Thr Gln Thr
      50              55              60
Leu Gln His Glu Arg Ala Arg Leu Asn Leu Lys Lys Lys Lys Phe Arg
65              70              75              80
Ala Pro Glu Gln Glu Leu Val Ser Ile Ile Asn Ser Glu Ser
      85              90

```

```

<210> 3385
<211> 720
<212> DNA
<213> Homo sapiens

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<400> 3385

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 60  
 gtaggggtga gccggcttgg ccagagggag gaggggtctat gctgaggtct actgatggta  
 120  
 gtgaaaacag tgacgggtgcg ggggtgggga gcaactgcggt ccacttcttc agccccccac  
 180  
 tatcctggaa gcttcagggt gggcccagg cagcctccag ctccagcgac caccctgtt  
 240  
 cctcttgcca ggttctttgt gaacttcccc tcggccaagc agtacttcag ccagttcaag  
 300  
 cacatggagg atccccctga gatggagcgg agccccagc tcggaagca cgcctgccga  
 360  
 gtcattgggg ccctcaacac tgctgtggag aacctgcag accccgacaa ggtgtctct  
 420  
 gtgctgcgcc ttgtggggaa agcccacgcc ctcaagcaca aggtggaacc ggtgtacttc  
 480  
 aagatcctct ctggggcat tctggagggt gtcgccgagg aatttgccag tgacttccca  
 540  
 cctgagacgc agagagcctg ggccaagctg cgtggcctca tctacagcca cgtgaccgct  
 600  
 gcctacaagg aagtgggctg ggtgcagcag gtccccaacg ccaccacccc accggccaca  
 660  
 ctgccctctt cggggccgta ggacccctcc ctccaccccc ctccctggca gcacctcgag  
 720

&lt;210&gt; 3386

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3386

Met	Val	Val	Lys	Thr	Val	Thr	Val	Arg	Gly	Trp	Gly	Ala	Leu	Arg	Ser
1				5					10					15	
Thr	Ser	Ser	Ala	Pro	His	Tyr	Pro	Gly	Ser	Phe	Arg	Val	Gly	Pro	Arg
			20					25					30		
Gln	Pro	Pro	Ala	Ser	Ala	Thr	Thr	Pro	Val	Pro	Leu	Ala	Arg	Phe	Phe
			35				40					45			
Val	Asn	Phe	Pro	Ser	Ala	Lys	Gln	Tyr	Phe	Ser	Gln	Phe	Lys	His	Met
	50					55					60				
Glu	Asp	Pro	Leu	Glu	Met	Glu	Arg	Ser	Pro	Gln	Leu	Arg	Lys	His	Ala
65					70					75				80	
Cys	Arg	Val	Met	Gly	Ala	Leu	Asn	Thr	Val	Val	Glu	Asn	Leu	His	Asp
			85					90						95	
Pro	Asp	Lys	Val	Ser	Ser	Val	Leu	Ala	Leu	Val	Gly	Lys	Ala	His	Ala
			100					105					110		
Leu	Lys	His	Lys	Val	Glu	Pro	Val	Tyr	Phe	Lys	Ile	Leu	Ser	Gly	Val
			115				120					125			
Ile	Leu	Glu	Val	Val	Ala	Glu	Glu	Phe	Ala	Ser	Asp	Phe	Pro	Pro	Glu
	130					135					140				
Thr	Gln	Arg	Ala	Trp	Ala	Lys	Leu	Arg	Gly	Leu	Ile	Tyr	Ser	His	Val
145					150					155				160	
Thr	Ala	Ala	Tyr	Lys	Glu	Val	Gly	Trp	Val	Gln	Gln	Val	Pro	Asn	Ala
			165					170						175	
Thr	Thr	Pro	Pro	Ala	Thr	Leu	Pro	Ser	Ser	Gly	Pro				

180

185

&lt;210&gt; 3387

&lt;211&gt; 3299

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3387

nacgcgtgaa ggggaagcag gcacgtccgg aagcgctcct ccagcagga cagctcactg  
60  
atgaggtcgg tgatggcggt ggtaaaggct tcctgggggt ttgccccgcc ggagtaatcc  
120  
ggaagaggcc tcttattagg gctctggtgg cggcggcggc ggacccttgg ggtctggacg  
180  
caacggcggc gggagcatga acgcccctcc agccttcgag tcgttcttgc tcttcgaggg  
240  
cgagaagaag taagtacgc cggtgcggc gggccgagga tcaccattaa caaggacacc  
300  
aaggtaccca atgcctgttt attcaccatc aacaaagaag accacacact gggaaacatc  
360  
attaaatcac aactcctaaa agaccgcga gtgctatttg ctggctacaa agtccccac  
420  
cccttgagc acaagatcat catccgagtg cagaccacgc cggactacag cccccaggaa  
480  
gcctttacca acgcatcac cgacctcgc agtgagctgt ccctgctgga ggagcgcttt  
540  
cgggtggcca taaaagacaa gcaggaagga attgagtagg ggccagaggg ggctctgctc  
600  
ggcctgtgag ccccgcttct acctgtgct gacctccgc tccaggtacc acaccagga  
660  
gagcggcgcg tcccagccat ggccgcctt gtggccaccc ctcacctga caccgacgtg  
720  
ttggccaccc ctcacctga caccgacgtg tcctgtacat agattaggtt ttatattcct  
780  
aataaagtat agcgaagag acctggatgt ggacttgagc agcggtgact tcgcaagcaa  
840  
atggattgtc aggttgatg caggcagatg acctgtttca ggggcgtccg gctggcaggg  
900  
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960  
ccggagagaa gtgtgcaaac ccatgagctc ccaagagtct ctgctctaga agcctcaact  
1020  
cctgggcctg cctgtcagtc aaagcaggaa cacttcttcc tgcataactc gaaacacctt  
1080  
tccacagget tcttgtccac agtagagttt aataaaaata ttcactgaaa gacccccccc  
1140  
acccccatcg gcccaggct gaataagtta gttagctgtg tccctggctc tttgcgatgg  
1200  
tgtgaggeta catcctcccc cagatggcta cgatgttga gtccgtcagg gcggtgaggt  
1260  
aggtgaagga ggcattggcc accactgtgt tcaccatggt cttggtcacc acctggccaa  
1320  
gggcccaggg ctggggccac ttcaggatct gtgtgggggc ctgcagggt gccggcagca  
1380

2565

ggggtggctg cttcaggatg ttgctgacgt cgtagagcca cacgttgccc tctcatccc  
1440  
cacagagcac aatcccccta tcagggcagg cgctgagcga gaagtaggcc aactcgggtg  
1500  
acgaccattg cagcgcgcc aggaccacca ctgccactgt ggactggctg cccggcccc  
1560  
cccacgtctg cctccagctc cacaggcaga tgggtgccag gccgctccc ttggaggcca  
1620  
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1680  
cagagaagac gaattccact tcacacacc cctctctttg gggctggctc agccgcacgt  
1740  
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1800  
cagggcagag gcgcaggggg atagaggtgg tgtccagtgt gagcagctgg ctggcctgga  
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1920  
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1980  
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2040  
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2100  
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2160  
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2220  
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2280  
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2340  
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2460  
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2520  
tagccttttg cacctgggtc ctactggcg ccaccagctc ctccagagat atccgcaccc  
2580  
gccactgggt gaactcgtg agggactcgg gcccgtagcg gacatccctg acagccgact  
2640  
tcacaaagtc cgctggggc ttctcagcct cctcttcagg acccagtgtg gccatgaact  
2700  
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2760  
aagttgagga cgcaccttg ccattgacct tacggagcgt gggcaggaga aaggagactt  
2820  
tcaggttgtc attgaccgtc aggaaggggt tgccctccag gctgagttcc tcgagcttgg  
2880  
ggaactggca caaggcagta acatccccca gctggttgtt gggcagcgg aggcacgca  
2940  
ggtgggacag gccaggttg tccggcagcg tctccaggtg gttgttagac aggtcaagct  
3000

cctgcagctg cgtcaggcgg cacaggagtt tgggggtccag gtgctcggaa agcagctcca  
 3060  
 atcctgacag gtccagactc cggatcttcc ccagccggtc gctcttgggg cgcccgcgct  
 3120  
 gcattagcag ccgcgccgag agggggccca tggcgaggag gcgcagcccg cgctgaccca  
 3180  
 gtcggccacc ccggcgtgtg gcgtcgccct gcgtctcctg gagcccgga ctggcgctccg  
 3240  
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 3299

<210> 3388

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3388

Ser Gly Arg Gly Leu Leu Gly Leu Trp Trp Arg Arg Arg Arg Thr  
 1 5 10 15  
 Leu Gly Val Trp Thr Gln Arg Arg Arg Glu His Glu Arg Pro Ser Ser  
 20 25 30  
 Leu Arg Val Val Leu Ala Leu Arg Gly Arg Glu Glu Val Ser Asp Ala  
 35 40 45  
 Gly Cys Gly Gly Pro Arg Ile Thr Ile Asn Lys Asp Thr Lys Val Pro  
 50 55 60  
 Asn Ala Cys Leu Phe Thr Ile Asn Lys Glu Asp His Thr Leu Gly Asn  
 65 70 75 80  
 Ile Ile Lys Ser Gln Leu Leu Lys Asp Pro Gln Val Leu Phe Ala Gly  
 85 90 95  
 Tyr Lys Val Pro His Pro Leu Glu His Lys Ile Ile Ile Arg Val Gln  
 100 105 110  
 Thr Thr Pro Asp Tyr Ser Pro Gln Glu Ala Phe Thr Asn Ala Ile Thr  
 115 120 125  
 Asp Leu Ile Ser Glu Leu Ser Leu Leu Glu Glu Arg Phe Arg Val Ala  
 130 135 140  
 Ile Lys Asp Lys Gln Glu Gly Ile Glu  
 145 150

<210> 3389

<211> 308

<212> DNA

<213> Homo sapiens

<400> 3389

nntgtctcca agcccttcca ccaccagcat gttctcattt ccaggtttct ctgtttaaaa  
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 aàcaaaagta gcgcatcggt ggtcttcacg acgtacaccc agaagcaccg gtccatcgag  
 120  
 gacgggcctc cgtttgtgga gccgctgctt aacttcattt ggttcctgct gctggctgtg  
 180  
 gacggggaac cttctgacca gcctcatggg ctctcagag caggaggatg gggaggagag  
 240  
 cccagcgac ggcagcccca tcgagctgga ctgaactggc caggccacgt ggagacacca  
 300

cggtcgac  
308

<210> 3390  
<211> 102  
<212> PRT  
<213> Homo sapiens

<400> 3390  
Xaa Val Ser Lys Pro Phe His His Gln His Val Leu Ile Ser Arg Phe  
1 5 10 15  
Leu Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr  
20 25 30  
Thr Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro  
35 40 45  
Leu Leu Asn Phe Ile Trp Phe Leu Leu Leu Ala Val Asp Gly Glu Pro  
50 55 60  
Ser Asp Gln Pro His Gly Leu Leu Arg Ala Gly Gly Trp Gly Gly Glu  
65 70 75 80  
Pro Gln Arg Arg Gln Pro His Arg Ala Gly Leu Asn Trp Pro Gly His  
85 90 95  
Val Glu Thr Pro Arg Ser  
100

<210> 3391  
<211> 1295  
<212> DNA  
<213> Homo sapiens

<400> 3391  
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gaagccctaa gtgacagttc agagcgtctt ttctcctttg gcgtcatcgc agatgttcaa  
120  
tttgcagact tagaagatgg ctttaatttc caaggaacca ggcggcgata ctacagacat  
180  
agtcttcttc acttacaggg tgccattgaa gactggaata atgaaagcag catgccctgt  
240  
tgtgtccttc agcttggaga tatcatcgat ggatataatg cacagtataa tgcattccaa  
300  
aagtccttag aacttggtat ggacatgttc aagaggctta aagttccagt tcatcataca  
360  
tggggaaacc atgaattcta taacttcagt agagagtatt taacacactc taaacttaac  
420  
actaagtttc tagaagatca gattgtacat catcctgaga ccatgccttc agaagattat  
480  
tatgcttata attttgtacc attccctaaa ttccggttca ttttacttga tgcatatgac  
540  
ttgagtgtct tgggcgtgga tcagtcttct ccaaatacag agcagtgtat gaagatattg  
600  
agggagcaca atccaaatac ggaactgaat agtcctcaag gactttctga gccccagttt  
660  
gtccagttta atggaggatt cagccaagaa cagctaaact ggttgaatga agtgctaaca  
720



ttctctgaca caaaccaaga aaaggtggtg attgtgagcc atcttcccat ttacccggac  
 780  
 gcctctgaca atgtgtgcct ggcttggaac tacagagatg ccttggcagt catttggctt  
 840  
 catgagtgtg tgggtgtgtt ctttctggt cacacccatg atgggtggcta ctctgaggat  
 900  
 ccttttggtg tataccacgt caacctagaa ggagttattg aaacagctcc agacagccaa  
 960  
 gcctttggca cagttcatgt ctatcctgac aaaatgatgt tgaaaggag aggcagagtt  
 1020  
 ccagatagaa ttatgaatta caagaaagaa agagccttcc attgttagtc taatttattt  
 1080  
 taacttgata gaaaatgagc tttgtgtttg tccctcctaa acaaaaaaat aaaaatcctc  
 1140  
 tgtctcattg tttagtattc agcttgcata acaaaatgta tttatagttt cagtgtgtga  
 1200  
 tggttgataa aatactcaga aatgttattt tggatcatgt atccattgta agttagaaac  
 1260  
 aaaccaggga ggaaactgag gcaggggtgt atagt  
 1295

<210> 3392

<211> 355

<212> PRT

<213> Homo sapiens

<400> 3392

Ile	Val	Phe	Leu	Leu	Tyr	Leu	Glu	Thr	Cys	Leu	Glu	Val	Met	Asp	Asp
1			5					10					15		
Lys	Pro	Asn	Pro	Glu	Ala	Leu	Ser	Asp	Ser	Ser	Glu	Arg	Leu	Phe	Ser
		20					25					30			
Phe	Gly	Val	Ile	Ala	Asp	Val	Gln	Phe	Ala	Asp	Leu	Glu	Asp	Gly	Phe
	35					40					45				
Asn	Phe	Gln	Gly	Thr	Arg	Arg	Tyr	Tyr	Arg	His	Ser	Leu	Leu	His	
	50				55				60						
Leu	Gln	Gly	Ala	Ile	Glu	Asp	Trp	Asn	Asn	Glu	Ser	Ser	Met	Pro	Cys
65			70					75					80		
Cys	Val	Leu	Gln	Leu	Gly	Asp	Ile	Ile	Asp	Gly	Tyr	Asn	Ala	Gln	Tyr
		85					90					95			
Asn	Ala	Ser	Lys	Lys	Ser	Leu	Glu	Leu	Val	Met	Asp	Met	Phe	Lys	Arg
		100					105					110			
Leu	Lys	Val	Pro	Val	His	His	Thr	Trp	Gly	Asn	His	Glu	Phe	Tyr	Asn
	115						120					125			
Phe	Ser	Arg	Glu	Tyr	Leu	Thr	His	Ser	Lys	Leu	Asn	Thr	Lys	Phe	Leu
	130					135					140				
Glu	Asp	Gln	Ile	Val	His	His	Pro	Glu	Thr	Met	Pro	Ser	Glu	Asp	Tyr
145			150					155					160		
Tyr	Ala	Tyr	His	Phe	Val	Pro	Phe	Pro	Lys	Phe	Arg	Phe	Ile	Leu	Leu
		165					170						175		
Asp	Ala	Tyr	Asp	Leu	Ser	Val	Leu	Gly	Val	Asp	Gln	Ser	Ser	Pro	Lys
		180					185					190			
Tyr	Glu	Gln	Cys	Met	Lys	Ile	Leu	Arg	Glu	His	Asn	Pro	Asn	Thr	Glu
	195					200						205			
Leu	Asn	Ser	Pro	Gln	Gly	Leu	Ser	Glu	Pro	Gln	Phe	Val	Gln	Phe	Asn

```

      210              215              220
Gly Gly Phe Ser Gln Glu Gln Leu Asn Trp Leu Asn Glu Val Leu Thr
225              230              235              240
Phe Ser Asp Thr Asn Gln Glu Lys Val Val Ile Val Ser His Leu Pro
      245              250              255
Ile Tyr Pro Asp Ala Ser Asp Asn Val Cys Leu Ala Trp Asn Tyr Arg
      260              265              270
Asp Ala Leu Ala Val Ile Trp Ser His Glu Cys Val Val Cys Phe Phe
      275              280              285
Ala Gly His Thr His Asp Gly Gly Tyr Ser Glu Asp Pro Phe Gly Val
      290              295              300
Tyr His Val Asn Leu Glu Gly Val Ile Glu Thr Ala Pro Asp Ser Gln
305              310              315              320
Ala Phe Gly Thr Val His Val Tyr Pro Asp Lys Met Met Leu Lys Gly
      325              330              335
Arg Gly Arg Val Pro Asp Arg Ile Met Asn Tyr Lys Lys Glu Arg Ala
      340              345              350
Phe His Cys
      355

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<210> 3393  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

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<400> 3393
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120
agtcggggcg ggtcaactt cgagtacttg aaacgggagc actcgctgtc gaagccctac
180
caggggtgtg gcacaggcag ttctcactg tggaaatctga tgggcaatng catggtgatg
240
accaggtata tccgccttac ccagatatg caaagtaaac aggggtgcctt gtggaaccgg
300
gtgccatgtt tcctgagaga ctgggagtgg caggtgcact tcaaaatcca tggacaagga
360
aagaagaatc tgcattggga tggcttggca atctggtaca caaaggatcg gatgcagcca
420
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480
cccaatgagg agaagcagcc cttcacgcgt
510

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<210> 3394  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

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<400> 3394
Xaa Arg Leu Trp Asp Pro Leu Gly Arg Gly Ser Ser Gly Gly Asp Val
1          5          10          15
Cys Arg Leu Gly Met Gly Pro Gly Xaa Val Thr Pro Ser Ser Phe Val

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<210> 3395
<211> 807
<212> DNA
<213> Homo sapiens
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2571

<210> 3396  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 3396  
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 1 5 10 15  
 Ser Ser Ser Leu Ser Ala Arg Met Met Ser Gly Ser Arg Gly Ser Ser  
 20 25 30  
 Leu Asn Asp Thr Tyr His Ser Arg Asp Ser Ser Phe Arg Leu Asp Ser  
 35 40 45  
 Glu Tyr Gln Ser Thr Ser Ala Ser Ala Ser Ala Ser Pro Phe Gln Ser  
 50 55 60  
 Ala Trp Tyr Ser Glu Ser Glu Ile Thr Gln Gly Ala Arg Ser Arg Ser  
 65 70 75 80  
 Gln Asn Gln Gln Arg Asp His Asp Ser Lys Arg Pro Lys Leu Ser Cys  
 85 90 95  
 Thr Asn Cys Thr Thr Ser Ala Gly Arg Asn Val Gly Asn Gly Leu Asn  
 100 105 110  
 Thr Leu Ser Asp Ser Ser Trp Arg His Ser Gln Val Pro Arg Ser Ser  
 115 120 125  
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<210> 3400

<211> 1069

<212> PRT

<213> Homo sapiens

<400> 3400

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Cys	Asp	Val	Leu	Leu	Ile	Val	Gly	Asp	Gln	Lys	Phe	Arg	Ala	His	Lys
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Asn	Val	Leu	Ala	Ala	Ser	Ser	Glu	Tyr	Phe	Gln	Ser	Leu	Phe	Thr	Asn
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Lys	Glu	Asn	Glu	Ser	Gln	Thr	Val	Phe	Gln	Leu	Asp	Phe	Cys	Glu	Pro
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Asp	Ala	Phe	Asp	Asn	Val	Leu	Asn	Tyr	Ile	Tyr	Ser	Ser	Ser	Leu	Phe
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Val	Glu	Lys	Ser	Ser	Leu	Ala	Ala	Val	Gln	Glu	Leu	Gly	Tyr	Ser	Leu
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Gly	Ile	Ser	Phe	Leu	Thr	Asn	Ile	Val	Ser	Lys	Thr	Pro	Gln	Ala	Pro
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Phe	Pro	Thr	Cys	Pro	Asn	Arg	Lys	Lys	Val	Phe	Val	Glu	Asp	Asp	Glu
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Ser	Arg	Pro	Ser	Pro	Ser	Ile	Ala	Val	Lys	Ala	Asn	Thr	Asn	Lys	Pro
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His	Val	Pro	Lys	Pro	Ile	Glu	Pro	Leu	His	Asn	Leu	Ser	Leu	Thr	Glu
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Lys	Ser	Trp	Pro	Lys	Asp	Ser	Ser	Val	Val	Tyr	Ala	Lys	Ser	Leu	Glu
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His	Ser	Gly	Ser	Leu	Asp	Asp	Pro	Asn	Arg	Ile	Ser	Leu	Val	Lys	Arg

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Leu Ala Leu Lys Arg Pro Arg Pro Pro Val Leu Ser Val Cys Ser Ser
          275          280          285
Ser Glu Thr Pro Tyr Leu Leu Lys Glu Thr Asn Lys Gly Asn Gly Gln
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Gly Glu Asp Arg Asn Leu Leu Tyr Tyr Ser Lys Leu Gly Leu Val Ile
305          310          315          320
Pro Ser Ser Gly Ser Gly Ser Gly Asn Gln Ser Ile Asp Arg Ser Gly
          325          330          335
Pro Leu Val Lys Ser Leu Leu Arg Arg Ser Leu Ser Met Asp Ser Gln
          340          345          350
Val Pro Val Tyr Ser Pro Ser Ile Asp Leu Lys Ser Ser Gln Gly Ser
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Ser Ser Val Ser Ser Asp Ala Pro Gly Asn Val Leu Cys Ala Leu Ser
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Gln Lys Ser Ser Leu Lys Asp Cys Ser Glu Lys Thr Ala Leu Asp Asp
385          390          395          400
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Gln Ser Thr Asp Arg Glu Gly Ala Ser Pro Val Thr Glu Val Arg Ile
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Lys Thr Glu Pro Ser Ser Pro Leu Ser Asp Pro Ser Asp Ile Ile Arg
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Val Thr Val Gly Asp Ala Ala Thr Thr Ala Ala Ala Ser Ser Ser Ser
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Val Thr Arg Asp Leu Ser Leu Lys Thr Glu Asp Asp Gln Lys Asp Met
465          470          475          480
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Phe Lys Lys Leu Lys Val Asn Glu His Gly Ser Pro Val Ser Glu Asp
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Asp Ser Asp Leu Asn Lys Asp Glu Phe Gly Glu Leu Glu Gly Thr Arg
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Pro Asn Lys Lys Phe Lys Cys Lys His Cys Leu Lys Ile Phe Arg Ser
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Thr Ala Gly Leu His Arg His Val Asn Met Tyr His Asn Pro Glu Lys
          565          570          575
Pro Tyr Ala Cys Asp Ile Cys His Lys Arg Phe His Thr Asn Phe Lys
          580          585          590
Val Trp Thr His Cys Gln Thr Gln His Gly Ile Val Lys Asn Pro Ser
          595          600          605
Pro Ala Ser Ser Ser His Ala Val Leu Asp Glu Lys Phe Gln Arg Lys
          610          615          620
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Lys Val Ala Lys Pro Lys Glu His Ala Pro Leu Ala Ser Pro Val Glu
705          710          715          720
Asn Lys Glu Val Tyr Gln Cys Arg Leu Cys Asn Ala Lys Leu Ser Ser
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Leu Leu Glu Gln Gly Ser His Glu Arg Leu-Cys Arg Asn Ala Ala Val
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Cys Pro Tyr Cys Ser Leu Arg Phe Phe Ser Pro Glu Leu Lys Gln Glu
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785          790          795          800
His Asn Gln Asn Asn Met Ala Pro Thr Glu Asn Phe Ser Leu Pro Val
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Leu Asp His Asn Gly Asp Val Thr Gly Ser Ser Arg Pro Gln Ser Gln
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Pro Glu Pro Asn Lys Val Asn His Ile Val Thr Thr Lys Asp Asp Asn
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        995          1000          1005
Gly Leu Ser Glu Asn Pro Thr Pro Ala Thr Glu Lys Leu Phe Val Pro
1010          1015          1020
Gln Glu Ser Asp Thr Leu Phe Tyr His Ala Pro Pro Leu Ser Ala Ile
1025          1030          1035          1040
Thr Phe Lys Arg Gln Phe Met Cys Lys Leu Cys His Arg Thr Phe Lys
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&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3401

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&lt;210&gt; 3402

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3402

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			35				40					45			
Glu	Leu	Leu	Glu	Leu	Asp	Ser	Ser	Ser	Ser	Leu	Cys	Val	Leu	Val	Ser
			50			55					60				
Thr	Val	Gly	Lys	Leu	Cys	Arg	Leu	Ile	Asn	Glu	Asp	Val	Asn	Glu	Gln
65				70					75				80		
Val	Met	Gln	Val	Leu	Gly	Pro	Glu	Asp	Leu	Gln	Ser	Ile	Ile	Tyr	Lys
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Asp	Leu	Leu	Glu	Ile	Leu	Glu	Ile	Asp	Asp	Ser	Gly	Cys	His	Cys	Thr
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Cys	Ser	Lys	Glu	Ile	Lys	Ser	Thr	Phe	Ile	Leu	Lys	Thr	Asn	Gln	Ile
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Ile	Phe	Thr	Val												
145															

&lt;210&gt; 3403

&lt;211&gt; 1696

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3403

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<211> 286

<212> PRT

<213> Homo sapiens

<400> 3404

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Ala	Ser	Glu	Cys	Thr	Glu	Leu	Pro	Lys	Ala	Glu	Lys	Trp	Arg	Arg	Gln
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Ile	Ile	Gly	Glu	Ile	Ser	Lys	Lys	Val	Ala	Gln	Ile	Gln	Asn	Ala	Gly
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Leu	Gly	Glu	Phe	Arg	Ile	Arg	Asp	Leu	Asn	Asp	Glu	Ile	Asn	Lys	Leu
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Pro	Asp	Tyr	Gly	Lys	Val	Gly	Pro	Lys	Met	Leu	Asp	His	Glu	Gly	Lys
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Glu	Val	Pro	Gly	Asn	Arg	Gly	Tyr	Lys	Tyr	Phe	Gly	Ala	Ala	Lys	Asp
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Leu	Pro	Gly	Val	Arg	Glu	Leu	Phe	Glu	Lys	Xaa	Thr	Ser	Ser	Ser	Ser
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Gln	Xaa	Lys	Thr	Arg	Ala	Glu	Leu	Met	Lys	Ala	Ile	Asp	Phe	Glu	Tyr
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Tyr	Gly	Tyr	Leu	Asp	Glu	Asp	Asp	Gly	Val	Ile	Val	Pro	Leu	Glu	Gln
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225				230					235					240	
Ile	Ala	His	Val	Pro	Val	Pro	Ser	Gln	Gln	Glu	Ile	Glu	Glu	Ala	Leu
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Val	Arg	Arg	Lys	Lys	Met	Glu	Leu	Leu	Gln	Lys	Tyr	Ala	Ser	Glu	Thr
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<210> 3405

<211> 402

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3405

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300
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402

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&lt;210&gt; 3406

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3406

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Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser Ala Lys Met Arg Arg Tyr
20     25     30
Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu Leu Ala Ser Ile Arg Lys
35     40     45
Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro Pro Pro Val Ala Ile Gly
50     55     60
Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser Pro Ala Pro Thr Gln Pro
65     70     75     80
Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro Arg Val Thr Leu Glu Gly
85     90     95
Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro Gly Leu Ala Lys Pro Gln
100    105    110
Met Pro Pro Gly Pro Cys Ser Pro Pro Ser Gly Pro Val Ala Glu Pro
115    120    125
Pro Ala Arg Leu Gln Ala
130

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&lt;210&gt; 3407

&lt;211&gt; 535

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3407

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<210> 3408
<211> 131
<212> PRT
<213> Homo sapiens
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<210> 3409
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<212> DNA
<213> Homo sapiens
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2584



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 720  
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 780  
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 840  
 tgggtctaca gagagggaat atggcgagag agctgggatg agtttgtacc acagatgttg  
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<210> 3410

<211> 144

<212> PRT

<213> Homo sapiens

<400> 3410

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Lys	Leu	Ser	Glu	Leu	Ser	Glu	Pro	Gly	Asp	Gly	Glu	Ala	Leu	Met	Tyr
			20					25					30		
His	Thr	His	Phe	Ser	Glu	Leu	Leu	Asp	Glu	Phe	Ser	Gln	Asn	Val	Leu
			35				40					45			
Gly	Gln	Leu	Leu	Asn	Asp	Pro	Phe	Leu	Ser	Glu	Lys	Ser	Val	Ser	Met
		50			55					60					
Glu	Val	Glu	Pro	Ser	Pro	Thr	Ser	Pro	Ala	Pro	Leu	Ile	Gln	Ala	Glu
65				70					75					80	
His	Ser	Tyr	Ser	Leu	Cys	Glu	Glu	Pro	Arg	Ala	Gln	Ser	Pro	Phe	Thr
			85					90						95	
His	Ile	Thr	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Asp	Glu	Val	Glu	Ser	Xaa
			100				105						110		
Arg	Asn	Gly	Thr	Cys	Leu	Gln	Thr	Ser	Leu	Gln	His	Pro	Ser	Arg	Gln
		115				120					125				
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<210> 3411

<211> 958

<212> DNA

<213> Homo sapiens

&lt;400&gt; 3411

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 660  
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 900  
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 958

&lt;210&gt; 3412

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3412

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Pro	Asn	Gln	Lys	Tyr	Ser	Asp	Gln	Thr	Ile	Ser	Cys	Phe	Leu	Asn	Trp
			20					25					30		
Thr	Val	Gly	Lys	Leu	Lys	Thr	His	Leu	Ser	Asn	Val	Tyr	Pro	Ser	Lys
		35					40				45				
Pro	Leu	Thr	Lys	Asp	Gln	Arg	Leu	Val	Tyr	Ser	Gly	Arg	Leu	Leu	Pro
	50					55					60				
Asp	His	Leu	Gln	Leu	Lys	Asp	Ile	Leu	Arg	Lys	Gln	Asp	Glu	Tyr	His
65					70					75				80	
Met	Val	His	Leu	Val	Cys	Thr	Ser	Arg	Thr	Pro	Pro	Ser	Ser	Pro	Lys
				85					90					95	
Ser	Ser	Thr	Asn	Arg	Glu	Ser	His	Glu	Ala	Leu	Ala	Ser	Ser	Ser	Asn

	100		105		110										
Ser	Ser	Ser	Asp	His	Ser	Gly	Ser	Thr	Thr	Pro	Ser	Ser	Gly	Gln	Glu
	115		120		125										
Thr	Leu	Ser	Leu	Ala	Val	Gly	Ser	Ser	Ser	Glu	Gly	Leu	Arg	Gln	Arg
	130		135		140										
Thr	Leu	Pro	Gln	Ala	Gln	Thr	Asp	Gln	Ala	Gln	Ser	His	Gln	Phe	Pro
145			150		155										160
Tyr	Val	Met	Gln	Gly	Asn	Val	Asp	Asn	Gln	Phe	Pro	Gly	Gln	Ala	Ala
			165		170										175
Pro	Pro	Gly	Phe	Pro	Val	Tyr	Pro	Ala							
			180					185							

&lt;210&gt; 3413

&lt;211&gt; 3344

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3413

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1080

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<212> PRT

<213> Homo sapiens

<400> 3414

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		20						25				30			
Tyr	Gly	Cys	Val	Gln	Gln	Pro	Lys	Thr	Gln	Glu	Ser	Lys	Leu	Lys	Ile
		35					40					45			
Gly	Gly	Val	Ser	Ser	Val	Asn	Glu	Arg	Pro	Ile	Ala	Gln	Gln	Leu	Asn
		50				55					60				
Pro	Gly	Phe	Gln	Leu	Ser	Phe	Ala	Ser	Ser	Gly	Pro	Ser	Val	Leu	Leu
65					70					75				80	
Pro	Ser	Val	Pro	Ala	Val	Ala	Ile	Lys	Val	Phe	Cys	Ser	Gly	Cys	Lys
			85						90					95	
Lys	Met	Leu	Tyr	Lys	Gly	Gln	Thr	Ala	Tyr	His	Lys	Thr	Gly	Ser	Thr
		100						105					110		
Gln	Leu	Phe	Cys	Ser	Thr	Arg	Cys	Ile	Thr	Arg	His	Ser	Ser	Pro	Ala
		115					120					125			
Cys	Leu	Pro	Pro	Pro	Pro	Lys	Lys	Thr	Cys	Thr	Asn	Cys	Ser	Lys	Asp
		130					135					140			
Ile	Leu	Asn	Pro	Lys	Asp	Val	Ile	Thr	Thr	Arg	Phe	Glu	Asn	Ser	Tyr
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Pro	Ser	Lys	Asp	Phe	Cys	Ser	Gln	Ser	Cys	Leu	Ser	Ser	Tyr	Glu	Leu
			165						170					175	
Lys	Lys	Lys	Pro	Val	Val	Thr	Ile	Tyr	Thr	Lys	Ser	Ile	Ser	Thr	Lys
			180					185					190		
Cys	Ser	Met	Cys	Gln	Lys	Asn	Ala	Asp	Thr	Arg	Phe	Glu	Val	Lys	Tyr

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  210              215              220
His Ser Thr Asn Asn Leu Thr Thr Asn Cys Cys Glu Asn Cys Gly Ser
  225              230              235              240
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Tyr Ala Leu Gly Lys Ser Leu Arg Ser Ser Ala Glu Met Ile Glu Asn
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  305              310              315              320
Cys His Ser Cys Lys Thr Ser Ala Ile Pro Gln Tyr His Leu Ala Met
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Ser Asp Gly Thr Ile Tyr Ser Phe Cys Ser Ser Ser Cys Val Val Ala
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Phe Gln Asn Val Phe Ser Lys Pro Lys Gly Thr Asn Ser Ser Ala Val
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Pro Leu Ser Gln Gly Gln Val Val Ser Pro Pro Ser Ser Arg Ser
      370              375              380
Ala Val Ser Ile Gly Gly Gly Asn Thr Ser Ala Val Ser Pro Ser Ser
  385              390              395              400
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Gln Gln Val Ala Leu Thr His Thr Val Val Lys Leu Lys Cys Gln His
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Cys Asn His Leu Phe Ala Thr Lys Pro Glu Leu Leu Phe Tyr Lys Gly
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Lys Met Phe Leu Phe Cys Gly Lys Asn Cys Ser Asp Glu Tyr Lys Lys
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Lys Asn Lys Val Val Ala Met Cys Glu Tyr Cys Lys Ile Glu Lys Ile
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Val Lys Glu Thr Val Arg Phe Ser Gly Ala Asp Lys Ser Phe Cys Ser
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Glu Gly Cys Lys Leu Leu Tyr Lys His Asp Leu Ala Lys Arg Trp Gly
      500              505              510
Asn His Cys Lys Met Cys Ser Tyr Cys Ser Gln Thr Ser Pro Asn Leu
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Val Gln Asn Arg Leu Glu Gly Lys Leu Glu Glu Phe Cys Cys Glu Asp
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Cys Met Ser Lys Phe Thr Val Leu Phe Tyr Gln Met Ala Lys Cys Asp
  545              550              555              560
Gly Cys Lys Arg Gln Gly Lys Leu Ser Glu Ser Ile Lys Trp Arg Gly
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Asn Ile Lys His Phe Cys Asn Leu Phe Cys Val Leu Glu Phe Cys His
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Gln Gln Ile Met Asn Asp Cys Leu Pro Gln Asn Lys Val Asn Ile Ser
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&lt;210&gt; 3416

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3416

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      180              185              190
Trp Lys Thr Arg Gln Leu Gln Ser Lys Leu His Glu Ala Asp Ile Val
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Val Leu Gly Ser Pro Lys Pro Glu Glu Ile Pro Leu Thr Trp Ile Gln
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Lys Met Met

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&lt;210&gt; 3417

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3417

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&lt;210&gt; 3418

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3418

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Ile Phe Arg Ser Leu His Thr Leu Val Gly Gln Leu Asp Leu Arg Asp
      35      40      45
Asp Val Val Lys Ile Thr Ile Asp Trp Asn Lys Leu Gln Ser Leu Ser
50      55      60
Ala Phe Gln Pro Ala Leu Leu Phe Ser Ala Leu Glu Gln His Ile Leu

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<210> 3419  
<211> 418  
<212> DNA  
<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

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35 40 45  
Cys Asp Thr Val Ala Leu Glu Ser Thr Thr Leu Arg Gly Thr Thr Arg  
50 55 60  
Glu Val Thr Arg Arg Ser Pro Ile Asn Met Lys His Pro Glu Gln Gly  
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<210> 3421  
<211> 2988  
<212> DNA  
<213> Homo sapiens

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&lt;210&gt; 3422

&lt;211&gt; 418

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3422

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<211> 1851
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3423

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 gctgcagctt ccacctagca gccaccagag gttacaaggg gagagtggcc cttccctcac  
 1680  
 aagtccgaca tctccaggcc ccactgaac tccggggacc tctactgact gcttgctggg  
 1740  
 acagtccacca ggggtggggg gaagggccac aaaatgaaac cattaaagac ccttaagagc  
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 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a  
 1851

<210> 3424

<211> 136

<212> PRT

<213> Homo sapiens

<400> 3424

Met	Leu	Trp	Pro	Gln	Val	Phe	Ser	Glu	Leu	Gly	Phe	Pro	Pro	Ala	Val
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Gln	Arg	Trp	Val	Ile	Gly	Arg	Cys	Leu	Cys	Val	Pro	Glu	Arg	Ser	Leu
			20					25					30		
Ala	Ser	Tyr	Gly	Val	Arg	Gln	Asp	Gly	Asp	Pro	Ala	Phe	Leu	Tyr	Leu
			35				40					45			
Leu	Ser	Ala	Pro	Arg	Glu	Ala	Pro	Ala	Thr	Gly	Pro	Ser	Pro	Gln	His
	50				55						60				
Pro	Gln	Lys	Met	Asp	Gly	Glu	Leu	Gly	Arg	Leu	Phe	Pro	Pro	Ser	Leu
65				70					75					80	
Gly	Leu	Pro	Pro	Gly	Pro	Gln	Pro	Ala	Ala	Ser	Ser	Leu	Pro	Ser	Pro
			85					90					95		
Leu	Gln	Pro	Ser	Trp	Ser	Cys	Pro	Ser	Cys	Thr	Phe	Ile	Asn	Ala	Pro
			100					105					110		
Asp	Arg	Pro	Gly	Cys	Glu	Met	Cys	Ser	Thr	Gln	Arg	Pro	Cys	Thr	Trp
	115					120						125			
Asp	Pro	Leu	Ala	Ala	Ala	Ser	Thr								
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<210> 3425

<211> 1416

<212> DNA

<213> Homo sapiens

<400> 3425

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 120  
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 180  
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 240  
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 300



gaatgcggct tctgctactg ccgccgccat gccgaggcgc acaggcagaa gttcctcagt  
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 420  
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 480  
 gcaggggaag agagtgagtc ggaggaagag agcgagtcag aggaagagag cgagacagag  
 540  
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 600  
 gatgagcaag aaagcgaggc cgaagaagac aaccaagaag aaggggaatc cgaggcggag  
 660  
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 720  
 gccaaagagga agtgtccgga ccatgggctt gatttgagta cctattgcc aagaatagg  
 780  
 cagctcatct gtgtcctgtg tccagtcatt ggggctcacc agggccacca actctccacc  
 840  
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 960  
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 1416

&lt;210&gt; 3426

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3426

Ser	Gly	Gly	Lys	Gly	Leu	Cys	Cys	Cys	Ala	Arg	Ala	Gly	Ala	Ala	Ala
1				5					10				15		
Ala	Pro	Gly	Pro	Ala	Ser	Arg	Arg	Gly	Ala	Val	Gln	Ala	Gly	Gly	Asp
			20					25				30			
Ser	Leu	Gly	Arg	Asp	Pro	Gly	Arg	Glu	Glu	Glu	Val	Arg	Pro	Arg	Gly
		35				40					45				
Arg	Lys	Ala	Ala	Ser	Pro	Gly	Ala	Pro	Arg	Pro	Trp	Pro	Arg	His	Ser
	50					55				60					
Thr	His	Met	Ala	Ser	Gly	Val	Gly	Ala	Ala	Phe	Glu	Glu	Leu	Pro	His

```

65          70          75          80
Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala Pro Gly Ala Glu
      85          90          95
Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg Arg His Ala Glu
      100          105          110
Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala Glu Tyr Val His
      115          120          125
Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu Gly Ala Gly Lys
      130          135          140
Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu Ile Glu Ser Glu
145          150          155          160
Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu Ser Glu Glu Glu
      165          170          175
Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp Glu Glu Ser Glu
      180          185          190
Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu Ser Glu Ala Glu
      195          200          205
Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu Gly Glu Thr Glu
      210          215          220
Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu Ala Glu Arg Val
225          230          235          240
Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu Ser Thr Tyr Cys
      245          250          255
Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro Val Ile Gly Ala
      260          265          270
His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala Phe Glu Glu Leu
      275          280          285
Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met Ile Glu Leu Val
      290          295          300
Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val Thr Arg Asp Gln
305          310          315          320
Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val Gln Lys Val Ile
      325          330          335
Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp Ile Gln Glu Ala
      340          345          350
Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp Ile Gln Ser His
      355          360          365
Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys Glu Gln Leu Asp
      370          375          380
Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly Asp Glu Glu Gly
385          390          395          400
Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
      405          410

```

&lt;210&gt; 3427

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3427

ggatccccc tcttcaaaat tgtagacgcg tctccgagtc ctttcactca tcggaggctg

60

ccggatttca atgtcatagt tcccattgtc aatgacatca tcggagaact tgacctgctg

120

gggctctggat tgagacttgg accttctgag cactggcaga tgtactggct tctcttcagg  
 180  
 caggatcttc tctggacaca actctgaact tagactcttt aaggactctg cactcctgtg  
 240  
 cagcatggaa gaggatcaaag ttcccatatt gctcatcttc tcacaatctt ctgtttccat  
 300  
 ctctcaaaaa ttttgcagag aatacaatga tggccttggc ttgttttctc catccaccga  
 360  
 agcccctgtg atattggaca atgccaaga atccatcgaa tcccgaacac ttgctctgg  
 420  
 tttcaggtct gacagacact ccagggaatc ttcataccac tgtgtttcat catgattata  
 480  
 ccctgaagcc ccatgggtcca gttccaattc ctgaagcctt ctactgcttg cagggcctgg  
 540  
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 580

<210> 3428

<211> 132

<212> PRT

<213> Homo sapiens

<400> 3428

Met	Asp	Ser	Leu	Ala	Leu	Ser	Asn	Ile	Thr	Gly	Ala	Ser	Val	Asp	Gly
1			5						10				15		
Glu	Asn	Lys	Pro	Arg	Pro	Ser	Leu	Tyr	Ser	Leu	Gln	Asn	Phe	Glu	Glu
			20					25					30		
Met	Glu	Thr	Glu	Asp	Cys	Glu	Lys	Met	Ser	Asn	Met	Gly	Thr	Leu	Asn
			35				40					45			
Ser	Ser	Met	Leu	His	Arg	Ser	Ala	Glu	Ser	Leu	Lys	Ser	Leu	Ser	Ser
			50				55				60				
Glu	Leu	Cys	Pro	Glu	Lys	Ile	Leu	Pro	Glu	Glu	Lys	Pro	Val	His	Leu
65					70					75				80	
Pro	Val	Leu	Arg	Arg	Ser	Lys	Ser	Gln	Ser	Arg	Pro	Gln	Gln	Val	Lys
			85					90					95		
Phe	Ser	Asp	Asp	Val	Ile	Asp	Asn	Gly	Asn	Tyr	Asp	Ile	Glu	Ile	Arg
			100					105					110		
Gln	Pro	Pro	Met	Ser	Glu	Arg	Thr	Arg	Arg	Arg	Val	Tyr	Asn	Phe	Glu
			115				120					125			
Glu	Arg	Gly	Ser												
			130												

<210> 3429

<211> 634

<212> DNA

<213> Homo sapiens

<400> 3429

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 120  
 gtcagcttcc ttttcatact ttcccgcggt tctctccacg agcaggtgca ccagggacct  
 180

gtccctctgt cctacacggt caccacagt acgacccaag gcttcccctt gcctacaggc  
 240  
 cagcacatcc ctggctgcag tgcccagcag ctcccagcat gctccgtgat gttcagtggg  
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 360  
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 420  
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 540  
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 600  
 ttgaaacact ctattacaa atgtgaacac gcgt  
 634

&lt;210&gt; 3430

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3430

Phe	Leu	Leu	Arg	Val	Ala	Leu	Ala	Val	Ser	Phe	Leu	Phe	Ile	Leu	Ser
1				5					10					15	
Arg	Arg	Ser	Leu	His	Glu	Gln	Val	His	Gln	Gly	Pro	Val	Pro	Leu	Ser
			20					25					30		
Tyr	Thr	Val	Thr	Thr	Val	Thr	Thr	Gln	Gly	Phe	Pro	Leu	Pro	Thr	Gly
		35					40					45			
Gln	His	Ile	Pro	Gly	Cys	Ser	Ala	Gln	Gln	Leu	Pro	Ala	Cys	Ser	Val
	50					55					60				
Met	Phe	Ser	Gly	Gln	His	Tyr	Pro	Leu	Cys	Cys	Leu	Pro	Pro	Pro	Leu
65					70					75					80
Ile	Gln	Ala	Cys	Thr	Met	Gln	Gln	Leu	Pro	Val	Pro	Tyr	Gln	Ala	Tyr
				85				90					95		
Pro	His	Leu	Ile	Ser	Ser	Asp	His	Tyr	Ile	Leu	His	Pro	Pro	Pro	Pro
			100					105					110		
Gly	Thr	His	Pro	Ala	Ala	Pro	Gly	Ser	Val						
			115				120								

&lt;210&gt; 3431

&lt;211&gt; 1396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3431

tgcagctcgg cctctgctgc ctgccggtgc tcttcgtggc tctgggcatg gcatcggacc  
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 ccattctcac gctggcgccc ccgctgcatt gccactacgg ggccttcccc cctaagtcc  
 120  
 ctgcgtggga gcagcgtccc aatgccagcg cgtcacgtcg ccagcgctgc cctagcacgc  
 180  
 agcgcgcca gccgtgtcgc caacagtacc aaatcgctcg gcagcgggctt cgccccgccg  
 240

gacttcaacc attgcctcaa ggattgggac tataatggcc ttctgtgct caccaccaac  
 300  
 gccatcgccc agtgggatct ggtgtgtgac ctgggctggc aggtgatcct ggagcagatc  
 360  
 ctcttcatct tgggctttgc ctccggctac ctgttcctgg gttaccccgc agacagattt  
 420  
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 480  
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 720  
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 1260  
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 1320  
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 1380  
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 1396

&lt;210&gt; 3432

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3432

Met Ala Leu Arg Phe Leu Leu Gly Phe Leu Leu Ala Gly Val Asp Leu  
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 Gly Val Tyr Leu Met Arg Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu  
 20 25 30  
 Arg Val Ala Leu Ala Gly Glu Leu Val Gly Val Gly Gly His Phe Leu  
 35 40 45  
 Phe Leu Gly Leu Ala Leu Val Ser Lys Asp Trp Arg Phe Leu Gln Arg

50	55	60
Met Ile Thr Ala Pro Cys Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly		
65	70	75
Leu Phe Leu Glu Ser Ala Arg Trp Leu Ile Val Lys Arg Gln Ile Glu		80
	85	90
Glu Ala Gln Ser Val Leu Arg Ile Leu Ala Glu Arg Asn Arg Pro His		95
	100	105
Gly Gln Met Leu Gly Glu Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu		110
	115	120
Asn Thr Cys Pro Leu Pro Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu		125
	130	135
Leu Asn Tyr Arg Asn Ile Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr		140
	145	150
Asn Phe Ile Ala His Ala Ile Arg His Cys Tyr Gln Pro Val Gly Gly		155
	165	170
Gly Gly Ser Pro Ser Asp Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly		175
	180	185
Thr Ala Ala Leu Ala Cys Val Phe Leu Gly Val Thr Val Asp Arg Phe		190
	195	200
Gly Arg Arg Gly Ile Leu Leu Ser Met Thr Leu Thr Gly Ile Ala		205
	210	215
Ser Leu Val Leu Leu Gly Leu Trp Asp Cys Glu His Pro Ile Phe Pro		220
	225	230
Thr Val Trp Ala Gln Gln Gly Asn Pro Asn Arg Asp Leu Asn Glu Ala		235
	245	250
Ala Ile Thr Thr Phe Ser Val Leu Gly Leu Phe Ser Ser Gln Ala Ala		255
	260	265
Ala Ile Leu Ser Thr Leu Leu Ala Glu Val Ile Pro Thr Thr Val		270
	275	280
Arg Gly Arg Gly Leu Gly Leu Ile		285
	290	295

&lt;210&gt; 3433

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3433

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 120  
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 180  
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 300  
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 480

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 540  
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<210> 3434

<211> 311

<212> PRT

<213> Homo sapiens

<400> 3434

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Arg	Pro	Ser	Ser	Val	Pro	Pro	Ser	Pro	Ser	Pro	Arg	Pro	Leu	Pro	Gly
			20					25					30		
Gly	Arg	Gln	Arg	Pro	Gln	Arg	Pro	Ser	His	Ser	Arg	Ser	His	Thr	Arg
			35				40					45			
Ser	Asn	Leu	Lys	Arg	Asp	Val	Ala	His	Leu	Tyr	Arg	Gly	Val	Gly	Ser
50						55				60					
Arg	Tyr	Ile	Met	Gly	Ser	Gly	Glu	Ser	Phe	Met	Gln	Leu	Gln	Gln	Arg
65					70				75					80	
Leu	Leu	Arg	Glu	Lys	Glu	Ala	Lys	Ile	Arg	Lys	Ala	Leu	Asp	Arg	Leu
			85					90						95	
Arg	Lys	Lys	Arg	His	Leu	Leu	Arg	Arg	Gln	Arg	Thr	Arg	Arg	Glu	Phe
			100					105						110	
Pro	Val	Ile	Ser	Val	Val	Gly	Tyr	Thr	Asn	Cys	Gly	Glu	His	Ala	Pro
			115				120					125			
Arg	Gly	Gly	Ala	Phe	Arg	Gly	Leu	Arg	Val	Thr	Gly	Glu	Asp	Ser	Pro
			130				135				140				
Gly	Gly	Gly	Gln	Gly	Val	Pro	Val	Val	Ser	Val	Val	Pro	Tyr	Asp	Ser
145					150				155					160	
Cys	Gly	Glu	His	Val	Pro	Arg	Arg	Gly	Gly	Ser	His	Gly	Arg	Arg	Val

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<210> 3435
<211> 1225
<212> DNA
<213> Homo sapiens
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180
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300
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360
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420
gatgttcgtc tccgaggggt caagatcaag tcatctagac agcgggaact aggggtgaat
480
gcagacctgt tccagccaac tagtctggtg cgatatccac gcctagaagg caccgacctt
540
gaagtactgt accgcagagc tgtcctcctg cagagattca tcaagatcct cgatagtgtc
600
ctgcaccacc tgggtacctg ctgggaccac aactgggca ctttcagtga gattaagcaa
660
gtgaagcagt tcctactgct gtcccgccag cggccaggcc tgggtggctca gtgcctgcgt
720
gactctgaga gcagcaagcc cagcttcatg ccacgcctat acatcaaccg ccgtcttgcc
780
atggaacacc gtgectgccc ctctcgagac cctgcctgca agaatgcagt cttcaccag
840

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&lt;210&gt; 3436

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3436

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		20						25					30		
Glu	Phe	Asn	Val	Ser	Cys	Leu	Thr	Asp	Ser	Asn	Ala	Asp	Thr	Tyr	Trp
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		100						105					110		
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	115						120					125			
Glu	Ile	Arg	Ile	Val	Glu	Cys	Arg	Asp	Asp	Gly	Ile	Asp	Val	Arg	Leu
	130					135					140				
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Ala	Asp	Leu	Phe	Gln	Pro	Thr	Ser	Leu	Val	Arg	Tyr	Pro	Arg	Leu	Glu
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&lt;210&gt; 3437

&lt;211&gt; 2081

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3437

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<211> 105

<212> PRT

<213> Homo sapiens

<400> 3438

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Glu	Ala	Glu	Pro	Gln	Trp	Glu	Arg	Glu	Gly	Ala	Arg	Phe	Thr	Thr	Pro

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<211> 287

<212> PRT

<213> Homo sapiens

<400> 3440

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Val	Ala	Ala	Ala	Ala	Arg	Trp	Pro	Arg	Gln	Pro	Arg	His	Pro	Arg	His
			35				40					45			
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Arg	Arg	Pro	Arg	Xaa	Pro	Gly	Gly	Pro	Gln	His	His	Gln	Pro	Gln	Pro
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Pro	Leu	Trp	Thr	Pro	Thr	Pro	Pro	Ser	Pro	Ala	Ser	Asp	Trp	Pro	Pro
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Leu	Pro	Pro	Asn	Arg	Pro	Pro	Gln	Asn	Pro	Gly	Pro	Thr	Leu	Pro	Trp
			100				105						110		
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Phe	Leu	Ser	Ala	Pro	Leu	Val	Pro	Arg	Ser	Pro	Gly	Gly	Glu	Ser	Ala
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Asp	Ser	Ser	Gln	Ala	Gly	Thr	Arg	Leu	Val	Pro	Glu	His	Ala	Ala	Ala
			165				170						175		
His	Thr	Gln	Gly	His	Gly	Pro	Ser	Gly	Pro	Gly	Thr	Trp	Ser	Gly	Ser
			180				185						190		
Glu	Arg	Pro	Gly	Cys	Leu	Ala	Asp	Arg	Thr	Ser	Glu	Thr	Thr	Gln	Pro
		195				200					205				
Ser	Phe	Glu	Asp	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Gly	Val	Pro	Trp	Arg
		210				215					220				
Thr	Thr	Leu	Ala	Glu	Thr	Leu	Leu	Ile	Pro	Gly	Leu	Glu	Leu	Leu	Gly
225					230				235					240	
Gly	Arg	Gln	Ala	Ser	Thr	Pro	Thr	Leu	Gly	Asn	Ala	Glu	Pro	Leu	Arg
			245				250						255		
Met	Cys	Ala	Arg	Gly	Arg	Val	Cys	Val	Phe	Leu	Arg	Val	Ser	Leu	Phe

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&lt;210&gt; 3441

&lt;211&gt; 2074

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3441

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<211> 374

<212> PRT

<213> Homo sapiens

<400> 3442

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&lt;210&gt; 3443

&lt;211&gt; 2070

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3443

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1560  
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gctaaccctt gggaccggaa agtagtggtc tacttagtgg acacatcgtt gccagacacc  
1680  
gatacctgga ttcattgatt tatgtcagag tatctgatag agctttcaaa agttaattaa  
1740  
tgactgcctc tgaaaccttg acaactaatt cagatttttt agcaataaca aaatgtagta  
1800  
ggcttaaaaa aaatcttaac tctgtacat ggctctgact gctgtggggg attgaaaaga  
1860  
atatgcttat gtttgatgaa agatatttaa caagttttgt ttaacagag ttgacttttc  
1920  
aaagaaaatt gtacttgaat tattactata atattagaat aaaaatgttt atcaatataa  
1980  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
2040  
aaaaaaaaaa aaaaaaaaaa aaaaaagggg  
2070

&lt;210&gt; 3444

&lt;211&gt; 579

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3444

```

Leu Ala Val Asn Ala Glu Glu Asp Ala Trp Leu Arg Ala Gln Val Ile
 1           5           10           15
Ser Thr Glu Glu Asn Lys Ile Lys Val Cys Tyr Val Asp Tyr Gly Phe
          20           25           30
Ser Glu Asn Val Glu Lys Ser Lys Ala Tyr Lys Leu Asn Pro Lys Phe
          35           40           45
Cys Ser Leu Ser Phe Gln Ala Thr Lys Cys Lys Leu Ala Gly Leu Glu
          50           55           60
Val Leu Ser Asp Asp Pro Asp Leu Val Lys Val Val Glu Ser Leu Thr
          65           70           75           80
Cys Gly Lys Ile Phe Ala Val Glu Ile Leu Asp Lys Ala Asp Ile Pro
          85           90           95
Leu Val Val Leu Tyr Asp Thr Ser Gly Glu Asp Asp Ile Asn Ile Asn
          100          105          110
Ala Thr Cys Leu Lys Ala Ile Cys Asp Lys Ser Leu Glu Val His Leu
          115          120          125
Gln Val Asp Ala Met Tyr Thr Asn Val Lys Ile Thr Asn Ile Cys Ser
          130          135          140
Asp Gly Thr Leu Tyr Cys Gln Val Pro Cys Lys Gly Leu Asn Lys Leu
          145          150          155          160
Ser Asp Leu Leu Arg Lys Ile Glu Asp Tyr Phe His Cys Lys His Met
          165          170          175
Thr Ser Glu Cys Phe Val Ser Leu Pro Phe Cys Gly Lys Ile Cys Leu
          180          185          190
Phe His Cys Lys Gly Lys Trp Leu Arg Val Glu Ile Thr Asn Val His
          195          200          205
Ser Ser Arg Ala Leu Asp Val Gln Phe Leu Asp Ser Gly Thr Val Thr
          210          215          220
Ser Val Lys Val Ser Glu Leu Arg Glu Ile Pro Pro Arg Phe Leu Gln
          225          230          235          240
Glu Met Ile Ala Ile Pro Pro Gln Ala Ile Lys Cys Cys Leu Ala Asp
          245          250          255
Leu Pro Gln Ser Ile Gly Met Trp Thr Pro Asp Ala Val Leu Trp Leu
          260          265          270
Arg Asp Ser Val Leu Asn Cys Ser Asp Cys Ser Ile Lys Val Thr Lys
          275          280          285
Val Asp Glu Thr Arg Gly Ile Ala His Val Tyr Leu Phe Thr Pro Lys
          290          295          300
Asn Phe Pro Asp Pro His Arg Ser Ile Asn Arg Gln Ile Thr Asn Ala
          305          310          315          320
Asp Leu Trp Lys His Gln Lys Asp Val Phe Leu Ser Ala Ile Ser Ser
          325          330          335
Gly Ala Asp Ser Pro Asn Ser Lys Asn Gly Asn Met Pro Met Ser Gly
          340          345          350
Asn Thr Gly Glu Asn Phe Arg Lys Asn Leu Thr Asp Val Ile Lys Lys
          355          360          365
Ser Met Val Asp His Thr Ser Ala Phe Ser Thr Glu Glu Leu Pro Pro
          370          375          380
Pro Val His Leu Ser Lys Pro Gly Glu His Met Asp Val Tyr Val Pro
          385          390          395          400
Val Ala Cys His Pro Gly Tyr Phe Val Ile Gln Pro Trp Gln Glu Ile

```

```

              405              410              415
His Lys Leu Glu Val Leu Met Glu Glu Met Ile Leu Tyr Tyr Ser Val
              420              425              430
Ser Glu Glu Arg His Ile Ala Val Glu Lys Asp Gln Val Tyr Ala Ala
              435              440              445
Lys Val Glu Asn Lys Trp His Arg Val Leu Leu Lys Gly Ile Leu Thr
              450              455              460
Asn Gly Leu Val Ser Val Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu
465              470              475              480
Val Asn Ile Arg Lys Val Gln Pro Leu Val Asp Met Phe Arg Lys Leu
              485              490              495
Pro Phe Gln Ala Val Thr Ala Gln Leu Ala Gly Val Lys Cys Asn Gln
              500              505              510
Trp Ser Glu Glu Ala Ser Met Val Phe Arg Asn His Val Glu Lys Lys
              515              520              525
Pro Leu Val Ala Leu Val Gln Thr Val Ile Glu Asn Ala Asn Pro Trp
              530              535              540
Asp Arg Lys Val Val Val Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr
545              550              555              560
Asp Thr Trp Ile His Asp Phe Met Ser Glu Tyr Leu Ile Glu Leu Ser
              565              570              575
Lys Val Asn

```

&lt;210&gt; 3445

&lt;211&gt; 2086

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3445

```

nnacgcgtgg cggcagaggg tatccaaggg cggacctggc gcgcaggcgc tgacccgacc
60
tggcagtggc ctggccgagg ccttggtgga gaggccttaa ccccgccggg cggcgcgcg
120
cctgcatgag agttgggccc cggcgggggg tggagcctac tcggggcgac tgcgatggac
180
gccttagaag gagagagctt tgcgctgtct ttctcctccg cctctgatgc agaatttgat
240
gctgtggttg gatatttaga ggacattatc atggatgacg agttccagtt attacagaga
300
aatttcattg acaagtacta cctggagttt gaagacacag aagagaataa actcatctac
360
acacctattt ttaatgaata catttctttg gtagaaaaat acattgaaga acagctgctg
420
cagcggattc ctgagttcaa catggcagcc ttcaccacaa cattacacca tctgttcctg
480
ttgaggcacc ataaggatga agtggtggtg gacatattcg acatgctgct caccttcaca
540
gattttctgg cttttaaaga aatgtttttg gactacagag cagaaaaaga aggccgagga
600
ctggacttaa gcagtggctt agtggtgact tcattgtgca aatcatcttc tctgccagct
660
tccagaaca atctgcggca ctaggtccta cctccagcca atgaatggga tcattctgga
720

```

tgtcaccagc ccaataggct cagctcatga tgacagaaca catcttgga agactgactc  
780  
tgttatgtaa ctcttcattt atgttaagta ttaataggtc aaaacaaaaa tgacctaacc  
840  
ctcctggacc tatttatcct gaaacacctt cttgtattca ttaaccatag tactcctccc  
900  
cacctcaagt agacacctct ctcaggagct tctgagtcag acgcctctgg agcgagccct  
960  
atgtcaggca ctccacctgg ggggcccttc ccagcctac ctgctggtgt gtaagtgtgg  
1020  
actaacccgc cgccaccacc ctctgttcca gcaggctctg catgaatctt tgtgcacttg  
1080  
cacctctttt tcacatgggc cacagtttca gtacttcagc ctcagtgggg ttctgatgt  
1140  
ttatctaggg tgttactcaa gccagtttg agattttgga gtctcctgtg atcacatctt  
1200  
gtctcggctg taggaatcaa cagaaggaga cgtcctctac ataaaagctc catgtgaaaa  
1260  
gctactccta gtcttaacat ttgcagtcct tgtgtcactg tcttctggtc ctgatgtagt  
1320  
cccactgttt ctagaagtct cttttaagca ttatttttga aaaaaaaaaat atttttatag  
1380  
atgaatactc aggctaacct agtggatgtg atcttggaac ttccatgatt atccacttaa  
1440  
agatcaaagt attatatgct gtgtgctttt taggtgtttg ttagtactgt gaaggcaaaa  
1500  
atgcttttcta cattgacatt cattcctatt ttactgggca cctatgaatg tatgtgtgtg  
1560  
gctagaaata gactaaaaca ttttctata gcatgttagt gtgtttgcat gtttgctgaa  
1620  
aatcctttgt gtataaacca gtttgtaagg ttctctgggt taggtaggga ctctgcagtt  
1680  
tcttctgtc aaaatctctc ctaccaagat ggtgttccac tgtccagccc agcatgagta  
1740  
gcaggtagag cacagcttta ctggctgttt gtatgctttg gtttagtgca atgtgtggta  
1800  
gattacttat cagaaaacat atatgtcatc tctagaacga agaaaaagca tagtagttca  
1860  
attcccagtg tgtccctttg attttttttt tttaatagta aaaataagaa tctgtactga  
1920  
cttttcactt ggccattctg gttttaaagg acaagctaca agctctgtgt ttctgtactg  
1980  
atgtgtcact tattaaatac ttttgtacca tgagtaaaac ttcagggtgtt tcgcaagaac  
2040  
caccattctc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa  
2086

&lt;210&gt; 3446

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3446

Met Asp Ala Leu Glu Gly Glu Ser Phe Ala Leu Ser Phe Ser Ser Ala

1	5	10	15
Ser Asp Ala Glu Phe Asp Ala Val Val Gly Tyr Leu Glu Asp Ile Ile			
20	25	30	
Met Asp Asp Glu Phe Gln Leu Leu Gln Arg Asn Phe Met Asp Lys Tyr			
35	40	45	
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro			
50	55	60	
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln			
65	70	75	80
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr			
85	90	95	
Leu His His Leu Phe Arg Leu Arg His His Lys Asp Glu Val Ala Gly			
100	105	110	
Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys			
115	120	125	
Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp			
130	135	140	
Leu Ser Ser Gly Leu Val Thr Ser Leu Cys Lys Ser Ser Ser Leu			
145	150	155	160
Pro Ala Ser Gln Asn Asn Leu Arg His			
165			

&lt;210&gt; 3447

&lt;211&gt; 936

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3447

acgcgtgaag gggttgccggg gaagatggag tatcccgccg cgccacagg gcaggccg

60

gacggcgagg cggccggggc ttacagcagc tcggagttgc tggagggcca ggagccggag

120

ggggtgagct ttgaccgga gagggcgccg cgcctgtggg aagccgtgtc cgggtgccag

180

ccggtgggta gagaggaagt ggagcacatg atccagaaga accaatgtct cttaccaaac

240

accagtgtga aggtttgctg cgccttgett atttctgagt ccagaagct ggcacattac

300

cagagcaaaa aacatgccaa caaagtgaag agatacctag caatccatgg aatggagaca

360

ttaaaggggg aaacgaagaa gctagactca gatcagaaga gcagcagaag caaagacaag

420

aaccagtgtc gcccacatct taacatgacc ttttctccc ctgtcgtggc ccagtcgcac

480

tacctgggga agaccacgc aaagaactta aagctgaagc agcagtcac taagtgga

540

gccttgacc agaatagaga gatgatagac ccagacaagt tctgcagcct ctgccatgca

600

actttcaacg accctgtcat ggctcaacaa cattatgtgg gcaagaaca cagaaaacag

660

gagaccaagc tcaaaactaat ggcacgctat gggcggtgg cgaccctgc tgtcactgac

720

ttccagctg gaaagggcta cccctgcaaa acatgtaaga tagtgctgaa ctccatagaa

780

cagtaccaag ctcatgtcag cggcttcaaa cacaagaacc agtcacacaaa aacagtggca  
 840  
 tcatcccttg gccagattcc aatgcaaagg caacccattc agaaagactc aaccaccttg  
 900  
 gaagactaga ggtgattctg cccagcatcc catatt  
 936

<210> 3448

<211> 302

<212> PRT

<213> Homo sapiens

<400> 3448

Thr	Arg	Glu	Gly	Phe	Ala	Gly	Lys	Met	Glu	Tyr	Pro	Ala	Pro	Ala	Thr
1				5					10					15	
Val	Gln	Ala	Ala	Asp	Gly	Gly	Ala	Ala	Gly	Pro	Tyr	Ser	Ser	Ser	Glu
		20					25					30			
Leu	Leu	Glu	Gly	Gln	Glu	Pro	Asp	Gly	Val	Arg	Phe	Asp	Arg	Glu	Arg
	35					40					45				
Ala	Arg	Arg	Leu	Trp	Glu	Ala	Val	Ser	Gly	Ala	Gln	Pro	Val	Gly	Arg
50					55				60						
Glu	Glu	Val	Glu	His	Met	Ile	Gln	Lys	Asn	Gln	Cys	Leu	Phe	Thr	Asn
65				70					75					80	
Thr	Gln	Cys	Lys	Val	Cys	Cys	Ala	Leu	Leu	Ile	Ser	Glu	Ser	Gln	Lys
		85						90					95		
Leu	Ala	His	Tyr	Gln	Ser	Lys	Lys	His	Ala	Asn	Lys	Val	Lys	Arg	Tyr
	100						105					110			
Leu	Ala	Ile	His	Gly	Met	Glu	Thr	Leu	Lys	Gly	Glu	Thr	Lys	Lys	Leu
	115					120					125				
Asp	Ser	Asp	Gln	Lys	Ser	Ser	Arg	Ser	Lys	Asp	Lys	Asn	Gln	Cys	Cys
130					135				140						
Pro	Ile	Cys	Asn	Met	Thr	Phe	Ser	Ser	Pro	Val	Val	Ala	Gln	Ser	His
145				150					155					160	
Tyr	Leu	Gly	Lys	Thr	His	Ala	Lys	Asn	Leu	Lys	Leu	Lys	Gln	Gln	Ser
	165							170					175		
Thr	Lys	Val	Glu	Ala	Leu	His	Gln	Asn	Arg	Glu	Met	Ile	Asp	Pro	Asp
	180						185					190			
Lys	Phe	Cys	Ser	Leu	Cys	His	Ala	Thr	Phe	Asn	Asp	Pro	Val	Met	Ala
	195					200						205			
Gln	Gln	His	Tyr	Val	Gly	Lys	Lys	His	Arg	Lys	Gln	Glu	Thr	Lys	Leu
210					215						220				
Lys	Leu	Met	Ala	Arg	Tyr	Gly	Arg	Leu	Ala	Asp	Pro	Ala	Val	Thr	Asp
225				230					235					240	
Phe	Pro	Ala	Gly	Lys	Gly	Tyr	Pro	Cys	Lys	Thr	Cys	Lys	Ile	Val	Leu
	245							250					255		
Asn	Ser	Ile	Glu	Gln	Tyr	Gln	Ala	His	Val	Ser	Gly	Phe	Lys	His	Lys
	260						265					270			
Asn	Gln	Ser	Pro	Lys	Thr	Val	Ala	Ser	Ser	Leu	Gly	Gln	Ile	Pro	Met
	275					280						285			
Gln	Arg	Gln	Pro	Ile	Gln	Lys	Asp	Ser	Thr	Thr	Leu	Glu	Asp		
290					295						300				

<210> 3449

<211> 877

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3449

```

ntgatcttca gcaaccatca ccaccggcta cagctgaagg cagctccggc ctcctccaat
60
ccccccggcg ccccggtctt gccgctgcac aattcctccg tgactgccaa ctcccagtec
120
ccggcccttc tggccggcac caaccocgtt gctgtcgtcg cggatggagg cagttgcccc
180
gcacactacc cgggtgcacga gtgcgtcttc aaggggggatg tgaggagact ctcctctctc
240
atccgcacgc acaatatcgg gcagaaagat aatcacggaa atactccttt acaccttgc
300
gtgatgttag gaaataaaga atgtgccccat ttacttttgg ctcacaatgc tccagtcaag
360
gtgaaaaatg ctcagggatg gagccctctg gcggaagcca tcagctatgg agataggcag
420
atgattacag ctcttttgag gaagcttaag cagcaatcca gggaaagtgt tgaagaaaaa
480
cgacctgat tattaagaag cctgaaagag ctagggtgact tttatctaga acttcactgg
540
gattttcaaa gctgggtgcc ttacttttcc cgaattctgc cttccgatgc atgtaaaata
600
tacaacaag gtatcaatat caggcttgac acaactctca tagactttac tgacatgaag
660
tgccaacgag gggatctaag cttcattttc aatggggatg cggcgccctc tgaatctttt
720
gtagtattag acaatgaaca aaaagtttat cagcgaatac atcatgaggc tcacatccca
780
ggaatcagag atggaaacag aagaagaggt ggatatttta atgagcagtg atatttactc
840
tgcaacttta tcaacaaaat caatttcttt cacgcgt
877

```

&lt;210&gt; 3450

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3450

```

Xaa Ile Phe Ser Asn His His His Arg Leu Gln Leu Lys Ala Ala Pro
1           5           10           15
Ala Ser Ser Asn Pro Pro Gly Ala Pro Ala Leu Pro Leu His Asn Ser
20           25           30
Ser Val Thr Ala Asn Ser Gln Ser Pro Ala Leu Leu Ala Gly Thr Asn
35           40           45
Pro Val Ala Val Val Ala Asp Gly Gly Ser Cys Pro Ala His Tyr Pro
50           55           60
Val His Glu Cys Val Phe Lys Gly Asp Val Arg Arg Leu Ser Ser Leu
65           70           75           80
Ile Arg Thr His Asn Ile Gly Gln Lys Asp Asn His Gly Asn Thr Pro
85           90           95
Leu His Leu Ala Val Met Leu Gly Asn Lys Glu Cys Ala His Leu Leu

```

```

      100      105      110
Leu Ala His Asn Ala Pro Val Lys Val Lys Asn Ala Gln Gly Trp Ser
      115      120      125
Pro Leu Ala Glu Ala Ile Ser Tyr Gly Asp Arg Gln Met Ile Thr Ala
      130      135      140
Leu Leu Arg Lys Leu Lys Gln Gln Ser Arg Glu Ser Val Glu Glu Lys
145      150      155      160
Arg Pro Arg Leu Leu Lys Ala Leu Lys Glu Leu Gly Asp Phe Tyr Leu
      165      170      175
Glu Leu His Trp Asp Phe Gln Ser Trp Val Pro Leu Leu Ser Arg Ile
      180      185      190
Leu Pro Ser Asp Ala Cys Lys Ile Tyr Lys Gln Gly Ile Asn Ile Arg
      195      200      205
Leu Asp Thr Thr Leu Ile Asp Phe Thr Asp Met Lys Cys Gln Arg Gly
      210      215      220
Asp Leu Ser Phe Ile Phe Asn Gly Asp Ala Ala Pro Ser Glu Ser Phe
225      230      235      240
Val Val Leu Asp Asn Glu Gln Lys Val Tyr Gln Arg Ile His His Glu
      245      250      255
Ala His Ile Pro Gly Ile Arg Asp Gly Asn Arg Arg Arg Gly Gly Tyr
      260      265      270
Phe Asn Glu Gln
      275

```

&lt;210&gt; 3451

&lt;211&gt; 595

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3451

```

gcattttttac agtttgtata tcccattttc aaggcttcag tggggctgct tagacaaaaa
60
cgatcttcag ggtttacaga atgggtcctc cttaaagctct ctgagccccc gccgtaggta
120
gaaatattca gtaagtagtg ccctgccatt gcaggtttgg atgtccttct gccagcaaaa
180
cccagcatga acctctggct tgtggagatg tcttcagct ggaaacctga gtgagcgaag
240
ttgaactgtg agggcggcac aactgagaga agattctgcc tccgaacct ctgaatgaga
300
gtctgaagga tctgatcttg ggttgcttta cttagtcctt cgtggtattg gtgtgtgtca
360
atgctggagt ccctcagctc cttagctgaa aagagctgaa ggggccttgg aacctggggg
420
agctgcttac tttgcaaggt tttgccagc tgctgctgcg tagctggatg ggactgtctc
480
tcattaactt cctctctggg gctattttct gttgtgttgg tagctatgag cgctcccatc
540
cccccttctt cttttgcagg caggggaacc gcttccattt caactttggg gagag
595

```

&lt;210&gt; 3452

&lt;211&gt; 192

&lt;212&gt; PRT



<213> Homo sapiens

<400> 3452

```

Met Glu Ala Val Pro Leu Pro Ala Lys Glu Glu Arg Gly Met Gly Ala
 1           5           10           15
Leu Ile Ala Thr Asn Thr Thr Glu Asn Ser Thr Arg Glu Glu Val Asn
           20           25           30
Glu Arg Gln Ser His Pro Ala Thr Gln Gln Gln Leu Gly Lys Thr Leu
           35           40           45
Gln Ser Lys Gln Leu Pro Gln Val Pro Arg Pro Leu Gln Leu Phe Ser
           50           55           60
Ala Lys Glu Leu Arg Asp Ser Ser Ile Asp Thr His Gln Tyr His Glu
65           70           75           80
Gly Leu Ser Lys Ala Thr Gln Asp Gln Ile Leu Gln Thr Leu Ile Gln
           85           90           95
Arg Val Arg Arg Gln Asn Leu Leu Ser Val Val Pro Pro Ser Gln Phe
           100          105          110
Asn Phe Ala His Ser Gly Phe Gln Leu Glu Asp Ile Ser Thr Ser Gln
           115          120          125
Arg Phe Met Leu Gly Phe Ala Gly Arg Arg Thr Ser Lys Pro Ala Met
           130          135          140
Ala Gly His Tyr Leu Leu Asn Ile Ser Thr Tyr Gly Arg Gly Ser Glu
145          150          155          160
Ser Phe Arg Arg Thr His Ser Val Asn Pro Glu Asp Arg Phe Cys Leu
           165          170          175
Ser Ser Pro Thr Glu Ala Leu Lys Met Gly Tyr Thr Asn Cys Lys Asn
           180          185          190

```

<210> 3453

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3453

```

nnacgcgtga aggggtcccg ccgcggggct ggcgggctga ggggagaaaa gatggcggcg
60
gcggcggcag ctggtgcggc ctccgggctg ccgggtccag tggcacaagg attaaaggaa
120
gcgttagtg atacgctcac cgggataccta tccccagtac aggaggtgcg ggcggctgct
180
gaagaacaga ttaaggtgct ggaggtgacg gaggaatttg gtgttcactt ggcagaactg
240
actgtagatc cccagggggc actggcaatc cgtcagctgg catcagtcac cttgaaacaa
300
tatgtggaga ctactggtg tgcccaatca gagaaattta ggctcctga aactacagaa
360
agggcaaaaa ttgttatccg ggagctattg cctaattggg tgagagaatc gataagcaaa
420
gtgcgctcca gtgtggccta tgcagtgtca gccattgcc actgggactg gcctgaa
477

```

<210> 3454

<211> 159

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3454

```

Xaa Arg Val Lys Gly Pro Gly Arg Gly Ala Gly Gly Leu Arg Gly Glu
 1           5           10           15
Lys Met Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly
 20           25           30
Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly
 35           40           45
Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile
 50           55           60
Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu
 65           70           75           80
Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val
 85           90           95
Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys
100           105           110
Phe Arg Pro Pro Glu Thr Thr Glu Arg Ala Lys Ile Val Ile Arg Glu
115           120           125
Leu Leu Pro Asn Gly Leu Arg Glu Ser Ile Ser Lys Val Arg Ser Ser
130           135           140
Val Ala Tyr Ala Val Ser Ala Ile Ala His Trp Asp Trp Pro Glu
145           150           155

```

&lt;210&gt; 3455

&lt;211&gt; 4886

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3455

```

nncttcggca caggattgat ccagtcctcc ttccttcact accacatgaa tgctgggcag
60
cccaggatca cactcactgc accctcaact cagaccgtta cctggcacac tggcctcact
120
cttgctcggag actgagctat tggcagtgcc ttcagctctg agctcaggca cctcgaacat
180
tggtttttgtc gttaaggatc ctaaagtgtc gtggggagtg atcacatttt tctcaacatc
240
cctggcccca cctcttctgc cacaacgtc agcatggtgg tatcagccgg ccctttgtcc
300
agcgagaagg cagagatgaa cattctagaa atcaatgaga aattgcgccc ccagttggca
360
gagaagaaac agcagttcag aaacctcaaa gagaaatgtt ttctaactca actggccggc
420
ttcctggcca accgacagaa gaaatacaaa tatgaagagt gtaaagatct cataaaat
480
atgctgagga atgagcgaca gttcaaggag gagaagcttg cagagcagct caagcaagct
540
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600
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<210> 3456

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3456

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Lys	Lys	Gln	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn	
			20				25					30			
Pro	Pro	Cys	Pro	Arg	Leu	Asn	Gly	Val	Leu	Met	Glu	Val	Glu	Glu	Pro
		35					40					45			
Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Met
	50					55					60				
Tyr	Phe	Glu	Leu	Pro	Asp	Ser	Phe	Gln	His	Tyr	Arg	Ser	Val	Phe	Tyr
65					70					75				80	
Ser	Phe	Glu	Glu	Glu	His	Ile	Ser	Phe	Ala	Leu	Tyr	Val	Asp	Asn	Arg
			85						90					95	
Phe	Phe	Thr	Leu	Thr	Val	Thr	Ser	Leu	His	Leu	Val	Phe	Gln	Met	Gly
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 <211> 646  
 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

<400> 3458  
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<210> 3459  
 <211> 592  
 <212> DNA  
 <213> Homo sapiens

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 240  
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<210> 3460

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3460

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Ser	Gly	Pro	Ala	Arg	Ile	Pro	Val	Leu	Pro	Cys	Ser	Pro	Gln	Leu	Pro
			20					25					30		
Gly	Pro	Ser	Leu	Cys	Ala	Ala	Ser	Val	Cys	Leu	Leu	Gln	Asn	Lys	His
			35				40					45			
His	Ala	Pro	Ser	Trp	Ala	Glu	Ala	Pro	Ala	Asp	Ser	Pro	Arg	Ala	Leu
	50					55				60					
Gln	Ala	Cys	Pro	Val	Leu	Cys	Gln	Ala	Gly	Pro	Gly	His	Val	Pro	Ala
65					70					75				80	
Pro	Gly	Ala	Gly	Leu	Gln	Arg	Gly	Gln	Trp	Ser	Ala	Leu	Lys	Thr	Val
			85					90					95		
Ile	Pro	Ala	Arg	Pro	Ala	Leu	Pro	Cys	Ser	Ala	Arg	Gly	Gln	Phe	Glu
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Leu	Lys	Leu													
			115												

<210> 3461

<211> 474

<212> DNA

<213> Homo sapiens

<400> 3461

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 180

ctggaagcca gcatcggggg ggctgggatg ctggcaagcc tctcggggg cactggctc  
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<210> 3462

<211> 101

<212> PRT

<213> Homo sapiens

<400> 3462

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Leu	Leu	Gly	Gly	His	Trp	Leu	Arg	Ala	Gln	Gly	Tyr	Ala	Asn	Pro	Phe
		20					25					30			
Trp	Leu	Ala	Leu	Ala	Leu	Leu	Ile	Ala	Met	Thr	Leu	Tyr	Ala	Ala	Phe
		35					40					45			
Cys	Phe	Gly	Glu	Thr	Leu	Lys	Glu	Pro	Lys	Ser	Thr	Arg	Leu	Phe	Thr
		50				55					60				
Phe	Arg	His	His	Arg	Ser	Ile	Val	Gln	Leu	Tyr	Val	Ala	Pro	Ala	Pro
65					70					75				80	
Glu	Lys	Ser	Arg	Lys	His	Leu	Ala	Leu	Tyr	Ser	Leu	Ala	Ile	Phe	Val
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Val	Ile	Thr	Val	His											
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<210> 3463

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 3463

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&lt;210&gt; 3464

&lt;211&gt; 434

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3464

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 20 25 30  
 Glu Leu Pro Glu Arg Arg Arg Arg Gln Gln Arg Gln Gly Lys His His

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Pro Asn Tyr Leu Met Ala	Asn Glu Arg Met Asn Leu Met Asn Met Ala	
50	55	60
Lys Leu Ser Ile Lys Gly Leu Ile Glu Ser Ala Leu Asn Leu Gly Arg		
65	70	75
Thr Leu Asp Ser Asp Tyr Ala Pro Leu Gln Gln Phe Phe Val Val Met		
85	90	95
Glu His Cys Leu Lys His Gly Leu Lys Ala Lys Lys Thr Phe Leu Gly		
100	105	110
Gln Asn Lys Ser Phe Trp Gly Pro Leu Glu Leu Val Glu Lys Leu Val		
115	120	125
Pro Glu Ala Ala Glu Ile Thr Ala Ser Val Lys Asp Leu Pro Gly Leu		
130	135	140
Lys Thr Pro Val Gly Arg Gly Arg Ala Trp Leu Arg Leu Ala Leu Met		
145	150	155
Gln Lys Lys Leu Ser Glu Tyr Met Lys Ala Leu Ile Asn Lys Lys Glu		
165	170	175
Leu Leu Ser Glu Phe Tyr Glu Pro Asn Ala Leu Met Met Glu Glu Glu		
180	185	190
Gly Ala Ile Ile Ala Gly Leu Leu Val Gly Leu Asn Val Ile Asp Ala		
195	200	205
Asn Phe Cys Met Lys Gly Glu Asp Leu Asp Ser Gln Val Gly Val Ile		
210	215	220
Asp Phe Ser Met Tyr Leu Lys Asp Gly Asn Ser Ser Lys Gly Thr Glu		
225	230	235
Gly Asp Gly Gln Ile Thr Ala Ile Leu Asp Gln Lys Asn Tyr Val Glu		
245	250	255
Glu Leu Asn Arg His Leu Asn Ala Thr Val Asn Asn Leu Gln Ala Lys		
260	265	270
Val Asp Ala Leu Glu Lys Ser Asn Thr Lys Leu Thr Glu Glu Leu Ala		
275	280	285
Val Ala Asn Asn Arg Ile Ile Thr Leu Gln Glu Glu Met Glu Arg Val		
290	295	300
Lys Glu Glu Ser Ser Tyr Ile Leu Glu Ser Asn Arg Lys Gly Pro Lys		
305	310	315
Gln Asp Arg Thr Ala Glu Gly Gln Ala Leu Ser Glu Ala Arg Lys His		
325	330	335
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340	345	350
Met Gln Ile Ser Met Arg Gln Glu Met Glu Leu Ala Met Lys Met Leu		
355	360	365
Glu Lys Asp Val Cys Glu Lys Gln Asp Ala Leu Val Ser Leu Arg Gln		
370	375	380
Gln Leu Asp Asp Leu Arg Ala Leu Lys His Glu Leu Ala Phe Lys Leu		
385	390	395
Gln Ser Ser Asp Leu Gly Val Lys Gln Lys Ser Glu Leu Asn Ser Arg		
405	410	415
Leu Glu Glu Lys Thr Asn Gln Met Ala Ala Thr Ile Lys Gln Leu Glu		
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Gln Arg		

&lt;210&gt; 3465

&lt;211&gt; 2904

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3465

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&lt;210&gt; 3466

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3466

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Gly Arg His Arg Lys Leu Pro Glu Asn Trp Thr Asp Thr Arg Glu Thr
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Leu Leu Glu Gly Met Leu Phe Ser Leu Lys Tyr Leu Gly Met Thr Leu
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Val Glu Gln Pro Lys Gly Glu Glu Leu Ser Ala Ala Ala Ile Lys Arg
          65           70           75           80
Ile Val Ala Thr Ala Lys Ala Ser Gly Lys Lys Leu Gln Lys Val Thr
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Leu Lys Val Ser Pro Arg Gly Ile Ile Leu Thr Asp Asn Leu Thr Asn
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Gln Leu Ile Glu Asn Val Ser Ile Tyr Arg Ile Ser Tyr Cys Thr Ala
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Asp Lys Met His Asp Lys Val Phe Ala Tyr Ile Ala Gln Ser Gln His
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Asn Gln Ser Leu Glu Cys His Ala Phe Leu Cys Thr Lys Arg Lys Met
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Pro Leu Lys Ser Leu Val Ala Thr Gly Asn Leu Leu Asp Leu Glu Glu
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Thr Ala Lys Ala Pro Leu Ser Thr Val Ser Ala Asn Thr Thr Asn Met
          225          230          235          240
Asp Glu Val Pro Arg Pro Gln Ala Leu Ser Gly Ser Ser Val Val Trp
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Glu Leu Asp Asp Gly Leu Asp Glu Ala Phe Ser Arg Leu Ala Gln Ser
          260          265          270
Arg Thr Asn Pro Gln Val Leu Asp Thr Gly Leu Thr Ala Gln Asp Met
          275          280          285
His Tyr Ala Gln Cys Leu Ser Pro Val Asp Trp Asp Lys Pro Asp Ser
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Ser Gly Thr Glu Gln Asp Asp Leu Phe Ser Phe
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&lt;210&gt; 3467

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3467

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180

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<210> 3468

<211> 88

<212> PRT

<213> Homo sapiens

<400> 3468

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			20					25					30		
Trp	Leu	Cys	Tyr	Thr	Ser	Cys	Tyr	Gln	Gln	Asn	Arg	Val	Ser	Leu	Gly
		35				40						45			
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		50				55				60					
Ala	Val	Lys	Leu	Arg	Thr	Lys	Val	Ile	Lys	Ile	Gln	Leu	Tyr	Tyr	Trp
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<210> 3469

<211> 1710

<212> DNA

<213> Homo sapiens

<400> 3469

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&lt;210&gt; 3470

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3470

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Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala
      35           40           45
Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala
      50           55           60
Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys
      65           70           75           80
Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val
      85           90           95
Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe
      100          105          110
Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu
      115          120          125
Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu
      130          135          140
Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val
      145          150          155          160
Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly
      165          170          175
Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln
      180          185          190
Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu
      195          200          205
Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln
      210          215          220
Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr
      225          230          235          240
Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile
      245          250          255
Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr
      260          265          270
Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met
      275          280          285
Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile
      290          295          300
Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser
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Gly Phe

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&lt;210&gt; 3471

&lt;211&gt; 2335

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3471

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<210> 3472

<211> 631

<212> PRT

<213> Homo sapiens

<400> 3472

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Lys	Val	Cys	Val	Ser	Val	Val	Ser	Glu	Lys	Cys	Arg	Ile	Asp	Thr	Glu
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Ile	Leu	Pro	Ser	Leu	Phe	Met	Arg	Cys	Thr	Thr	Asp	Leu	Asn	Arg	Lys
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His	Asp	Gly	Ser	Val	His	Ile	Val	His	Arg	Leu	Ser	Leu	Gln	Thr	Met
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Ala	Val	Phe	Tyr	Ser	Ser	Ala	Ala	Pro	Arg	Pro	Val	Asp	Glu	Pro	Ala
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Met	Lys	Arg	Pro	Arg	Thr	Ala	Gly	Pro	Ala	Val	His	Leu	Lys	Ala	Met
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<210> 3473  
<211> 1660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3473

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 1660

<210> 3474

<211> 474

<212> PRT

<213> Homo sapiens

<400> 3474

Met	Ala	Tyr	Ile	Gln	Leu	Glu	Pro	Leu	Asn	Glu	Gly	Phe	Leu	Ser	Arg
1				5					10					15	
Ile	Ser	Gly	Leu	Leu	Leu	Cys	Arg	Trp	Thr	Cys	Arg	His	Cys	Cys	Gln
			20				25						30		
Lys	Cys	Tyr	Glu	Ser	Ser	Cys	Cys	Gln	Ser	Ser	Glu	Asp	Glu	Val	Glu
			35				40					45			
Ile	Leu	Gly	Pro	Phe	Pro	Ala	Gln	Thr	Pro	Pro	Trp	Leu	Met	Ala	Ser
			50			55					60				
Arg	Ser	Ser	Asp	Lys	Asp	Gly	Asp	Ser	Val	His	Thr	Ala	Ser	Glu	Val
65					70					75				80	
Pro	Leu	Thr	Pro	Arg	Thr	Asn	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Ser	Ser
				85					90					95	
Asp	Thr	Ser	Lys	Ser	Thr	Tyr	Ser	Leu	Thr	Arg	Arg	Ile	Ser	Ser	Leu
			100					105					110		
Glu	Ser	Arg	Arg	Pro	Ser	Ser	Pro	Leu	Ile	Asp	Ile	Lys	Pro	Ile	Glu
			115				120					125			
Phe	Gly	Val	Leu	Ser	Ala	Lys	Lys	Glu	Pro	Ile	Gln	Pro	Ser	Val	Leu
			130				135				140				
Arg	Arg	Thr	Tyr	Asn	Pro	Asp	Asp	Tyr	Phe	Arg	Lys	Phe	Glu	Pro	His
145					150					155				160	
Leu	Tyr	Ser	Leu	Asp	Ser	Asn	Ser	Asp	Asp	Val	Asp	Ser	Leu	Thr	Asp
				165					170					175	
Glu	Glu	Ile	Leu	Ser	Lys	Tyr	Gln	Leu	Gly	Met	Leu	His	Phe	Ser	Thr
			180					185					190		
Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val	Ile	Glu	Ala
			195				200					205			
Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg	Gln	Asp	Met
			210			215					220				
Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro	Asp	Gln	Lys
225					230					235				240	
Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys	Pro	Val	Phe
				245					250					255	
Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala	Gln	Arg	Arg
				260				265					270		
Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser	Arg	His	Cys
			275				280					285			
Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp	Leu	Val	Lys
			290			295					300				
Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln	Asn	Glu	Val
305					310					315				320	
Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro	Ser	Ala	Gly

```

          325          330          335
Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln Thr Asp
          340          345          350
Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val His Gly
          355          360          365
Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly Thr Ile
          370          375          380
Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln Glu Glu
385          390          395          400
Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn Met Lys
          405          410          415
Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr Ser Ser
          420          425          430
Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr His Arg
          435          440          445
Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu Cys Asp
          450          455          460
Arg Val Ser Pro Ala Ser Leu Glu Val Thr
465          470

```

&lt;210&gt; 3475

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3475

```

acgcgtctgaggaggctggtttcttctgcacgcccgcgcgaagctgctctggctggtgctg
60
cagcccttcttctactcactacggcgcctctgcgtccaccccaaggccgtgacccgcatg
120
gaggtgctcaacacgctggtgcagctggcgccgacctggccatctttgcctttggggg
180
ctcaagcccgtaggtctacctgctggccagctccttctctgggctggggcctgcaccccatc
240
tcggggccacttcgtggccgaactacatgttctcaaggccacgagacctactcctac
300
tatggggcctctcaactggatcaccttcaatgtgggctaccacgtggagcaccacgacttc
360
cccagcatcccggtctacaaactgcccgtgtgcggaagatcgcgcccgagtactacgac
420
cacctgcccagcaccactcctgggtgaaggtgctctgggattttgtgtttgaggactcc
480
ctggggccctatgccagggtgaagcgggtgtacata
514

```

&lt;210&gt; 3476

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3476

```

Thr Arg Leu Glu Gly Trp Phe Phe Cys Thr Pro Ala Arg Lys Leu Leu
1          5          10          15
Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro Leu Cys Val

```

```

                20                25                30
His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr Leu Val Gln
      35                40                45
Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu Lys Pro Val
      50                55                60
Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu His Pro Ile
      65                70                75                80
Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys Gly His Glu
      85                90                95
Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe Asn Val Gly
      100                105                110
Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly Tyr Asn Leu
      115                120                125
Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His Leu Pro Gln
      130                135                140
His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe Glu Asp Ser
      145                150                155                160
Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr
      165                170

```

&lt;210&gt; 3477

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3477

```

gcgcgcctcg gctgcctgcc cggcgggtctc cgggtcctcg tccagaccgg ccaccggagc
60
ttgacctcct gcatcgaccc ttccatggga cttaatgaag agcagaaaga atttcaaaaa
120
gtggcctttg actttgctgc ccgagagatg gctccaaata tggcagagtg ggaccagaag
180
gtaggcgttt ttcttgtgct tagacgttct aacaacagat gtctcaggca gacctttatc
240
tttgtctccc gataatgtaa ttgttaaag tctcctccac ttaccaactc ttactgcaag
300
tgagaatacc ggtagtggat gatttttctt agaaggcatc ctgatcatct tgtaca
356

```

&lt;210&gt; 3478

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3478

```

Met Ile Arg Met Pro Ser Arg Lys Asn His Pro Leu Pro Val Phe Ser
  1                5                10                15
Leu Ala Val Arg Val Gly Lys Trp Arg Arg His Leu Thr Ile Thr Leu
      20                25                30
Ser Gly Asp Lys Asp Lys Gly Leu Pro Glu Thr Ser Val Val Arg Thr
      35                40                45
Ser Lys His Lys Lys Asn Ala Tyr Leu Leu Val Pro Leu Cys His Ile
      50                55                60
Trp Ser His Leu Ser Gly Ser Lys Val Lys Gly His Phe Leu Lys Phe

```

```

65              70              75              80
Phe Leu Leu Phe Ile Lys Ser His Gly Arg Val Asp Ala Gly Gly Gln
              85              90              95
Ala Pro Val Ala Gly Leu Asp Glu Asp Pro Glu Thr Ala Gly Gln Ala
              100              105              110
Ala Glu Ala Arg
              115

```

&lt;210&gt; 3479

&lt;211&gt; 797

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3479

```

nctttccaac ccagcctgaa ggggaaagcc acctcggagg acaccctcaa tctaaggaga
60
taccgccggct ctgacaggat catgctgcag aagtggcaga aaagggacat cagcaatttt
120
gagtatctca tgtacctcaa caccgcggtt gggagaacct gcaatgacta catgcagtac
180
ccagtgttcc cctgggtcct cgcagactac acctcagaga cattgaactt ggcaaatccg
240
aagattttcc gggatctttc aaagcccatg ggggctcaga ccaaggaaag gaagctgaaa
300
tttatccaga ggtttaaaga agttgagaaa actgaaggag acatgactgc ccagtgccac
360
tactacaccc actactcctc ggccatcctc gtggcctcct acctggtccg gatgccaccc
420
ttcaccagg ccttctgcgc tctgcagggt agctgctgcc actctctgta cacacacaca
480
cacacacaca cacacacata cgctgtatc acaagactaa gacctgtgct tgaacaaaga
540
caggatgcct ctgctaaaaa cttagtcatt agccagtgat tcccagttga cattggctcc
600
aggattctgg ctcaccagcc aaggcaggct gttcttctc agttacacct gcacatctgc
660
ccaacaaagt cttgcaaaat gattctaaaa aataagaaat gagacatgaa aaaaatgatt
720
taacataaat aagatttagt ggaaaaagaa aaagcaggaa acttgagagac tagaaaggca
780
ggcgggtcaag gattaga
797

```

&lt;210&gt; 3480

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3480

```

Xaa Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser Glu Asp Thr Leu
 1              5              10              15
Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met Leu Gln Lys Trp
              20              25              30
Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met Tyr Leu Asn Thr

```



```
<210> 3481
<211> 1794
<212> DNA
<213> Homo sapiens
```

```
<400> 3481
nncaacgtgg tcaccacctc acgaactata agaagcgtgt ggcagccttg gaagccacgc
60
aaaagcccag cacttcccag agccaggggac tgacacaaca gaaagtctgc aagcaatgcc
120
atgaggtcct gaccagaggg tcttctgcca atgcctccaa gtggtcacca cctcagctct
180
gcagaccctg cggtgctggg agccaccatg gagagtaggt gctacggctg cgctgtcaag
240
ttcaccctct tcaagaagga gtacggctgt aagaattgtg gcaggngctt ctgttcaggc
300
tgctaagct tcagtgcagc agtgcctcgg actgggaaca cccaacagaa agtctgcaag
360
caatgccatg aggtcctgac cagaggggtct tctgccaatg cctccaagtg gtcaccacct
420
cagaactata agaagcgtgt ggcagccttg gaagccaagc aaaagcccag cacttcccag
480
agccaggggac tgacacgaca agaccagatg attgctgagc gcctagcacg actccgccag
540
gagaacaagc ccaagttagt cccctcacag gcagagatag aggcacggct ggctgcccta
600
aaggatgaac gtcagggttc catcccttcc acccaggaaa tggaggcacg acttgcacgc
660
ttgcaggggc gagttctacc ttctcaaacc cccagcccg gcacatcaca caccggacac
720
caggacccaa gcccagcaga cacaggatct gctaacgcag ctggcagctg aggtggctat
780
cgatgaaagc tggaaaggag gaggcccagc tgctctcttc cagaatgatc tcaaccaggg
840
```

tggcccagg agcactaatt ccaagaggca ggccacttgg ttcttggaga aggagaagag  
 900  
 cagactgctg gctgaggcag cacttgagtt gcgggaggag aacacgaggc aggaacggat  
 960  
 tctggccctg gccaagcgac tagccatgct gcggggacag gaccccgaga gagtgacct  
 1020  
 ccaggactat cgctcccag acagtgatga cgacgaggat gaggagacag ccatccaaag  
 1080  
 agtcctgcag cagctcactg aagaagcttc cctggatgag gcaagtggct ttaacatccc  
 1140  
 tgcagagcag gcttctcgac cctggacgca accccgcggg gcagagcctg agggccagga  
 1200  
 tgtggacccc aggcctgagg ctgaggaaga ggagctcccc tgggtgctga tctgcaatga  
 1260  
 ggatgccacc ctacgtgctg ctggctgca tggggacctc ttctgtgccc gctgcttcg  
 1320  
 agagggccat gatgcctttg agcttaaaga gcaccagaca tctgcctact ctctccacg  
 1380  
 tgcaggccaa gagcactgaa gacaccctgg tcctcccga agggcagtcc cacaggcagc  
 1440  
 ggcacccatt tctgggcccc gccacaggac gtccgatggg agagcttgct tggctctact  
 1500  
 gatgatggat agggcccttc ctgagccttg gtgtccctgg aatgaggaaa gattctccat  
 1560  
 tcgagagaat gactgggagg gaagaagtcg gggccctcct attagaagcc cagactggaa  
 1620  
 gtgagaggca tgatggggag agaccagact gaatctacgg gtgagccctg taacctggct  
 1680  
 ctagggcaca ggccctccc ctggcactta gtgggtctaa taaagtatgt tgattcattg  
 1740  
 ggaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa  
 1794

&lt;210&gt; 3482

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3482

Met	Pro	Pro	Ser	Gly	His	His	Leu	Ser	Ser	Ala	Asp	Pro	Ala	Val	Leu
1				5					10					15	
Gly	Ala	Thr	Met	Glu	Ser	Arg	Cys	Tyr	Gly	Cys	Ala	Val	Lys	Phe	Thr
			20					25					30		
Leu	Phe	Lys	Lys	Glu	Tyr	Gly	Cys	Lys	Asn	Cys	Gly	Arg	Xaa	Phe	Cys
		35					40					45			
Ser	Gly	Cys	Leu	Ser	Phe	Ser	Ala	Ala	Val	Pro	Arg	Thr	Gly	Asn	Thr
	50					55				60					
Gln	Gln	Lys	Val	Cys	Lys	Gln	Cys	His	Glu	Val	Leu	Thr	Arg	Gly	Ser
65					70					75				80	
Ser	Ala	Asn	Ala	Ser	Lys	Trp	Ser	Pro	Pro	Gln	Asn	Tyr	Lys	Lys	Arg
				85					90					95	
Val	Ala	Ala	Leu	Glu	Ala	Lys	Gln	Lys	Pro	Ser	Thr	Ser	Gln	Ser	Gln
			100					105					110		
Gly	Leu	Thr	Arg	Gln	Asp	Gln	Met	Ile	Ala	Glu	Arg	Leu	Ala	Arg	Leu

```

      115      120      125
Arg Gln Glu Asn Lys Pro Lys Leu Val Pro Ser Gln Ala Glu Ile Glu
      130      135      140
Ala Arg Leu Ala Ala Leu Lys Asp Glu Arg Gln Gly Ser Ile Pro Ser
145      150      155      160
Thr Gln Glu Met Glu Ala Arg Leu Ala Ala Leu Gln Gly Arg Val Leu
      165      170      175
Pro Ser Gln Thr Pro Gln Pro Gly Thr Ser His Thr Gly His Gln Asp
      180      185      190
Pro Ser Pro Ala Asp Thr Gly Ser Ala Asn Ala Ala Gly Ser
      195      200      205

```

&lt;210&gt; 3483

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3483

```

nccggccgcgg cgcggaacgg cgccctccgc cccaccatgg gcaacagcgc gagccgcaac
60
gacttcgagt gggctctacac cgaccagccg cacacgcagc ggcgcaagga gatactggcc
120
aagtaccggg ccatcaaggc cctgatgcgg ccagaccgcg gcctcaagtg ggcggggctg
180
gtgctggtgc tggctcagat gctggcctgc tggctggtgc gcgggctggc ctggcgctgg
240
ctgctgttct gggcctacgc ctttggtggc tgcgtgaacc actcgtgac gctggccatc
300
cagacatct cgcacaacgc ggccttcggc acggggccgtg cggcacgcaa ccgetggctg
360
gccgtgttcg ccaacctgcc cgtgggtgtg ccctacgccg cctccttcaa gaagtaccac
420
gtggaccacc accgctacct gggcgggcgac ggactggacg tggacgtgcc cacgcgt
477

```

&lt;210&gt; 3484

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3484

```

Met Gly Asn Ser Ala Ser Arg Asn Asp Phe Glu Trp Val Tyr Thr Asp
1      5      10      15
Gln Pro His Thr Gln Arg Arg Lys Glu Ile Leu Ala Lys Tyr Pro Ala
      20      25      30
Ile Lys Ala Leu Met Arg Pro Asp Pro Arg Leu Lys Trp Ala Gly Leu
      35      40      45
Val Leu Val Leu Val Gln Met Leu Ala Cys Trp Leu Val Arg Gly Leu
      50      55      60
Ala Trp Arg Trp Leu Leu Phe Trp Ala Tyr Ala Phe Gly Gly Cys Val
65      70      75      80
Asn His Ser Leu Thr Leu Ala Ile His Asp Ile Ser His Asn Ala Ala
      85      90      95
Phe Gly Thr Gly Arg Ala Ala Arg Asn Arg Trp Leu Ala Val Phe Ala

```

```

          100          105          110
Asn Leu Pro Val Gly Val Pro Tyr Ala Ala Ser Phe Lys Lys Tyr His
          115          120          125
Val Asp His His Arg Tyr Leu Gly Gly Asp Gly Leu Asp Val Asp Val
          130          135          140
Pro Thr Arg
145

```

<210> 3485  
 <211> 812  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3485
tattttattta tagtcacaaa aactgttcag gaagaaatgt tatgaaaaga acatttttac
60
tgcattgctta aaacatttaa ttttctatta tacagttaaa catttgcttg aattcagtga
120
gtctaaaaaaa tcttattgtt ctcaggtag cagttagttg agcagagtc attggtgaag
180
caatctagtt attggcaaatt tctaacacat ggtaagggtgt gggggaaagg atttaaaata
240
acagaaaaaat gtaagtacaa acatacataa cagcaaaata aaactcactt taacaaaaat
300
ttatttaaaa tggtaccccc atatttcctc aatgaccaac ttgtttcagt tttatctccc
360
cctcatccgg ttattttatg tctttttggg aggaaggagg atgaggggtt ttgtttttta
420
acaaaatcac tggcttttta aaaagtgtta ctgcagtcatt ttataagatg catgttatgt
480
ggaagtgata cctgagttgt ttgcattggc aatggaagag gcagcagctc tgaaaggagt
540
atgagtcagg aaaaaaatcc ttcaggaacc ttcaagattg aagaaagaac ttcttttaac
600
attaaagacc aagtattatt ggccagagtc tcttctgaga ttgtgagttt ttcattaact
660
ccttgtgtaa aagtcagtaa aatatcaatg atatcattct gaattttctg ttcattacta
720
tccaaacgac ctgagagggg gatagagcac aggagcatat gtaaagtaac aagcgctgaa
780
ggaacacgca tgcctttaa ctcaaaggat cc
812

```

<210> 3486  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

```

<400> 3486
Met Arg Val Pro Ser Ala Leu Val Thr Leu His Met Leu Leu Cys Ser
1          5          10          15
Ile Pro Leu Ser Gly Arg Leu Asp Ser Asp Glu Gln Lys Ile Gln Asn
20          25          30
Asp Ile Ile Asp Ile Leu Leu Thr Phe Thr Gln Gly Val Asn Glu Lys

```

```

          35              40              45
Leu Thr Ile Ser Glu Glu Thr Leu Ala Asn Asn Thr Trp Ser Leu Met
          50              55              60
Leu Lys Glu Val Leu Ser Ser Ile Leu Lys Val Pro Glu Gly Phe Phe
65          70          75          80
Ser Gly Leu Ile Leu Leu Ser Glu Leu Leu Pro Leu Pro Leu Pro Met
          85          90          95
Gln Thr Thr Gln Val Ser Leu Pro His Asn Met His Leu Ile Asn Asp
          100          105          110
Cys Ser Asn Thr Phe
          115

```

&lt;210&gt; 3487

&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3487

```

nnattgtatc aaaatcctag atttgaataa cttattatct taaataatca gtaactaaaa
60
ccaagcaatc catcacacaa agaggggaaa gggtaatat ctgagttata aattttttac
120
cctgtctgat aaaaatagaa gcctgaaagt ttaaattttt cctggattta aatttaaaga
180
taaatttggt tttcagtga atactctcaa tagcaatttt accaaagagg ctttcttctg
240
aaggccacct ctgaaataat tagaggataa atgtcaatgg catgatatta agatattact
300
tggccaggcg tggtcgtcac gcgtgtaatc ccagcacttt gggaggccga ggcagggtgga
360
tcacgaggtc aagaaatcga gaccagcctg gctaacacag tgaaaccccg tctcattctg
420
agcttcttga caccttttaa tccagtcact gaaattagca tctgcaccta gaaagaaaaa
480
actgactata acatcactca tctgcacaac ctattaatca gcaaatactt actgaatacc
540
tactacatcc caggcagtgt tctaggcact ggggagtcgg cagcgaacaa aacctgtctt
600
aacagacctt atcaccaact ctactatagt tataaacata ccaatagttt aacatttagt
660
tgtaaatcat gaaacatttt gatattttta aaattttaac tacagtcaac ctttaattca
720
cagatacaaa taatctgcat ttcccccaat cccgctgctc ttagagaagc tt
772

```

&lt;210&gt; 3488

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3488

```

Asp Ile Thr Trp Pro Gly Val Val Val Thr Arg Val Ile Pro Ala Leu
1          5          10          15
Trp Glu Ala Glu Ala Gly Gly Ser Arg Gly Gln Glu Ile Glu Thr Ser

```

```

                20                25                30
Leu Ala Asn Thr Val Lys Pro Arg Leu Ile Leu Ser Phe Leu Thr Pro
                35                40                45
Phe Asn Pro Val Thr Glu Ile Ser Ile Cys Thr
                50                55

```

<210> 3489  
 <211> 288  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3489
tagctaacac tccactatgg gagcccatct cctcccaggg ccagggagac cagggagacc
60
agggagacca ggtctggccc ccaactctaa ggctcatctt agaggcgaga ttcaggccca
120
gcccgagggtg ccccatgagg cctggtggtt ggaggcagag ggtatccctt gcccaaattc
180
gtgccacatt cacagtcaact gggaaagcta cggggatggg ccgggcgcgg tggctcacac
240
ctgtaatccc agcactttgg agagccccaa gacgacggat cacgagtc
288

```

<210> 3490  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

```

<400> 3490
Met Gly Ala His Leu Leu Pro Gly Pro Gly Arg Pro Gly Arg Pro Gly
1                5                10                15
Arg Pro Gly Leu Ala Pro Asn Ser Lys Ala His Leu Arg Gly Glu Ile
                20                25                30
Gln Ala Gln Pro Arg Val Pro His Glu Ala Trp Trp Leu Glu Ala Glu
                35                40                45
Gly Ile Pro Cys Pro Asn Ser Cys His Ile His Ser His Trp Glu Ser
                50                55                60
Tyr Gly Asp Gly Pro Gly Ala Val Ala His Thr Cys Asn Pro Ser Thr
65                70                75                80
Leu Glu Ser Pro Lys Thr Thr Asp His Glu
                85                90

```

<210> 3491  
 <211> 568  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3491
gggaaccgac gtccctctgt ggtgaaattc cacccttca cgcctgcat cgccgtagcc
60
gacaaggaca gcatctgctt ttgggactgg gagaaagggg agaagctgga ttatttccac
120
aatgggaacc ctcggtacac gagggtcact gccatggagt atctgaatgg ccaggactgc
180

```

tcgcttctgc tgacggccac agacgatggt gccatcaggg tctggaagaa ttttgctgat  
 240  
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<210> 3492

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3492

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		20						25					30		
Gly	Glu	Lys	Leu	Asp	Tyr	Phe	His	Asn	Gly	Asn	Pro	Arg	Tyr	Thr	Arg
		35					40					45			
Val	Thr	Ala	Met	Glu	Tyr	Leu	Asn	Gly	Gln	Asp	Cys	Ser	Leu	Leu	Leu
	50					55					60				
Thr	Ala	Thr	Asp	Asp	Gly	Ala	Ile	Arg	Val	Trp	Lys	Asn	Phe	Ala	Asp
65					70				75					80	
Leu	Glu	Lys	Asn	Pro	Glu	Met	Val	Thr	Ala	Trp	Gln	Gly	Leu	Ser	Asp
			85						90				95		
Met	Leu	Pro	Thr	Thr	Arg	Gly	Ala	Gly	Met	Val	Val	Asp	Trp	Glu	Gln
		100						105					110		
Glu	Thr	Gly	Leu	Leu	Met	Ser	Ser	Gly	Asp	Val	Arg	Ile	Val	Arg	Ile
		115					120					125			
Trp	Asp	Thr	Asp	Arg	Glu	Met	Lys	Val	Gln	Asp	Ile	Pro	Thr	Gly	Ala
	130					135					140				
Asp	Ser	Cys	Val	Thr	Ser	Leu	Ser	Cys	Asp	Ser	His	Arg	Ser	Leu	Ile
145					150					155				160	
Val	Ala	Gly	Leu	Gly	Asp	Gly	Ser	Ile	Arg	Val	Tyr	Asp	Arg	Arg	Met
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Ala	Leu	Ser	Glu	Cys	Arg	Val	Met	Thr	Tyr	Arg	Glu	His			
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<210> 3493

<211> 2244

<212> DNA

<213> Homo sapiens

<400> 3493

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1680



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<210> 3494

<211> 628

<212> PRT

<213> Homo sapiens

<400> 3494

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			20					25					30		
Ala	Ser	His	His	Ser	Gly	Ser	Asp	Asn	His	Ser	Glu	Arg	Ser	Asp	Asn
		35					40					45			
Arg	Ser	Glu	Ala	Ser	Glu	Arg	Ser	Asp	His	Glu	Asp	Asn	Asp	Pro	Ser
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Asp	Val	Asp	Gln	His	Ser	Gly	Ser	Glu	Ala	Pro	Asn	Asp	Asp	Glu	Asp
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Glu	Gly	His	Arg	Ser	Asp	Gly	Gly	Ser	His	His	Ser	Glu	Ala	Glu	Gly
			85					90						95	
Ser	Glu	Lys	Ala	His	Ser	Asp	Asp	Glu	Lys	Trp	Gly	Arg	Glu	Asp	Lys
			100					105					110		
Ser	Asp	Gln	Ser	Asp	Asp	Glu	Lys	Ile	Gln	Asn	Ser	Asp	Asp	Glu	Glu
		115				120						125			
Arg	Ala	Gln	Gly	Ser	Asp	Glu	Asp	Lys	Leu	Gln	Asn	Ser	Asp	Asp	Asp
	130					135					140				
Glu	Lys	Met	Gln	Asn	Thr	Asp	Asp	Glu	Glu	Arg	Pro	Gln	Leu	Ser	Asp
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Asp	Glu	Arg	Gln	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Ala	Asn	Ser	Asp	Asp
			165					170					175		
Glu	Arg	Pro	Val	Ala	Ser	Asp	Asn	Asp	Asp	Glu	Lys	Gln	Asn	Ser	Asp
		180						185					190		
Asp	Glu	Glu	Gln	Pro	Gln	Leu	Ser	Asp	Glu	Glu	Lys	Met	Gln	Asn	Ser
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Asp	Asp	Glu	Arg	Pro	Gln	Ala	Pro	Asp	Glu	Glu	His	Arg	His	Ser	Asp

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      245              250              255
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      260              265              270
Thr Met Asp Leu Phe Gly Gly Ala Asp Asp Ile Ser Ser Gly Ser Asp
      275              280              285
Gly Glu Asp Lys Pro Pro Thr Pro Gly Gln Pro Val Asp Glu Asn Gly
      290              295              300
Leu Pro Gln Asp Gln Gln Glu Glu Glu Pro Ile Pro Glu Thr Arg Ile
305              310              315              320
Glu Val Glu Ile Pro Lys Val Asn Thr Asp Leu Gly Asn Asp Leu Tyr
      325              330              335
Phe Val Lys Leu Pro Asn Phe Leu Ser Val Glu Pro Arg Pro Phe Asp
      340              345              350
Pro Gln Tyr Tyr Glu Asp Glu Phe Glu Asp Glu Glu Met Leu Asp Glu
      355              360              365
Glu Gly Arg Thr Arg Leu Lys Leu Lys Val Glu Asn Thr Ile Arg Trp
      370              375              380
Arg Ile Arg Arg Asp Glu Glu Gly Asn Glu Ile Lys Glu Ser Asn Ala
385              390              395              400
Arg Ile Val Lys Trp Ser Asp Gly Ser Met Ser Leu His Leu Gly Asn
      405              410              415
Glu Val Phe Asp Val Tyr Lys Ala Pro Leu Gln Gly Asp His Asn His
      420              425              430
Leu Phe Ile Arg Gln Gly Thr Gly Leu Gln Gly Gln Ala Val Phe Lys
      435              440              445
Ala Lys Leu Thr Phe Arg Pro His Ser Thr Asp Ser Ala Thr His Arg
      450              455              460
Lys Met Thr Leu Ser Leu Ala Asp Arg Cys Ser Lys Thr Gln Lys Ile
465              470              475              480
Arg Ile Leu Pro Met Ala Gly Arg Asp Pro Glu Cys Gln Arg Thr Glu
      485              490              495
Met Ile Lys Lys Glu Glu Glu Arg Leu Arg Ala Ser Ile Arg Arg Glu
      500              505              510
Ser Gln Gln Arg Arg Met Arg Glu Lys Gln His Gln Arg Gly Leu Ser
      515              520              525
Ala Ser Tyr Leu Glu Pro Asp Arg Tyr Asp Glu Glu Glu Glu Gly Glu
      530              535              540
Glu Ser Ile Ser Leu Ala Ala Ile Lys Asn Arg Tyr Lys Gly Gly Ile
545              550              555              560
Arg Glu Glu Arg Ala Arg Ile Tyr Ser Ser Asp Ser Asp Glu Gly Ser
      565              570              575
Glu Glu Asp Lys Ala Gln Arg Leu Leu Lys Ala Lys Lys Leu Thr Ser
      580              585              590
Asp Glu Glu Gly Glu Pro Ser Gly Lys Arg Lys Ala Glu Asp Asp Asp
      595              600              605
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Glu Asp Asp Asp
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<210> 3495  
 <211> 1085  
 <212> DNA  
 <213> Homo sapiens

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 180  
 aagaaccgg atgagggcga gaagtttaaa ctcatatccc aggcataatga agtgctttca  
 240  
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 360  
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 420  
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 480  
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 960  
 aagcacgggg acctgagatg cgtgcgcgat gaaggaatgc ccatctacaa agcaccctg  
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<210> 3496  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 3496  
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Asp Gln Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ser Gly Ser Pro
65      70      75      80
Ser Phe Ser Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly
      85      90      95
Gly Arg Met Ala Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu
      100      105      110
Ser Val Thr Leu Glu Asp Leu Tyr Asn Gly Val Thr Lys Lys Leu Ala
      115      120      125
Leu Gln Lys Asn Val Ile Cys Glu Lys Cys Glu Gly Val Gly Gly Lys
      130      135      140
Lys Gly Ser Val Glu Lys Cys Pro Leu Cys Lys Gly Arg Gly Met Gln
145      150      155      160
Ile His Ile Gln Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Thr
      165      170      175
Val Cys Ile Glu Cys Lys Gly Gln Gly Glu Arg Ile Asn Pro Lys Asp
      180      185      190
Arg Cys Glu Ser Cys Ser Gly Ala Lys Val Ile Arg Glu Lys Lys Ile
      195      200      205
Ile Glu Val His Val Glu Lys Gly Met Lys Asp Gly Gln Lys Ile Leu
      210      215      220
Phe His Gly Glu Gly Asp Gln Glu Pro Glu Leu Glu Pro Gly Asp Val
225      230      235      240
Ile Ile Val Leu Asp Gln Lys Asp His Ser Val Phe Gln Arg Arg Gly
      245      250      255
His Asp Leu Ile Met Lys Met Lys Ile Gln Leu Ser Glu Ala Leu Cys
      260      265      270
Gly Phe Lys Lys Thr Ile Lys Thr Leu Asp Asn Arg Ile Leu Val Ile
      275      280      285
Thr Ser Lys Ala Gly Glu Val Ile Lys His Gly Asp Leu Arg Cys Val
      290      295      300
Arg Asp Glu Gly Met Pro Ile Tyr Lys Ala Pro Leu Glu Lys Gly Ile
305      310      315      320
Leu Ile Ile Gln Phe Leu Val Ile Phe Pro Xaa Lys His Trp Leu Ser
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Leu

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&lt;210&gt; 3497

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3497

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120
tttttagtat atccttctaa aaagttttcc tgagaatttt tagtttggcc tctcaagttt
180

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300  
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1020  
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&lt;210&gt; 3498

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3498

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          20           25           30
Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg Asn Glu Glu Arg
          35           40           45
Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys Met Glu Ser Ile
          50           55           60
Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu Glu Val Leu Ser
65           70           75           80
Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro Ala Gly Arg Asn
          85           90           95
Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu Glu Asn Leu Leu
          100          105          110
Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln Asn Lys Lys Val
          115          120          125
Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr Ile Ser Ile Leu
130          135          140
Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg Glu Val Ile Asn
145          150          155          160
Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu Asp Ala Gln Leu
          165          170          175
Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro Arg Phe Leu Asn
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Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala Gly Ser Ser Ser
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Glu Ser
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&lt;210&gt; 3499

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3499

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540

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<210> 3500

<211> 168

<212> PRT

<213> Homo sapiens

<400> 3500

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		20						25					30		
Ala	Ser	Thr	Gly	Lys	Gln	Gly	Ala	Pro	Gly	Pro	Asp	Trp	Ala	Cys	Ile
		35					40					45			
Phe	His	Val	Val	Leu	Gln	Pro	Ser	Arg	His	Gly	Pro	Glu	Ala	Thr	Ala
	50					55					60				
Ala	Pro	Gln	Ser	Pro	Pro	Thr	Pro	Ala	Val	Pro	Pro	Gly	His	Gly	Ala
65					70					75				80	
His	Asp	Ser	Gly	Pro	Gly	Gln	Arg	Gln	Arg	Gln	Gly	Ala	Gly	Ser	Thr
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Pro	Ala	Arg	Val	Pro	Val	His	Gly	Ser	Pro	Ser	Ser	Cys	Arg	Ala	Leu
		100						105					110		
Arg	Pro	Ala	Gly	Arg	Ser	Ser	Arg	Ala	Ala	Pro	Arg	Ala	Ser	Pro	Ala
		115					120					125			
Gly	Gln	Ala	Ser	Ser	Arg	Pro	Xaa	Ser	Gly	Ala	Met	His	Arg	Leu	Gly
	130					135					140				
Glu	Gly	Asn	Arg	Ala	Gly	Glu	Lys	Val	Phe	Arg	Arg	Thr	Ala	Val	Gln
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Lys	Arg	Arg	Val	Gly	Gly	Gly	Thr								
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<210> 3501

<211> 691

<212> DNA

<213> Homo sapiens

<400> 3501

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<211> 196

<212> PRT

<213> Homo sapiens

<400> 3502

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<210> 3503

<211> 857

<212> DNA

<213> Homo sapiens

<400> 3503



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<211> 285

<212> PRT

<213> Homo sapiens

<400> 3504

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	165	170
Thr Arg Gln Val Val Lys Lys Tyr Trp Ala Ile Thr Val His Val Pro		175
	180	185
Met Pro Ser Ala Gly Val Val Asp Ile Pro Ile Val Glu Lys Glu Gly		190
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Gln Gly Gln Gln Gln His Pro Arg Met Thr Leu Ser Pro Ser Ser Arg		205
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Met Asp Asp Gly Lys Met Val Lys Val Arg Arg Ser Arg Asn Ala Gln		220
225	230	235
Val Ala Val Thr Gln Tyr Gln Val Leu Ser Ser Thr Leu Ser Ser Ala		240
	245	250
Leu Val Glu Leu Gln Pro Ile Thr Gly Ile Lys His Gln Leu Arg Val		255
	260	265
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		285

&lt;210&gt; 3505

&lt;211&gt; 1612

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3505

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&lt;210&gt; 3506

&lt;211&gt; 502

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3506

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Met	Leu	Leu	Ala	Trp	Pro	Leu	Ala	Leu	Val	Ala	Ser	Leu	Gly	Ser	Ala
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Phe	Leu	Leu	Lys	Ala	Ile	Met	Arg	Thr	Met	Trp	Phe	Ala	Gly	Gly	Phe
65			70				75							80	
His	Arg	Val	Ala	Val	Lys	Gly	Arg	Gln	Ala	Leu	Pro	Thr	Glu	Ala	Ala
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Ile	Leu	Thr	Leu	Ala	Pro	His	Ser	Ser	Tyr	Phe	Asp	Ala	Ile	Pro	Val
	100						105					110			
Thr	Met	Thr	Met	Ser	Ser	Ile	Val	Met	Lys	Thr	Glu	Ser	Arg	Asp	Ile
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Pro	Ile	Trp	Gly	Thr	Leu	Ile	Gln	Tyr	Ile	Arg	Pro	Val	Phe	Val	Ser
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Arg	Ser	Asp	Gln	Asp	Ser	Arg	Arg	Lys	Thr	Val	Glu	Glu	Ile	Lys	Arg
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 Glu Met Tyr Pro Ala Phe Ala Glu Glu Tyr Leu Tyr Pro Asp Gln Thr  
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&lt;211&gt; 885

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3507

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&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3508

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Ser	Val	Val	Gly	Thr	Trp	Tyr	Val	Thr	Ala	Ile	Val	Ile	Ile	Lys	Tyr
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&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3512

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&lt;212&gt; PRT

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&lt;400&gt; 3514

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Ser	Asp	Ser	Ser	Glu	Gly	Phe	Leu	Gln	Leu	Pro	His	Gln	Asp	Ser	Gln
	130					135					140				
Asp	Ser	Ser	Ser	Val	Gly	Ser	Asn	Ser	Leu	Glu	Asp	Gly	Gln	Thr	Leu
145				150						155				160	
Gly	Thr	Lys	Lys	Ser	Ser	Thr	Met	Asn	Asp	Leu	Val	Gln	Ser	Met	Val
			165					170					175		
Leu	Ala	Gly	Gln	Trp	Thr	Gly	Ser	Thr	Glu	Asn	Leu	Glu	Val	Pro	Asp
		180						185				190			
Asp	Ile	Ser	Thr	Gly	Lys	Arg	Arg	Lys	Glu	Leu	Gly	Ala	Met	Ala	Phe
		195					200					205			
Ser	Thr	Thr	Ala	Ile	Asn	Phe	Ser	Thr	Val	Asn	Ser	Ser	Ala	Gly	Phe
	210					215					220				
Arg	Ser	Lys	Gln	Leu	Val	Asn	Asn	Lys	Asp	Thr	Thr	Ser	Phe	Glu	Asp
225			230						235					240	
Ile	Ser	Pro	Gln	Gly	Val	Ser	Asp	Asp	Ser	Ser	Thr	Gly	Ser	Arg	Val
			245					250					255		
His	Ala	Ser	Arg	Pro	Ala	Ser	Leu	Asp	Ser	Gly	Arg	Thr	Ser	Thr	Ser
		260						265				270			
Asn	Ser	Asn	Asn	Asn	Ala	Ser	Leu	His	Glu	Val	Lys	Ala	Gly	Ala	Val



275 280 285  
 Asn Asn Gln Ser Arg Pro Gln Ser His Ser Ser Gly Glu Phe Ser Leu  
 290 295 300  
 Leu His Asp His Glu Ala Trp Ser Ser Ser Gly Ser Ser Pro Ile Gln  
 305 310 315 320  
 Tyr Leu Lys Arg Gln Thr Arg Ser Ser Pro Val Leu Gln His Lys Ile  
 325 330 335  
 Ser Glu Thr Leu Glu Ser Arg His His Lys Ile Lys Thr Gly Ser Pro  
 340 345 350  
 Gly Ser Glu Val Val Thr Leu Gln Gln Phe Leu Glu Glu Ser Asn Lys  
 355 360 365  
 Leu Thr Ser Val Gln Ile Lys Ser Ser Ser Gln Glu Asn Leu Leu Asp  
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 Glu Val Met Lys Ser Leu Ser Val Ser Ser Asp Phe Leu Gly Lys Asp  
 385 390 395 400  
 Lys Pro Val Ser Cys Gly Leu Ala Arg Ser Val Ser Gly Lys Thr Pro  
 405 410 415  
 Gly Asp Phe Tyr Asp Arg Arg Thr Thr Lys Pro Glu Phe Leu Arg Pro  
 420 425 430  
 Gly Pro Arg Lys Thr Glu Asp Thr Tyr Phe Ile Ser Ser Ala Gly Lys  
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 Pro Thr Pro Gly Thr Gln Gly Lys Ile Lys Leu Val Lys Glu Ser Ser  
 450 455 460  
 Leu Ser Arg Gln Ser Lys Asp Ser Asn Pro Tyr Ala Thr Leu Pro Arg  
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 Ala Ser Ser Val Ile Ser Thr Ala Glu Gly Thr Thr Arg Arg Thr Ser  
 485 490 495  
 Ile His Asp Phe Leu Thr Lys Asp Ser Arg Leu Pro Ile Ser Val Asp  
 500 505 510  
 Ser Pro Pro Ala Ala Ala Asp Ser Asn Thr Thr Ala Ala Ser Asn Val  
 515 520 525  
 Asp Lys Val Gln Glu Ser Arg Asn Ser Lys Ser Arg Ser Arg Glu Gln  
 530 535 540  
 Gln Ser Ser  
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&lt;210&gt; 3517

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3517

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 cctttgcttt ccatccgcta tagtgacctc ctttgctcctt gcggggggaaa ccgaggccac  
 180  
 agccttgtag cgcattgctg atcgcccgac ttcccgcccc ctgctcgtgc gggcctcact  
 240  
 gtctccttct gggctggggg cttgcgacac cgccctccgg ccgactcgct cgtgggggtgc  
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 342

<210> 3518  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

<400> 3518  
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 Trp Pro Asp Pro Asp Phe Ser Ala Gly Arg Leu Cys Phe Pro Ser Ala  
 20 25 30  
 Ile Val Ala Ser Phe Val Leu Ala Gly Glu Thr Glu Ala Thr Ala Leu  
 35 40 45  
 Gln Arg Met Pro Asp Arg Pro Thr Ser Arg Pro Leu Leu Val Arg Ala  
 50 55 60  
 Ser Leu Ser Pro Ser Gly Leu Gly Ala Cys Asp Thr Ala Leu Arg Pro  
 65 70 75 80  
 Thr Arg Ser Trp Gly Ala Cys Trp Gln Trp Leu Gly His Ser Cys Ser  
 85 90 95  
 Gly Gln Gly

<210> 3519  
 <211> 2207  
 <212> DNA  
 <213> Homo sapiens

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 240  
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 420  
 ggggaactca ctgacacca cacctccttc gctgacggac acacttttct actcgagaag  
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 660  
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<210> 3520
<211> 303
<212> PRT
<213> Homo sapiens
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&lt;400&gt; 3520

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 20          25          30
Val Val Asn Leu Pro Pro Ala Gln Leu Ser Ser Ser Asp Glu Glu Thr
 35          40          45
Arg Glu Glu Leu Ala Arg Ile Gly Leu Val Pro Pro Pro Glu Glu Phe
 50          55          60
Ala Asn Gly Val Leu Leu Ala Thr Pro Leu Ala Gly Pro Gly Pro Ser
 65          70          75          80
Pro Thr Thr Val Pro Ser Pro Ala Ser Gly Lys Pro Ser Ser Glu Pro
 85          90          95
Pro Pro Ala Pro Glu Ser Ala Ala Asp Ser Gly Val Glu Glu Ala Asp
100          105          110
Thr Arg Ser Ser Ser Asp Pro His Leu Glu Thr Thr Ser Thr Ile Ser
115          120          125
Thr Val Ser Ser Met Ser Thr Leu Ser Ser Glu Ser Gly Glu Leu Thr
130          135          140
Asp Thr His Thr Ser Phe Ala Asp Gly His Thr Phe Leu Leu Glu Lys
145          150          155          160
Pro Pro Val Pro Pro Lys Pro Lys Leu Lys Ser Pro Leu Gly Lys Gly
165          170          175
Pro Val Thr Phe Arg Asp Pro Leu Leu Lys Gln Ser Ser Asp Ser Glu
180          185          190
Leu Met Ala Gln Gln His His Ala Ala Ser Ala Gly Leu Ala Ser Ala
195          200          205
Ala Gly Pro Ala Arg Pro Arg Tyr Leu Phe Gln Arg Arg Ser Lys Leu
210          215          220
Trp Gly Asp Pro Val Glu Ser Arg Gly Leu Pro Gly Pro Glu Asp Asp
225          230          235          240
Lys Pro Thr Val Ile Ser Glu Leu Ser Ser Arg Leu Gln Gln Leu Asn
245          250          255
Lys Asp Thr Arg Ser Leu Gly Glu Glu Pro Val Gly Gly Leu Gly Ser
260          265          270
Leu Leu Asp Pro Ala Lys Lys Ser Pro Ile Ala Ala Ala Arg Ser Pro
275          280          285
Leu Ser Ser Leu Gly Leu Gly Gly Trp Tyr Val Asp Ala Thr Ser
290          295          300

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&lt;210&gt; 3521

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3521

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120
attcctctac accttcgct acttctgcac accccacgac ttctctgact tctctctga
180
ccgcatcaac agcacgctga ccagggccca ccaggacccc acctcgacct tcaccaagat
240

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 360  
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 420  
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 480  
 gacccttcaa cgccctctgt aagaggctct cagaggacgg catctccagg aagagcttcc  
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 cctggaggct gccccgaggc aacgggctgg tgctgcccgc acacaaggag cgccctaca  
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<210> 3522

<211> 181

<212> PRT

<213> Homo sapiens

<400> 3522

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 20 25 30  
 Gln His Ala Asp Gln Gly Pro Pro Gly Pro His Leu Asp Leu His Gln  
 35 40 45  
 Asp Leu Gln Ala Glu Pro Leu Arg Pro Ala Gly Leu Gly Gly Gly Leu  
 50 55 60  
 Leu Arg Cys Gly Leu Pro Ser Glu Gln Arg Ala Ala Gly Glu Ala Arg  
 65 70 75 80  
 Gly Leu His Leu Leu Gln Asp Pro Thr Pro Gly Arg Leu Cys Gln Ala  
 85 90 95  
 Pro Ala Gly Pro Pro Gly Gly Gly His Gly Pro Ala Gly Arg Gly Gln  
 100 105 110  
 Pro Ser Arg His Arg Pro Gly Glu Pro Gln Gly Gly Arg Gly Gly Xaa  
 115 120 125  
 Pro Asp Pro Ser Thr Pro Ser Val Arg Gly Ser Gln Arg Thr Ala Ser  
 130 135 140  
 Pro Gly Arg Ala Ser Pro Gly Gly Cys Pro Glu Ala Thr Gly Trp Cys  
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 Cys Arg His Thr Arg Ser Ala Pro Thr Pro Leu Leu Pro Pro Cys Pro  
 165 170 175  
 Ser Pro Ala Ser Ser  
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<210> 3523

<211> 2614

<212> DNA

<213> Homo sapiens

<400> 3523

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120  
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180  
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420  
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 2160  
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 2460  
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 2520  
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 2580  
 aagaattaaa atactctttt acgtaaaaaa aata  
 2614

&lt;210&gt; 3524

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3524

Met	Ala	Pro	Asp	Pro	Leu	Ala	Ala	Glu	Thr	Ala	Ala	Gln	Gly	Leu	Thr
1				5				10					15		
Pro	Arg	Tyr	Phe	Thr	Trp	Asp	Glu	Val	Ala	Gln	Arg	Ser	Gly	Cys	Glu
	20					25						30			
Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	Ile	Ser	Asp	Phe
	35					40					45				
Ser	Arg	Arg	His	Pro	Gly	Gly	Ser	Arg	Val	Ile	Ser	His	Tyr	Ala	Gly
	50				55				60						
Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val	Ala	Phe	His	Ile	Asn	Lys	Gly	Leu
	65			70				75					80		
Val	Lys	Lys	Tyr	Met	Asn	Ser	Leu	Leu	Ile	Gly	Glu	Leu	Ser	Pro	Glu
	85						90						95		
Gln	Pro	Ser	Phe	Glu	Pro	Thr	Lys	Asn	Lys	Glu	Leu	Thr	Asp	Glu	Phe
	100						105					110			
Arg	Glu	Leu	Arg	Ala	Thr	Val	Glu	Arg	Met	Gly	Leu	Met	Lys	Ala	Asn

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      115              120              125
His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly
      130              135              140
Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe
      145              150              155              160
Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp
      165              170              175
Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
      180              185              190
Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala Pro
      195              200              205
Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys Pro Asn
      210              215              220
Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe Phe Phe Ala
      225              230              235              240
Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln Lys Lys Lys Tyr
      245              250              255
Met Pro Tyr Asn His Gln His Lys Tyr Phe Phe Leu Ile Gly Pro Pro
      260              265              270
Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr Ile Phe Tyr Phe Val Ile
      275              280              285
Gln Arg Lys Lys Trp Val Asp Leu Val Trp Met Ile Thr Phe Tyr Val
      290              295              300
Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
      305              310              315              320
Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
      325              330              335
Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
      340              345              350
Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
      355              360              365
Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
      370              375              380
His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Lys Val Ala
      385              390              395              400
Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
      405              410              415
Lys Pro Leu Leu Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu
      420              425              430
Ser Gly Gln Leu Trp Leu Asp Ala Tyr Leu His Gln
      435              440

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&lt;210&gt; 3525

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3525

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120
tggaacagaa accagatgat gcacaatatt attgtcaaag agcttattgt cacattcttc
180

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 300  
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 360  
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 1116

&lt;210&gt; 3526

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3526

Ile	Thr	Asp	Glu	Lys	Arg	Ile	Phe	Phe	Tyr	Ile	Val	Ala	Val	Ala	Asp
1				5					10					15	
Ala	Lys	Lys	Ser	Arg	Glu	Phe	Asn	Pro	Asn	Asn	Ser	Thr	Ala	Val	Leu
			20					25					30		
Arg	Lys	Gly	Ile	Cys	Glu	Tyr	His	Leu	Lys	Asn	Tyr	Ala	Ala	Ala	Leu
		35					40					45			
Glu	Thr	Phe	Ile	Gly	Gly	Gln	Lys	Leu	Xaa	Ala	Asp	Ala	Asn	Phe	Ser
	50					55					60				
Asp	Trp	Ile	Lys	Arg	Cys	Gln	Glu	Ala	Gln	Asn	Gly	Ser	Glu	Ser	Glu
65					70					75				80	
Val	Val	Met	Glu	Pro	Ala	Leu	Glu	Gly	Thr	Gly	Lys	Glu	Gly	Lys	Lys
			85						90					95	
Ala	Ser	Ser	Arg	Lys	Arg	Thr	Leu	Ala	Glu	Pro	Pro	Ala	Lys	Gly	Leu
			100					105						110	
Leu	Gln	Pro	Val	Lys	Leu	Ser	Arg	Ala	Glu	Leu	Tyr	Lys	Glu	Pro	Thr

115	120	125
Asn Glu Glu Leu Asn Arg Leu Arg Glu Thr Glu Ile Leu Phe His Ser		
130	135	140
Ser Leu Leu Arg Leu Gln Val Glu Glu Leu Leu Lys Glu Val Arg Leu		
145	150	155
Ser Glu Lys Lys Lys Asp Arg Ile Asp Ala Phe Leu Arg Glu Val Asn		
165	170	175
Gln Arg Val Val Arg Val Pro Ser Val Pro Glu Thr Glu Leu Thr Asp		
180	185	190
Gln Ala Trp Leu Pro Ala Gly Val Arg Val Pro Leu His Gln Val Pro		
195	200	205
Tyr Ala Val Lys Gly Cys Phe Arg Phe Leu Pro Pro Ala Gln Val Thr		
210	215	220
Val Val Gly Ser Tyr Leu Leu Gly Thr Cys Ile Arg Pro Asp Ile Asn		
225	230	235
Val Asp Val Ala Leu Thr Met Pro Arg Glu Ile Leu Gln Asp Lys Asp		
245	250	255
Gly Leu Asn Gln Arg Tyr Phe Arg Lys Arg Ala Leu Tyr Leu Ala His		
260	265	270
Leu Ala His His Leu Ala Gln Asp Pro Leu Phe Gly Ser Val Cys Phe		
275	280	285
Ser Tyr Thr Asn Gly Cys His Leu Lys Pro Ser Leu Leu Leu Arg Pro		
290	295	300

&lt;210&gt; 3527

&lt;211&gt; 2838

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3527

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<211> 281

<212> PRT

<213> Homo sapiens

<400> 3528

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&lt;210&gt; 3529

&lt;211&gt; 3026

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3529

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<211> 206

<212> PRT

<213> Homo sapiens

<400> 3530

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<211> 879

<212> DNA

<213> Homo sapiens

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&lt;210&gt; 3532

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3532

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&lt;210&gt; 3533

&lt;211&gt; 1151

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3533

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<211> 313

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<213> Homo sapiens

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Lys	His	Gly	Ala	Ile	Pro	Gly	Gly	Leu	Ser	Ile	Gly	Pro	Pro	Gly	Lys
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Pro	Leu	Gly	Trp	Thr	Ser	Ser	Tyr	Ser	Ser	Gly	Ser	Ala	Trp	Ser	Thr
			260				265						270		
Asp	Thr	Ser	Gly	Arg	Thr	Ser	Ser	Trp	Leu	Val	Leu	Arg	Asn	Leu	Thr
		275				280					285				
Pro	Gln	Val	Gln	Tyr	Gly	Ala	Pro	Ala	Ser	Leu	Ser	Met	Ile	Gln	Gly
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<210> 3535

<211> 723

<212> DNA

<213> Homo sapiens

<400> 3535  
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 aagatcagct tagagaagaa gtggtccaga gagtttctct tctccttctc tattacatta  
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 480  
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<210> 3536  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 3536  
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 20 25 30  
 Arg Val Ser Leu Leu Leu Tyr Tyr Ile Ile His Gln Glu Glu Ile  
 35 40 45  
 Cys Ser Ser Lys Leu Asn Met Ser Asn Lys Glu Tyr Lys Phe Tyr Leu  
 50 55 60  
 His Ser Leu Leu Ser Leu Arg Gln Asp Glu Asp Ser Ser Phe Leu Ser  
 65 70 75 80  
 Gln Asn Glu Thr Glu Asp Ile Leu Ala Phe Thr Arg Gln Tyr Phe Asp  
 85 90 95  
 Thr Ser Gln Ser Gln Cys Met Glu Thr Lys Thr Leu Gln Lys Lys Ser  
 100 105 110  
 Gly Ile Val Ser Ser Glu Gly Ala Asn Glu Ser Thr Leu Pro Gln Leu  
 115 120 125  
 Ala Ala Met Ile Ile Thr Leu Ser Leu Gln Gly Val Cys Leu Gly Gln  
 130 135 140  
 Gly Asn Leu Pro Ser Pro Asp Tyr Phe Thr Glu Tyr Ile Phe Ser Ser

WO 00/58473

PCT/US00/08621

145  
Leu Asn Arg

150

155

160

&lt;210&gt; 3537

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3537

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&lt;210&gt; 3538

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3538

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1           5           10           15
Ser Trp Thr Leu Cys Lys His Phe Cys Ala Cys Trp Val Gly Ala Arg
20           25           30
Leu Lys Asp Pro Ser Ser Asn Pro Ala Gly Pro Arg Ala Thr Ala Gly
35           40           45
Gln Gly Val Ala Pro Gly Phe Arg His Ala Thr Thr Arg Ala Arg
50           55           60
Ala Thr His Ala Ser Cys Ala His Leu Thr His Thr Pro Leu Pro Gly
65           70           75           80
His Ala Asp Thr Pro Gln Pro His Thr Ser His Ala Val His Leu Arg
85           90           95
Leu Leu Thr Ser His Ala Gln Cys Trp Cys Thr Phe Ala Ser His Met

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100 105 110  
 Leu Pro Ser Pro Pro Thr Gln Gly His Pro Thr Ala Pro Pro Cys Pro  
 115 120 125  
 Cys Pro Ser Pro Ser Leu Glu Val Pro Cys Pro Ala Gly Pro Val Asn  
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<210> 3539

<211> 818

<212> DNA

<213> Homo sapiens

<400> 3539

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 120  
 cggggggcgg aggttgagct gagccgagat cgcgccaggta cgctccagtc tgggcgacaa  
 180  
 gagcgaaact cgatatcaaa aaaaaaaaaa acgtcctgat ccagagcct cttcacgcgt  
 240  
 ccctaccac agcacttcag agaagcaggt ctttaatcag tgtgtctaga tgcagctgct  
 300  
 gactgtcacc cctaccccg cttctctcca gtctgaggac ggccagtcac cccattgcc  
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 720  
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<210> 3540

<211> 180

<212> PRT

<213> Homo sapiens

<400> 3540

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 20 25 30  
 Thr Leu Gly Ser Ser Arg Ala Lys Leu Gly Asn Phe Pro Trp Gln Ala

```

      35          40          45
Phe Thr Ser Ile His Gly Arg Gly Gly Gly Ala Leu Leu Gly Asp Arg
      50          55          60
Trp Ile Leu Thr Ala Ala His Thr Val Tyr Pro Lys Asp Ser Val Ser
      65          70          75          80
Leu Arg Lys Asn Gln Ser Val Asn Val Phe Leu Gly His Thr Ala Ile
      85          90          95
Asp Glu Met Leu Lys Leu Gly Asn His Pro Val His Arg Val Val Val
      100          105          110
His Pro Asp Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile
      115          120          125
Ala Leu Leu Glu Leu Gln His Ser Ile Pro Leu Gly Pro Asn Val Leu
      130          135          140
Pro Val Cys Leu Pro Asp Asn Glu Thr Leu Tyr Arg Ser Gly Leu Leu
      145          150          155          160
Gly Tyr Val Ser Gly Phe Gly Met Glu Met Gly Trp Leu Thr Thr Glu
      165          170          175
Leu Lys Tyr Ser
      180

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&lt;210&gt; 3541

&lt;211&gt; 722

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3541

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120
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180
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240
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300
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aa
722

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&lt;210&gt; 3542

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3542

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Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
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Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
      20             25             30
Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      35             40             45
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
      50             55             60
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
65             70             75             80
Ala Ile Lys Gln Asn Pro Leu Leu Ala Glu Ala Tyr Ser Asn Leu Gly
      85             90             95
Asn Val Tyr Lys Glu Arg Gly Gln Leu Gln Glu Ala Ile Glu His Tyr
      100            105            110
Arg His Ala Leu Arg Leu Lys Pro Asp Phe Ile Asp Gly Tyr Ile Asn
      115            120            125
Ala Ala Ala Ala Leu Val Ala Ala Gly Asp Met Glu Gly Ala Val Gln
      130            135            140
Ala Tyr Val Ser Ala Leu Gln Pro Gly
145                    150

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&lt;210&gt; 3543

&lt;211&gt; 1206

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3543

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120
gtttggttgt tgctcaggat gtgtaatagt ttctcttcag ccataagcca cgcttggtag
180
atattaattg agtggagaga tcttgcacct cttccagtta tgcatttgtg gtttgtcgtc
240
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aaccccaaga tcccatgag agaaaggag ttctgggaat tatgtaacaa gtgtaatttg
660

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 780  
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<210> 3544

<211> 273

<212> PRT

<213> Homo sapiens

<400> 3544

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Met	Gly	Leu	Ile	Val	Phe	Val	Trp	Leu	Tyr	Asn	Ile	Val	Leu	Ile	Pro
			20					25					30		
Lys	Ile	Val	Leu	Phe	Pro	His	Tyr	Glu	Glu	Gly	His	Ile	Pro	Gly	Ile
		35					40					45			
Leu	Ile	Ile	Ile	Phe	Tyr	Gly	Ile	Ser	Ile	Phe	Cys	Leu	Val	Ala	Leu
	50					55					60				
Val	Arg	Ala	Ser	Ile	Thr	Asp	Pro	Gly	Arg	Leu	Pro	Glu	Asn	Pro	Lys
65					70				75					80	
Ile	Pro	His	Gly	Glu	Arg	Glu	Phe	Trp	Glu	Leu	Cys	Asn	Lys	Cys	Asn
			85					90					95		
Leu	Met	Arg	Pro	Lys	Arg	Ser	His	His	Cys	Ser	Arg	Cys	Gly	His	Cys
			100					105					110		
Val	Arg	Arg	Met	Asp	His	His	Cys	Pro	Trp	Ile	Asn	Asn	Cys	Val	Gly
		115					120					125			
Glu	Asp	Asn	His	Trp	Leu	Phe	Leu	Gln	Leu	Cys	Phe	Tyr	Thr	Glu	Leu
	130					135					140				
Leu	Thr	Cys	Tyr	Ala	Leu	Met	Phe	Ser	Phe	Cys	His	Tyr	Tyr	Tyr	Phe
145					150					155				160	
Leu	Pro	Leu	Lys	Lys	Arg	Asn	Leu	Asp	Leu	Phe	Val	Phe	Arg	His	Glu
			165					170					175		
Leu	Ala	Ile	Met	Arg	Leu	Ala	Ala	Phe	Met	Gly	Ile	Thr	Met	Leu	Val
		180						185					190		
Gly	Ile	Thr	Gly	Leu	Phe	Tyr	Thr	Gln	Leu	Ile	Gly	Ile	Ile	Thr	Pro
		195					200					205			
Cys	Ser	Leu	Ile	Leu	Leu	Lys	Cys	Gly	Ser	Val	Ser	Asn	Asn	Ser	Leu



210		215		220	
Gly Asp Leu Met Lys Ile Ser Glu Thr Phe Ala Leu Arg Ile Pro Ser					
225		230		235	240
Phe Val Val Met Cys Pro Glu Asn Ser Ser Leu Arg Val Phe Asn Ser					
	245		250		255
Val Lys Leu Leu Leu Cys Leu Asp Ser Pro Leu Ile Gln Trp Ser Thr					
	260	265		270	
Lys					

&lt;210&gt; 3545

&lt;211&gt; 3657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3545

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1140

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<210> 3546

<211> 792

<212> PRT

<213> Homo sapiens

<400> 3546

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Gln	Glu	Val	Trp	Pro	Ile	Ile	Trp	Leu	Arg	Leu	Thr	Leu	Ala	Leu	Thr
		20						25				30			
Leu	Ala	Asp	Pro	Gly	Trp	Ala	Ser	Ile	Ser	Arg	Gly	Val	Leu	Val	Cys
		35					40					45			
Asp	Glu	Cys	Cys	Ser	Val	His	Arg	Ser	Leu	Gly	Arg	His	Ile	Ser	Ile
		50				55					60				
Val	Lys	His	Leu	Arg	His	Ser	Ala	Trp	Pro	Pro	Thr	Leu	Leu	Gln	Met
65					70					75				80	
Val	His	Thr	Leu	Ala	Ser	Asn	Gly	Ala	Asn	Ser	Ile	Trp	Glu	His	Ser
			85					90					95		
Leu	Leu	Asp	Pro	Ala	Gln	Val	Gln	Ser	Gly	Arg	Arg	Lys	Ala	Asn	Pro
		100						105					110		
Gln	Asp	Lys	Val	His	Pro	Ile	Lys	Ser	Glu	Phe	Ile	Arg	Ala	Lys	Tyr
		115					120					125			
Gln	Met	Leu	Ala	Phe	Val	His	Lys	Leu	Pro	Cys	Arg	Asp	Asp	Asp	Gly

130 135 140  
 Val Thr Ala Lys Asp Leu Ser Lys Gln Leu His Ser Ser Val Arg Thr  
 145 150 155 160  
 Gly Asn Leu Glu Thr Cys Leu Arg Leu Leu Ser Leu Gly Ala Gln Ala  
 165 170 175  
 Asn Phe Phe His Pro Glu Lys Gly Thr Thr Pro Leu His Val Ala Ala  
 180 185 190  
 Lys Ala Gly Gln Thr Leu Gln Ala Glu Leu Leu Val Val Tyr Gly Ala  
 195 200 205  
 Asp Pro Gly Ser Pro Asp Val Asn Gly Arg Thr Pro Ile Asp Tyr Ala  
 210 215 220  
 Arg Gln Ala Gly His His Glu Leu Ala Glu Arg Leu Val Glu Cys Gln  
 225 230 235 240  
 Tyr Glu Leu Thr Asp Arg Leu Ala Phe Tyr Leu Cys Gly Arg Lys Pro  
 245 250 255  
 Asp His Lys Asn Gly His Tyr Ile Ile Pro Gln Met Ala Asp Arg Ser  
 260 265 270  
 Arg Gln Lys Cys Met Ser Gln Ser Leu Asp Leu Ser Glu Leu Ala Lys  
 275 280 285  
 Ala Ala Lys Lys Lys Leu Gln Ala Leu Ser Asn Arg Leu Phe Glu Glu  
 290 295 300  
 Leu Ala Met Asp Val Tyr Asp Glu Val Asp Arg Arg Glu Asn Asp Ala  
 305 310 315 320  
 Val Trp Leu Ala Thr Gln Asn His Ser Thr Leu Val Thr Glu Arg Ser  
 325 330 335  
 Ala Val Pro Phe Leu Pro Val Asn Pro Glu Tyr Ser Ala Thr Arg Asn  
 340 345 350  
 Gln Gly Arg Gln Lys Leu Ala Arg Phe Asn Ala Arg Glu Phe Ala Thr  
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 Leu Ile Ile Asp Ile Leu Ser Glu Ala Lys Arg Arg Gln Gln Gly Lys  
 370 375 380  
 Ser Leu Ser Ser Pro Thr Asp Asn Leu Glu Leu Ser Leu Arg Ser Gln  
 385 390 395 400  
 Ser Asp Leu Asp Asp Gln His Asp Tyr Asp Ser Val Ala Ser Asp Glu  
 405 410 415  
 Asp Thr Asp Gln Glu Pro Leu Arg Ser Thr Gly Ala Thr Arg Ser Asn  
 420 425 430  
 Arg Ala Arg Ser Met Asp Ser Ser Asp Leu Ser Asp Gly Ala Val Thr  
 435 440 445  
 Leu Gln Glu Tyr Leu Glu Leu Lys Lys Ala Leu Ala Thr Ser Glu Ala  
 450 455 460  
 Lys Val Gln Gln Leu Met Lys Val Asn Ser Ser Leu Ser Asp Glu Leu  
 465 470 475 480  
 Arg Arg Leu Gln Arg Glu His Phe Ala Pro Ile Ile His Lys Leu Gln  
 485 490 495  
 Ala Glu Asn Leu Gln Leu Arg Gln Pro Pro Gly Pro Val Pro Thr Pro  
 500 505 510  
 Pro Leu Pro Ser Glu Arg Ala Glu His Thr Pro Met Ala Pro Gly Gly  
 515 520 525  
 Ser Thr His Arg Arg Asp Arg Gln Ala Phe Ser Met Tyr Glu Pro Gly  
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<210> 3547
<211> 1039
<212> DNA
<213> Homo sapiens
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gcttggtggac ggcagcacac ttctgctttt gtcccttcac caggacgaat ttactctttt
240
gggcttggtg gtaatgggca gctgggaacc ggttcaacaa gcaacaggaa aagccccctt
300
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gaatatttct gtgtaaaag aattttctca gggggagatc aaagcttttc acattactct
420
agtccccaga actgtggggc accagatgac ttcagatgtc ccaatccgac aaagcagatc
480
tggacagtga atgaagctct aattcagaaa tggctgagct atccttctgg aaggtttcct
540
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720  
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900  
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1039

<210> 3548

<211> 346

<212> PRT

<213> Homo sapiens

<400> 3548

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			20				25						30		
Gly	Gln	Leu	Gly	His	Asn	Ser	Thr	Ser	His	Glu	Ile	Asn	Pro	Arg	Lys
		35					40					45			
Val	Phe	Glu	Leu	Met	Gly	Ser	Ile	Val	Thr	Glu	Ile	Ala	Cys	Gly	Arg
	50				55						60				
Gln	His	Thr	Ser	Ala	Phe	Val	Pro	Ser	Ser	Gly	Arg	Ile	Tyr	Ser	Phe
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Gly	Leu	Gly	Gly	Asn	Gly	Gln	Leu	Gly	Thr	Gly	Ser	Thr	Ser	Asn	Arg
			85					90						95	
Lys	Ser	Pro	Phe	Thr	Val	Lys	Gly	Asn	Trp	Tyr	Pro	Tyr	Asn	Gly	Gln
			100					105					110		
Cys	Leu	Pro	Asp	Ile	Asp	Ser	Glu	Glu	Tyr	Phe	Cys	Val	Lys	Arg	Ile
		115					120					125			
Phe	Ser	Gly	Gly	Asp	Gln	Ser	Phe	Ser	His	Tyr	Ser	Ser	Pro	Gln	Asn
	130				135						140				
Cys	Gly	Pro	Pro	Asp	Asp	Phe	Arg	Cys	Pro	Asn	Pro	Thr	Lys	Gln	Ile
145					150					155				160	
Trp	Thr	Val	Asn	Glu	Ala	Leu	Ile	Gln	Lys	Trp	Leu	Ser	Tyr	Pro	Ser
			165						170					175	
Gly	Arg	Phe	Pro	Val	Glu	Ile	Ala	Asn	Glu	Ile	Asp	Gly	Thr	Phe	Ser
			180					185					190		
Ser	Ser	Gly	Cys	Leu	Asn	Gly	Ser	Phe	Leu	Ala	Val	Ser	Asn	Asp	Asp
		195					200					205			
His	Tyr	Arg	Thr	Gly	Thr	Arg	Phe	Ser	Gly	Val	Asp	Met	Asn	Ala	Ala
	210					215						220			
Arg	Leu	Leu	Phe	His	Lys	Leu	Ile	Gln	Pro	Asp	His	Pro	Gln	Ile	Ser

225		230		235		240									
Gln	Gln	Val	Ala	Ala	Ser	Leu	Glu	Lys	Asn	Leu	Ile	Pro	Lys	Leu	Thr
			245						250					255	
Ser	Ser	Leu	Pro	Asp	Val	Glu	Ala	Leu	Arg	Phe	Tyr	Leu	Thr	Leu	Pro
			260						265					270	
Glu	Cys	Pro	Leu	Met	Ser	Asp	Ser	Asn	Asn	Phe	Ile	Thr	Ile	Ala	Ile
		275						280					285		
Pro	Phe	Gly	Thr	Ala	Leu	Val	Asn	Leu	Glu	Lys	Ala	Pro	Leu	Lys	Val
	290						295					300			
Leu	Glu	Asn	Trp	Trp	Ser	Val	Leu	Glu	Pro	Pro	Leu	Phe	Leu	Lys	Ile
305					310					315				320	
Val	Glu	Leu	Phe	Lys	Glu	Val	Val	Val	His	Leu	Leu	Lys	Leu	Tyr	Lys
			325						330					335	
Ile	Gly	Ile	Pro	Pro	Ser	Glu	Arg	Ile	Ile						
			340					345							

&lt;210&gt; 3549

&lt;211&gt; 2542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3549

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agatatgaga aaattcatgg aagaagtaag gaaaaggaga gagctagtct agataaaaaa
180
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240
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300
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360
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420
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480
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720
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780
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840
agcttcgaaa gatatcccaa aaatttcagt gactccagaa gaaatgagcc tccaccacca
900
agaaatgaac ttagagaatc agacaggcga gaagtacgag gggagcgaga cgaaaggaga
960

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acgggtgatta ttcattgacag gcctgatata actcatccta gacatcctcg agaggcaggg  
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1080  
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1140  
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1380  
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2160  
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2520  
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2542



&lt;210&gt; 3550

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3550

Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu Glu Lys Lys Arg Ile Ser  
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 20 25 30  
 His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Ile His Gly Arg  
 35 40 45  
 Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg Asp Lys Asp  
 50 55 60  
 Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln Arg  
 65 70 75 80  
 Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Arg Arg Ala Met Glu  
 85 90 95  
 Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg Glu Arg Arg Glu Arg Glu  
 100 105 110  
 Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg Leu Gln Arg  
 115 120 125  
 Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg Glu Arg  
 130 135 140  
 Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile Glu Gln Glu  
 145 150 155 160  
 Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu Leu Arg  
 165 170 175  
 Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn Ser Leu  
 180 185 190  
 Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr Trp Ser  
 195 200 205  
 Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp Ala Arg Phe Gly His Gly  
 210 215 220  
 Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe Asn Asp Phe Asp His Arg  
 225 230 235 240  
 Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala Val Gln Ser Ser Ser Phe  
 245 250 255  
 Glu Arg Arg Asp Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Ala Arg  
 260 265 270  
 Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe Glu Arg Tyr Pro Lys Asn  
 275 280 285  
 Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg Asn Glu Leu  
 290 295 300  
 Arg Glu Ser Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg Arg  
 305 310 315 320  
 Thr Val Ile Ile His Asp Arg Pro Asp Ile Thr His Pro Arg His Pro  
 325 330 335  
 Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser Asp  
 340 345 350  
 Gly Ser Met Ser Thr Asp Lys Arg Glu Thr Arg Val Glu Arg Pro Glu  
 355 360 365  
 Arg Ser Gly Arg Glu Val Ser Gly His Ser Val Arg Gly Ala Pro Pro

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385      390      395      400
Gly Val Ile Thr Asp Arg Gly Gly Gly Ser Gln His Tyr Pro Glu Glu
      405      410      415
Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg Lys
      420      425      430
Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr Arg
      435      440      445
Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His Ser
      450      455      460
Ser Asn Ala Ser Pro Ile Asn Arg Ile Val Gln Ile Ser Gly Asn Ser
465      470      475      480
Met Pro Arg Gly Ser Gly Ser Gly Phe Lys Pro Phe Lys Gly Gly Pro
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Pro Arg Arg Phe
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<210> 3551  
 <211> 545  
 <212> DNA  
 <213> Homo sapiens

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<400> 3551
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120
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180
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420
ctggaggaac tgaagaagct gtgtctccga gaagctgtaa gcctttccta gtcacatccc
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545

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<210> 3552  
 <211> 55  
 <212> PRT  
 <213> Homo sapiens

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<400> 3552
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1      5      10      15
Ala Lys Lys Asp Met Leu Ala Ala Leu Lys Ser Arg Gln Glu Ala Leu

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Glu	Glu	Thr	Leu	Arg	Gln
			Arg	Leu	Glu
				Glu	Leu
				Lys	Lys
					Leu
					Cys
					Leu
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Arg	Glu	Ala	Val	Ser	Leu
				Ser	
	50		55		

&lt;210&gt; 3553

&lt;211&gt; 1412

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3553

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1140
tctcccaatg atctccagat gctctccgat gcaccttctc accatctctt ctgccttctg
1200
cctcctgtgc cccccacca gaatgccctt ccaaaagtgc ttgctgttat ccaggtag
1260

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 1412

<210> 3554

<211> 419

<212> PRT

<213> Homo sapiens

<400> 3554

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Gln	Asp	Val	Val	Gly	Arg	Phe	Asn	Glu	Arg	Phe	Ile	Leu	Ser	Leu	Ala
			20					25					30		
Ser	Cys	Lys	Lys	Cys	Leu	Val	Ile	Asp	Asp	Gln	Leu	Asn	Ile	Leu	Pro
	35						40					45			
Ile	Ser	Ser	His	Val	Ala	Thr	Met	Glu	Ala	Leu	Pro	Pro	Gln	Thr	Pro
	50					55					60				
Asp	Glu	Ser	Leu	Gly	Pro	Ser	Asp	Leu	Glu	Leu	Arg	Glu	Leu	Lys	Glu
65				70					75					80	
Ser	Leu	Gln	Asp	Thr	Gln	Pro	Val	Gly	Val	Leu	Val	Asp	Cys	Cys	Lys
			85					90					95		
Thr	Leu	Asp	Gln	Ala	Lys	Ala	Val	Leu	Lys	Phe	Ile	Glu	Gly	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Leu	Arg	Ser	Thr	Val	Ala	Leu	Thr	Ala	Ala	Arg	Gly	Arg
	115						120					125			
Gly	Lys	Ser	Ala	Ala	Leu	Gly	Leu	Ala	Ile	Ala	Gly	Ala	Val	Ala	Phe
	130					135					140				
Gly	Tyr	Ser	Asn	Ile	Phe	Val	Thr	Ser	Pro	Ser	Pro	Asp	Asn	Leu	His
145			150						155					160	
Thr	Leu	Phe	Glu	Phe	Val	Phe	Lys	Gly	Phe	Asp	Ala	Leu	Gln	Tyr	Gln
			165					170					175		
Glu	His	Leu	Asp	Tyr	Glu	Ile	Ile	Gln	Ser	Leu	Asn	Pro	Glu	Phe	Asn
			180					185					190		
Lys	Ala	Val	Ile	Ile	Val	Asn	Val	Phe	Arg	Glu	His	Arg	Gln	Thr	Ile
	195					200					205				
Gln	Tyr	Ile	His	Pro	Ala	Asp	Ala	Val	Lys	Leu	Gly	Gln	Ala	Glu	Leu
	210					215					220				
Val	Val	Ile	Asp	Glu	Ala	Ala	Ala	Ile	Pro	Leu	Pro	Leu	Val	Lys	Ser
225				230					235					240	
Leu	Leu	Gly	Pro	Tyr	Leu	Val	Phe	Met	Ala	Ser	Thr	Ile	Asn	Gly	Tyr
			245					250					255		
Glu	Gly	Thr	Gly	Arg	Ser	Leu	Ser	Leu	Lys	Leu	Ile	Gln	Gln	Leu	Arg
		260					265					270			
Gln	Gln	Ser	Ala	Gln	Ser	Gln	Val	Ser	Thr	Thr	Ala	Glu	Asn	Lys	Thr
		275					280					285			
Thr	Thr	Thr	Ala	Arg	Leu	Ala	Ser	Ala	Arg	Thr	Leu	His	Glu	Val	Ser
	290					295					300				
Leu	Gln	Glu	Ser	Ile	Arg	Tyr	Ala	Pro	Gly	Asp	Ala	Val	Glu	Lys	Trp
305				310					315				320		
Leu	Asn	Asp	Leu	Leu	Cys	Leu	Asp	Cys	Leu	Asn	Ile	Thr	Arg	Ile	Val

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<400> 3555
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120
atgaaccagg cgttgcagag gcgcttcgcc aagggggtgc agtacaacat gaagatagt
180
atccggggag acaggaacac gggcaagaca gcgctgtggc accgcctgca gggccggccg
240
ttcgtggagg agtacatccc cacacaggag atccagggtca ccagcatcca ctggagctac
300
aagaccacgg atgacatcgt gaagggtgaa gtctgggatg tagtagacaa aggaaaatgc
360
aaaaagcgag gcgacggctt aaagatggag aacgaccccc aggaggcgga gtctgaaatg
420
gccctggatg ctgagttcct ggacgtgtac aagaactgca acggggtggg catgatgttc
480
gacattacca agcagtggac cttcaattac attctccggg agcttccaaa agtgcccacc
540
cacgtgccag tgtgcgtgct ggggaactac cgggacatgg gcgagcaccg agtcatcnnc
600
tgccggacgn acgtgcgtga cttcatcgac aacctggaca gacctccagg ttctctctac
660
ttccgctatg ctgagcttct catgaagaac agcttcggcc taaagtacct tcataagttc
720
ttcaatatcc catttttgca gcttcagagg gagacgctgt tgcggcagct ggagacgaac
780
cagctggaca tggacgccac gctggaggag ctgtcgggtgc agcaggagac ggaggaccag
840
aactacggca tcttctctgga gatgatggag gctcgcagcc gtggccatgc gtccccactg
900
gcggccaacg ggcagagccc atccccgggc tcccagtcac cagtgggtgcc tgcaggcgct
960
gtgtccacgg ggagctccag ccccggcaca gccagcccc cccacagct gccctcaat
1020

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ggttgccccca ccatacctc  
1038

<210> 3556

<211> 333

<212> PRT

<213> Homo sapiens

<400> 3556

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly
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Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu
			20					25					30		
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile
			35				40					45			
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln
	50					55					60				
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val
65					70				75					80	
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Thr	Asp	Asp	Ile	Val	Lys	Val
			85					90					95		
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp
			100					105					110		
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Ala	Glu	Ser	Glu	Met	Ala
		115					120					125			
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val
	130					135						140			
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg
145					150					155				160	
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn
			165					170					175		
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Xaa	Cys	Arg	Thr	Xaa	Val
		180					185						190		
Arg	Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe
		195					200				205				
Arg	Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu
	210					215					220				
His	Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu
225				230					235					240	
Leu	Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu
			245					250					255		
Glu	Leu	Ser	Val	Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe
			260				265						270		
Leu	Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala
		275				280					285				
Ala	Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Val	Pro
	290				295						300				
Ala	Gly	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Ala	Gln	Pro
305				310						315				320	
Ala	Pro	Gln	Leu	Pro	Leu	Asn	Gly	Cys	Pro	Thr	Ile	Leu			
			325				330								

<210> 3557

<211> 486

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3557

tcagtgcacaa ggaggacgtt tgggcacagc ggcattgcag tgcacacgtg gtagtgcattg  
60  
ccggcattga tcaagtccat ctgggctatg gccataagcc aacaccagtt ctatctggac  
120  
agaaagcaga gtaagtccaa aatccatgca gcacgcagcc tgagtgcagat cgccatcgac  
180  
ctgaccgaga cggggacgct gaagacctcg aagctggcca acatgggtag caaggggaag  
240  
atcatcagcg gcagcagcgg cagcctgctg tcttcaggat ctggtgccag gagacactgc  
300  
attctactcc caggtttctca ggaatcagat agctgcagat cggccaagaa ggacatgctg  
360  
gctgccttga agtccaggca ggaagctctg gaggaacccc tgcgtcagag gctggaggaa  
420  
ctgaagaagc tgtgtctccg agaagctgag ctcacgggca agctgccagt agaatatccc  
480  
ctggat  
486

&lt;210&gt; 3558

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3558

Ser	Val	Thr	Arg	Arg	Thr	Phe	Gly	His	Ser	Gly	Ile	Ala	Val	His	Thr
1				5					10					15	
Trp	Tyr	Ala	Cys	Pro	Ala	Leu	Ile	Lys	Ser	Ile	Trp	Ala	Met	Ala	Ile
			20					25					30		
Ser	Gln	His	Gln	Phe	Tyr	Leu	Asp	Arg	Lys	Gln	Ser	Lys	Ser	Lys	Ile
		35					40					45			
His	Ala	Ala	Arg	Ser	Leu	Ser	Glu	Ile	Ala	Ile	Asp	Leu	Thr	Glu	Thr
		50					55				60				
Gly	Thr	Leu	Lys	Thr	Ser	Lys	Leu	Ala	Asn	Met	Gly	Ser	Lys	Gly	Lys
65					70					75				80	
Ile	Ile	Ser	Gly	Ser	Ser	Gly	Ser	Leu	Leu	Ser	Ser	Gly	Ser	Gly	Ala
			85					90						95	
Arg	Arg	His	Cys	Ile	Leu	Leu	Pro	Gly	Ser	Gln	Glu	Ser	Asp	Ser	Ser
			100					105					110		
Gln	Ser	Ala	Lys	Lys	Asp	Met	Leu	Ala	Ala	Leu	Lys	Ser	Arg	Gln	Glu
		115					120					125			
Ala	Leu	Glu	Glu	Thr	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		130				135					140				
Cys	Leu	Arg	Glu	Ala	Glu	Leu	Thr	Gly	Lys	Leu	Pro	Val	Glu	Tyr	Pro
145					150					155					160
Leu	Asp														

&lt;210&gt; 3559

&lt;211&gt; 673

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3559

```

gaaggagcga gcgggggcgc gaggcgttta cctggaggca gcggcttggg cgcgcagagc
60
ggccgcgggt ccccgccacc tgcggccatg gatgaggagc gcgccctcta catcgccgg
120
gccggcgaag caggggctat cgagcgggtc ctgagggatt acagcgacaa gcatagggct
180
actttcaaat ttgaatcaac agatgaagat aaaagaaaga aactctgtga aggcataatt
240
aaagtcccta taaaggacat cccaacaaca tgtcaagtgt cctgcctgga agtactccgc
300
attctctcca gagacaaaaa ggtttttagtt cctgtgacaa ctaaggaaaa tatgcagata
360
ctgctgcgac tagccaagct aaatgagtta gatgattctt tggagaaagt atcagagttc
420
ccagttattg tggagtcatt aaaatgtctg tgtaatatag tgttcaacag tcagatggca
480
cagcagctca gcctggaact taatcttgct gcaaagctct gtaacctcct gagaaagtgc
540
aaggaccgga aatttatcaa tgacattaag tgctttgact tgcgcttgct cttccttctg
600
tcacttttgc acaccgacat caggtcacaa ttgcgctatg agctccaggg actaccgctg
660
ctaacgcaga tcg
673

```

&lt;210&gt; 3560

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3560

```

Met Asp Glu Glu Arg Ala Leu Tyr Ile Val Arg Ala Gly Glu Ala Gly
 1             5             10             15
Ala Ile Glu Arg Val Leu Arg Asp Tyr Ser Asp Lys His Arg Ala Thr
      20             25             30
Phe Lys Phe Glu Ser Thr Asp Glu Asp Lys Arg Lys Lys Leu Cys Glu
      35             40             45
Gly Ile Phe Lys Val Leu Ile Lys Asp Ile Pro Thr Thr Cys Gln Val
      50             55             60
Ser Cys Leu Glu Val Leu Arg Ile Leu Ser Arg Asp Lys Lys Val Leu
65             70             75             80
Val Pro Val Thr Thr Lys Glu Asn Met Gln Ile Leu Leu Arg Leu Ala
      85             90             95
Lys Leu Asn Glu Leu Asp Asp Ser Leu Glu Lys Val Ser Glu Phe Pro
      100            105            110
Val Ile Val Glu Ser Leu Lys Cys Leu Cys Asn Ile Val Phe Asn Ser
      115            120            125
Gln Met Ala Gln Gln Leu Ser Leu Glu Leu Asn Leu Ala Ala Lys Leu
      130            135            140
Cys Asn Leu Leu Arg Lys Cys Lys Asp Arg Lys Phe Ile Asn Asp Ile

```



```

145             150             155             160
Lys Cys Phe Asp Leu Arg Leu Leu Phe Leu Leu Ser Leu Leu His Thr
             165             170             175
Asp Ile Arg Ser Gln Leu Arg Tyr Glu Leu Gln Gly Leu Pro Leu Leu
             180             185             190
Thr Gln Ile .
             195

```

&lt;210&gt; 3561

&lt;211&gt; 523

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3561

```

acgcgtgcct gtaggcagac gaggggccag tgggcagagc agacatgaat gccccctgaa
60
ggctcacaga gctgactcag aagggccatt gtcacacact ggtaagagct gattctgagg
120
ggagggcatg agacgcctat tgcagagctg ctcaccagaa ggtcacagga atttagaaga
180
gaagctccta cctgcccccg atcatgcacg tggccactga ggatgccaga cgaggtgatg
240
ctggctctcat agagaatgta cccgaaggac tgtccatttc cccattgac tggcaggttc
300
tccatggtga tgggcttttc agacttgatt ggctgcgtac agaagagatg gaggggtggg
360
caggctcagg aggagtgggg tcacagacag actctgcttg ggggctggca catgggggtgg
420
aagcggaggt ttggtgggtg ttttctactt tgacttctca ttgcactaaa catacaactc
480
tccaggggtga cggggaagag gagtggggca aaggggtgtg cac
523

```

&lt;210&gt; 3562

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3562

```

Met His Val Ala Thr Glu Asp Ala Arg Arg Gly Asp Ala Gly Leu Ile
 1             5             10             15
Glu Asn Val Pro Glu Gly Leu Ser Ile Ser Pro Ile Asp Trp Gln Val
             20             25             30
Leu His Val Asp Gly Leu Phe Arg Leu Asp Trp Leu Arg Thr Glu Glu
             35             40             45
Met Glu Gly Trp Ala Gly Ser Gly Gly Val Gly Ser Gln Thr Asp Ser
             50             55             60
Ala Trp Gly Leu Ala His Gly Val Glu Ala Glu Val Trp Trp Val Phe
             65             70             75             80
Ser Thr Leu Thr Ser His Cys Thr Lys His Thr Thr Leu Gln Gly Asp
             85             90             95
Gly Glu Glu Glu Trp Gly Lys Gly Val Cys
             100             105

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<210> 3563  
 <211> 359  
 <212> DNA  
 <213> Homo sapiens

<400> 3563  
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 60  
 cgaagccagg ggcgcgcggc gatgtgagcc atgagcgcca cgtggacgct gtcgccggag  
 120  
 cccctgccgc cgtcgacggg gccccagtg ggcgcgggcc tggacgcgga gcagcgcacg  
 180  
 gtgttcgctt tcgtgctctg cctgctcgtg gtgctggtgc tgttgatggt gcgctgcgtg  
 240  
 cgcctcctgc tcgacccta cagccgcagtg cccgcctcgt cctggaccga ccacaaggag  
 300  
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 359

<210> 3564  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 3564  
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 1 5 10 15  
 Gly Pro Pro Val Gly Ala Gly Leu Asp Ala Glu Gln Arg Thr Val Phe  
 20 25 30  
 Ala Phe Val Leu Cys Leu Leu Val Val Leu Val Leu Leu Met Val Arg  
 35 40 45  
 Cys Val Arg Ile Leu Leu Asp Pro Tyr Ser Arg Met Pro Ala Ser Ser  
 50 55 60  
 Trp Thr Asp His Lys Glu Ala Leu Glu Arg Gly Gln Phe Asp Tyr Ala  
 65 70 75 80  
 Leu Val

<210> 3565  
 <211> 580  
 <212> DNA  
 <213> Homo sapiens

<400> 3565  
 acgcgtcgtg ggtgggaaaa gggatgccag gacaccagaa gagcaatata aaacagctcc  
 60  
 cgtgagcagg cacaggagac cttccgcgcc gccggccggg cgaccccgca ggaagtagga  
 120  
 aggacgagcg cgcacttcaa gtcccagaag ccccgcttcc ctggagcccg cgccgtgccg  
 180  
 cgctacgccc gccgggagcc gggcagagcg gccaatatgt cgcagcccaa gaaaagaaag  
 240  
 cttgagtcgg gggcgccgcg cgaaggaggg gaggggaactg aagaggaaga tggcgccggag  
 300

cgggaggcgg ccctggagcg accccggacg actaagcggg aacgggacca gctgtactac  
 360  
 gagtgctact cggacgtttc ggtccacgag gagatgatcg cggaccgcgt ccgcaccgat  
 420  
 gcctaccgct ggggtttccct tcggaactgg gcagcactgc gaggcaagac ggtactggac  
 480  
 gtgggcgcgg gcaccggcat tctgagcatc ttctgtgccc aggccggggc ccggcgcgtg  
 540  
 tacgcggtag aggccagcgc catctggcaa caggcccggg  
 580

<210> 3566

<211> 193

<212> PRT

<213> Homo sapiens

<400> 3566

Thr	Arg	Arg	Gly	Trp	Glu	Lys	Gly	Cys	Gln	Asp	Thr	Arg	Arg	Ala	Ile
1			5						10					15	
Gln	Asn	Ser	Ser	Arg	Glu	Gln	Ala	Gln	Glu	Thr	Phe	Arg	Ala	Ala	Gly
		20					25					30			
Arg	Ala	Thr	Pro	Gln	Glu	Val	Gly	Arg	Thr	Ser	Ala	His	Phe	Lys	Ser
		35				40				45					
Gln	Lys	Pro	Pro	Phe	Pro	Gly	Ala	Arg	Ala	Val	Pro	Arg	Tyr	Ala	Arg
	50					55				60					
Arg	Glu	Pro	Gly	Arg	Ala	Ala	Lys	Met	Ser	Gln	Pro	Lys	Lys	Arg	Lys
65				70					75					80	
Leu	Glu	Ser	Gly	Gly	Gly	Ala	Glu	Gly	Gly	Glu	Gly	Thr	Glu	Glu	Glu
			85					90					95		
Asp	Gly	Ala	Glu	Arg	Glu	Ala	Ala	Leu	Glu	Arg	Pro	Arg	Thr	Thr	Lys
		100					105					110			
Arg	Glu	Arg	Asp	Gln	Leu	Tyr	Tyr	Glu	Cys	Tyr	Ser	Asp	Val	Ser	Val
		115				120						125			
His	Glu	Glu	Met	Ile	Ala	Asp	Arg	Val	Arg	Thr	Asp	Ala	Tyr	Arg	Trp
	130					135					140				
Val	Ser	Leu	Arg	Asn	Trp	Ala	Ala	Leu	Arg	Gly	Lys	Thr	Val	Leu	Asp
145				150					155					160	
Val	Gly	Ala	Gly	Thr	Gly	Ile	Leu	Ser	Ile	Phe	Cys	Ala	Gln	Ala	Gly
			165				170						175		
Ala	Arg	Arg	Val	Tyr	Ala	Val	Glu	Ala	Ser	Ala	Ile	Trp	Gln	Gln	Ala
			180				185						190		

Arg

<210> 3567

<211> 2811

<212> DNA

<213> Homo sapiens

<400> 3567

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 ccttgacgaa gagccagaag gaagctgaac tgaccctga actggagaaa cagaaggaaa  
 120

ataagcaggt ggaagagatc ctccgtctgg agaaagaaat cgaggacctg cagcgcatga  
180  
aggagcagca ggagctgtcg ctgaccgagg cttccctgca gaagctgcag gagcggcggg  
240  
accaggagct cgcgaggctg gaggaggaga tttttgcacc tgaaaaaggc agccatagtt  
300  
ttccagaagc aactcagagg tcagattgct cggagagttt acagacaatt gctggcagag  
360  
aaaagggagc aagaagaaaa gaagaaacag gaagaggaag aaaagaagaa acgggaggaa  
420  
gaagaaagag aaagagagag agagcgaaga gaagccgagc tccgcgcca gcaggaagaa  
480  
gaaacgagga agcagcaaga actcgaagcc ttgcagaaga gccagaagga agctgaactg  
540  
acccgtgaac tggagaaaca gaagggaaat aagcaggtgg aagagatcct ccgtctggag  
600  
aaagaaatcg aggacctgca gcgcatgaag gagcagcagg agctgtcgct gaccgaggct  
660  
tccctgcaga agctgcagga gcggcgggac caggagctcc gcaggctgga ggaggaagcg  
720  
tgcagggcgg cccaggagtt cctcgagtcc ctcaatttcg acgagatcga cgagtgtgct  
780  
cggaatatcg agcggtcctt gtcgggggga agcgaatttt ccagcgagct ggctgagagc  
840  
gcatgcgagg agaagcccaa cttcaacttc agccagccct acccagagga ggaggtcgat  
900  
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960  
cactcagacc agcgaacaag tggcatccgg accagcgatg actcttcaga ggaggaccca  
1020  
tacatgaacg acacgggtgt gccaccagc cccagtgcgg acagcacggc gctgctcgcc  
1080  
ccatcagtgc aggactccgg gagcctacac aactcctcca gcggcgagtc cacctactgc  
1140  
atgccccaga acgctgggga cttgccctcc ccagacggcg actacgacta cgaccaggat  
1200  
gactatgagg acggtgccat cacttcgggc agcagcgtga cttcttccaa ctctacggc  
1260  
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1380  
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1500  
cgctgggtgc tcctcaagga tgaaaccttc ttgtgggtcc gctccaagca ggaggccctc  
1560  
aagcaaggct ggctccacaa aaaagggggg ggctcctcca cgctgtccag gagaaattgg  
1620  
aagaagcgct ggtttgcct cgcgcagtc aagctgatgt actttgaaaa cgacagcgag  
1680  
gagaagctca agggcaccgt agaagtgcga acggcaaaag agatcataga taacaccacc  
1740

aaggagaatg ggatcgacat cattatggcc gataggactt tccacctgat tgcagagtcc  
1800  
ccagaagatg ccagccagtg gttcagcgtg ctgagtcagg tccacgcgtc cacggaccag  
1860  
gagatccagg agatgcatga tgagcaggca aaccacaga atgctgtggg caccttggat  
1920  
gtggggctga ttgattctgt gtgtgcctct gacagccctg atagacccaa ctggtttgtg  
1980  
atcatcacgg ccaaccgggt gctgcactgc aacgccgaca cgccggagga gatgcaccac  
2040  
tgataaacc tgctgcagag gtccaaaggg gacaccagag tggagggcca ggaattcatc  
2100  
gtgagaggat ggttgacaaa agaggtgaag aacagtccaa agatgtcttc actgaaactg  
2160  
aagaaacggt ggtttgtact caccacaaat tccctggatt actacaagag ttcagagaag  
2220  
aacgcgtca aactggggac cctggctctc aacagcctct gctctgtcgt cccccagat  
2280  
gagaagatat tcaaagagac aggctactgg aacgtcacccg tgtacgggag caagcactgt  
2340  
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2400  
gtgactgaca ccaaggcccc gatcgacacc cccaccagc agctgattca agatatcaag  
2460  
gagaactgcc tgaactcgga tgtggtgga cagatttaca agcgggaacc gatccttcga  
2520  
tacacccatc accccttgca ctccccactc ctgccccctc cgtatgggga cataaatctc  
2580  
aacttgctca aagacaaagg ctataccacc cttcaggatg aggccatcaa gatattcaat  
2640  
tccctgcagc aactggagtc catgtctgac ccaattccaa taatccaggg catcctacag  
2700  
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2760  
aacaagtgc cccaccccg cagtgtgggc aacctgtaca gctggcagat c  
2811

&lt;210&gt; 3568

&lt;211&gt; 869

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3568

Pro	Arg	Leu	Pro	Cys	Arg	Ser	Cys	Arg	Ser	Gly	Gly	Thr	Arg	Ser	Ser
1				5					10					15	
Ala	Gly	Trp	Arg	Arg	Arg	Phe	Leu	His	Leu	Lys	Lys	Ala	Ala	Ile	Val
			20					25					30		
Phe	Gln	Lys	Gln	Leu	Arg	Gly	Gln	Ile	Ala	Arg	Arg	Val	Tyr	Arg	Gln
		35				40						45			
Leu	Leu	Ala	Glu	Lys	Arg	Glu	Gln	Glu	Glu	Lys	Lys	Lys	Gln	Glu	Glu
	50					55				60					
Glu	Glu	Lys	Lys	Lys	Arg	Glu	Glu	Glu	Glu	Arg	Glu	Arg	Glu	Arg	Glu
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Leu	Arg	Leu	Glu	Lys	Glu	Ile	Glu	Asp	Leu	Gln	Arg	Met	Lys	Glu	Gln								
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Pro	Tyr	Pro	Glu	Glu	Glu	Val	Asp	Glu	Gly	Phe	Glu	Ala	Asp	Asp	Asp								
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Ala	Phe	Lys	Asp	Ser	Pro	Asn	Pro	Ser	Glu	His	Gly	His	Ser	Asp	Gln								
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Arg	Thr	Ser	Gly	Ile	Arg	Thr	Ser	Asp	Asp	Ser	Ser	Glu	Glu	Asp	Pro								
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Tyr	Met	Asn	Asp	Thr	Val	Val	Pro	Thr	Ser	Pro	Ser	Ala	Asp	Ser	Thr								
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Val	Leu	Leu	Ala	Pro	Ser	Val	Gln	Asp	Ser	Gly	Ser	Leu	His	Asn	Ser								
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Ser	Ser	Gly	Glu	Ser	Thr	Tyr	Cys	Met	Pro	Gln	Asn	Ala	Gly	Asp	Leu								
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Pro	Ser	Pro	Asp	Gly	Asp	Tyr	Asp	Tyr	Asp	Gln	Asp	Asp	Tyr	Glu	Asp								
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Asp	Ser	Glu	Glu	Asp	Phe	Asp	Ser	Arg	Phe	Asp	Thr	Asp	Asp	Glu	Leu								
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Glu Met His His Trp Ile Thr Leu Leu Gln Arg Ser Lys Gly Asp Thr		
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Phe Val Leu Thr His Asn Ser Leu Asp Tyr Tyr Lys Ser Ser Glu Lys		
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Val Pro Pro Asp Glu Lys Ile Phe Lys Glu Thr Gly Tyr Trp Asn Val		
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Asn Glu Ala Thr Arg Trp Ser Ser Val Ser Gln Asn Val Thr Asp Thr		
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Lys Ala Pro Ile Asp Thr Pro Thr Gln Gln Leu Ile Gln Asp Ile Lys		
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Pro Ile Leu Arg Tyr Thr His His Pro Leu His Ser Pro Leu Leu Pro		
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785	790	795
Thr Thr Leu Gln Asp Glu Ala Ile Lys Ile Phe Asn Ser Leu Gln Gln		800
805	810	815
Leu Glu Ser Met Ser Asp Pro Ile Pro Ile Ile Gln Gly Ile Leu Gln		
820	825	830
Thr Gly His Asp Leu Arg Pro Leu Arg Asp Glu Leu Tyr Cys Gln Leu		
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Ile Lys Gln Thr Asn Lys Val Pro His Pro Gly Ser Val Gly Asn Leu		
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Tyr Ser Trp Gln Ile		
865		

&lt;210&gt; 3569

&lt;211&gt; 5070

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3569

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 <212> PRT  
 <213> Homo sapiens

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 Arg Ala Pro Ser Pro Pro Trp Pro Gln Gly Pro Leu Ser Pro Gly  
 35 40 45  
 Pro Gly Ser Leu Pro Leu Ser Ile Ala Arg Val Gln Thr Pro Pro Trp  
 50 55 60  
 His Pro Pro Gly Ala Pro Ser Pro Gly Leu Leu Gln Asp Ser Asp Ser  
 65 70 75 80  
 Leu Ser Gly Ser Tyr Leu Asp Pro Asn Tyr Gln Ser Ile Lys Trp Gln  
 85 90 95  
 Pro His Gln Gln Asn Lys Trp Ala Thr Leu Tyr Asp Ala Asn Tyr Lys  
 100 105 110  
 Glu Leu Pro Met Leu Thr Tyr Arg Val Asp Ala Asp Lys Gly Phe Asn  
 115 120 125  
 Phe Ser Val Gly Asp Asp Ala Phe Val Cys Gln Lys Lys Asn His Phe  
 130 135 140  
 Gln Val Thr Val Tyr Ile Gly Met Leu Gly Glu Pro Lys Tyr Val Lys  
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 Thr Pro Glu Gly Leu Lys Pro Leu Asp Cys Phe Tyr Leu Lys Leu His  
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 Gly Val Lys Leu Glu Ala Leu Asn Gln Ser Ile Asn Ile Glu Gln Ser  
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 Gln Ser Asp Arg Ser Lys Arg Pro Phe Asn Pro Val Thr Val Asn Leu  
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 Pro Pro Glu Gln Val Thr Lys Val Thr Val Gly Arg Leu His Phe Ser  
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 Gln Arg Tyr Phe Met Leu Val Val Ala Leu Gln Ala His Ala Gln Asn  
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 Arg Ala Gln Val Pro Asp Thr Val Phe His His Gly Arg Val Gly Ile  
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 Asn Thr Asp Arg Pro Asp Glu Ala Leu Val Val His Gly Asn Val Lys  
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Ile Glu Ala Thr Ala Pro Glu Thr Gly Val Ile Ala Gln Glu Val Lys
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Glu Ile Leu Pro Glu Ala Val Lys Asp Thr Gly Asp Met Val Phe Ala
385      390      395      400
Asn Gly Lys Thr Ile Glu Asn Phe Leu Val Val Asn Lys Glu Arg Ile
      405      410      415
Phe Met Glu Asn Val Gly Ala Val Lys Glu Leu Cys Lys Leu Thr Asp
      420      425      430
Asn Leu Glu Thr Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu
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Ala Lys Leu Arg Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly
      450      455      460
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465      470      475      480
His Lys Lys Arg Pro Lys Val Ala Ser Lys Ser Ser Ser Val Val
      485      490      495
Pro Asp Gln Ala Cys Ile Ser Gln Arg Phe Leu Gln Gly Thr Ile Ile
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      530      535      540
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Pro Pro Gly Gly Ser Glu Ala Leu Cys Pro Trp Ser Ser Gln Ser Phe
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      580      585      590
Ile Gln Pro Ser Leu Leu Leu Val Thr Thr Ser Leu Thr Ser Ser Ala
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Pro Gly Ser Ala Val Arg Thr Leu Asp Met Cys Ser Ser His Pro Cys
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Pro Val Ile Cys Cys Ser Ser Pro Thr Thr Asn Pro Thr Thr Gly Pro
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Ser Pro Ser Thr Asn Arg Ser Gly Pro Ser Gln Met Ala Leu Leu Pro
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Val Thr Asn Ile Arg Ala Lys Ser Trp Gly Leu Ser Val Asn Gly Ile
      675      680      685
Asp His Ser Lys His His Lys Ser Leu Glu Pro Leu Ala Ser Pro Ala
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Val Pro Phe Pro Gly Gly Gln Gly Lys Ala Lys Asn Ser Pro Ser Leu
705      710      715      720
Gly Phe His Gly Arg Ala Arg Arg Gly Ala Leu Gln Ser Ser Val Gly
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Pro Ala Glu Pro Thr Trp Ala Gln Gly Gln Ser Ala Ser Leu Leu Ala
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Glu Pro Val Pro Ser Leu Thr Ser Ile Gln Val Leu Glu Asn Ser Met
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Ser Ile Thr Ser Gln Tyr Cys Ala Pro Gly Asp Ala Cys Arg Pro Gly

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Ser Leu Thr Leu Gln Met Asn Ser Ser Ser Pro Val Ser Val Val Leu
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Cys Ser Leu Arg Ser Lys Glu Glu Pro Cys Glu Glu Gly Ser Leu Pro
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Gln Ser Leu His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp
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Pro Ile Thr Ile Leu Ser Phe Arg Glu Phe Thr Tyr His Phe Arg Val
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&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3571

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&lt;210&gt; 3572

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&lt;400&gt; 3572

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Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His

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&lt;213&gt; Homo sapiens

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<210> 3574

<211> 361

<212> PRT

<213> Homo sapiens

<400> 3574

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Thr	Leu	Thr	Ala	Thr	Asn	Pro	Arg	Ser	His	Ala	His	Ala	Asp	Ala	Pro
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Cys	Gly	Thr	Cys	Thr	His	Asn	His	Thr	Cys	Val	Gln	Ser	Gly	Arg	His
				85					90					95	
Thr	His	Thr	Cys	Ile	Glu	Ala	Ser	Leu	Trp	Thr	Pro	Ser	Ala	Ser	His
			100					105					110		
Arg	Gly	Gly	Ser	Pro	Ala	Val	Phe	Asp	Trp	Phe	Phe	Glu	Ala	Ala	Cys
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Pro	Ala	Ser	Val	Gln	Glu	Asp	Pro	Pro	Ile	Leu	Arg	Gln	Phe	Pro	Pro
	130					135					140				
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Pro	Phe	Asp	Val	Glu	Arg	Gly	Pro	Pro	Ser	Pro	Ala	Val	Gln	His	Phe
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225					230					235					240
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Gly	Ser	Gly	Val	Thr	Val	Ser	Ser	Gly	Gln	Gly	Ile	Pro	Pro	Pro	Thr
			260					265					270		
Arg	Gly	Asn	Ser	Lys	Pro	Leu	Ser	Cys	Phe	Val	Ala	Pro	Asp	Ser	Gly
		275					280						285		
Arg	Leu	Pro	Ser	Ile	Pro	Glu	Asn	Arg	Asn	Leu	Thr	Glu	Leu	Val	Val
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Ala	Val	Thr	Asp	Glu	Asn	Ile	Val	Gly	Leu	Phe	Ala	Ala	Leu	Leu	Ala
305					310					315					320
Glu	Arg	Arg	Val	Leu	Leu	Thr	Ala	Ser	Lys	Leu	Ser	Thr	Leu	Arg	Arg
				325					330					335	
Gly	Pro	Pro	Gly	Arg	Gly	Gly	Ser	Arg	Ala	Trp	Leu	Arg	Pro	Gly	Gly
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355

360

&lt;210&gt; 3575

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3575

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&lt;210&gt; 3576

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3576

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 Ser Thr Thr Lys Gln Asp Lys Ile Ile Ser Phe Ile Phe Ala Leu Thr  
 35 40 45  
 Ile Pro Lys Met Met Phe Leu Pro Asn Glu Cys Leu His Phe Ile Phe  
 50 55 60  
 Gln Thr Cys Ser Leu Lys Pro Ile Ile Ala Pro Leu Arg Asn Ile Phe  
 65 70 75 80  
 Thr Ser Ser Ser Gly Met Ser Leu Ser Ala Gly Ser Ser Pro Leu His  
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120
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180
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1020

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<210> 3578

<211> 195

<212> PRT

<213> Homo sapiens

<400> 3578

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		50				55					60				
Lys	Asn	Pro	Glu	Glu	Ile	Arg	Gly	Gly	Gly	Leu	Leu	Lys	Tyr	Ser	Asn
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Leu	Leu	Val	Arg	Asp	Phe	Arg	Pro	Thr	Asp	Gln	Glu	Glu	Ile	Lys	Thr
			85						90					95	
Leu	Glu	Arg	Tyr	Met	Cys	Ser	Arg	Phe	Phe	Ile	Asp	Phe	Pro	Asp	Ile
			100					105					110		
Leu	Glu	Gln	Gln	Arg	Lys	Leu	Glu	Thr	Tyr	Leu	Gln	Asn	His	Phe	Ala
		115					120					125			
Glu	Glu	Glu	Arg	Ser	Lys	Tyr	Asp	Tyr	Leu	Met	Ile	Leu	Arg	Arg	Val
		130				135					140				
Val	Asn	Glu	Ser	Thr	Val	Cys	Leu	Met	Gly	His	Glu	Arg	Arg	Gln	Thr
145				150					155					160	
Leu	Asn	Leu	Ile	Ser	Leu	Leu	Ala	Leu	Arg	Val	Leu	Gly	Gly	Thr	Lys
			165						170					175	
His	His	Pro	Pro	Val	Pro	Pro	Arg	Ser	Pro	Val	Thr	Thr	Ser	Gly	Pro
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<210> 3579

<211> 755

<212> DNA

<213> Homo sapiens

<400> 3579

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 300  
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<210> 3580

<211> 121

<212> PRT

<213> Homo sapiens

<400> 3580

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			20						25					30	
Glu	Thr	Lys	Gln	His	Glu	Lys	Trp	Leu	Ser	Gln	Pro	Thr	Cys	Ser	Asp
		35					40					45			
Met	Pro	Arg	Asn	Phe	Ser	Ser	Gly	Pro	Gly	Ser	Gly	Gly	Leu	Leu	Ile
		50				55					60				
Phe	Ser	Gln	Asp	Ile	Val	Leu	Ser	Trp	Asn	Leu	Ala	Gly	Gly	Trp	Ser
65				70						75				80	
Ile	Cys	Ile	Trp	Ser	Ile	Ala	Arg	Leu	Ser	His	Leu	Ser	Ser	Asp	Gln
				85					90					95	
Lys	Cys	Ile	Ser	Lys	Ile	Ile	Thr	Ser	Thr	Lys	Thr	Ile	Ile	Asp	Cys
			100					105						110	
Glu	Gln	Thr	Phe	Ser	Val	Thr	Ser	Arg							
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<210> 3581

<211> 2132

<212> DNA

<213> Homo sapiens

<400> 3581

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<210> 3582

<211> 138

<212> PRT

<213> Homo sapiens

<400> 3582

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Pro	Arg	Thr	Gly	Cys	Thr	Thr	Ala	Ser	Ala	Cys	Ser	Thr	Gly	Thr	Cys
			20					25					30		
Ala	Ala	Pro	Gly	Val	Ala	Pro	Arg	Gly	Ala	Cys	Trp	Thr	Cys	Thr	Arg
		35					40					45			
Arg	Ala	Ser	Ser	Ala	Cys	Thr	Arg	Arg	Gly	Thr	Ala	Ala	Ala	Trp	Ser
	50					55				60					
Ser	Arg	Pro	Arg	Pro	Ser	Thr	Thr	Ala	Thr	Ser	Arg	Cys	Ser	Ser	Ala
65					70					75				80	
Arg	Trp	Arg	Arg	Arg	Thr	Arg	Gly	Cys	Thr	Pro	Ala	Thr	Cys	Thr	Ile
			85					90					95		
Thr	Thr	Ala	Thr	Ser	Thr	Arg	Ala	Trp	Pro	Ser	Ala	Trp	Arg	Ser	Pro
			100					105					110		
Thr	Ala	Pro	Arg	Pro	Pro	Pro	Pro	Thr	Gly	Thr	Ala	Arg	Arg	Arg	Cys
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Trp	Arg	Trp	Arg	Ala	Ala	His	Pro	Arg	Phe						
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<210> 3583

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 3583

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&lt;210&gt; 3584

&lt;211&gt; 356

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3584

Met Ser Arg Pro Leu Leu Ile Thr Phe Thr Pro Ala Thr Asp Pro Ser  
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 Asp Leu Trp Lys Asp Gly Gln Gln Gln Pro Gln Pro Glu Lys Pro Glu

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Ser Thr Leu Asp Gly Ala Ala Ala Arg Ala Phe Tyr Glu Ala Leu Ile
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Gly Asp Glu Ser Ser Ala Pro Asp Ser Gln Arg Ser Gln Thr Glu Pro
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Ala Arg Glu Arg Lys Arg Lys Lys Arg Arg Ile Met Lys Ala Pro Ala
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Ala Glu Ala Val Ala Glu Gly Ala Ser Gly Arg His Gly Gln Gly Arg
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Ser Leu Glu Ala Glu Asp Lys Met Thr His Arg Ile Leu Arg Ala Ala
                100                105                110
Gln Glu Gly Asp Leu Pro Glu Leu Arg Arg Leu Leu Glu Pro His Glu
                115                120                125
Ala Gly Gly Ala Gly Gly Asn Ile Asn Ala Arg Asp Ala Phe Trp Trp
130                135                140
Thr Pro Leu Met Cys Ala Ala Arg Ala Gly Gln Gly Ala Ala Val Ser
145                150                155                160
Tyr Leu Leu Gly Arg Gly Ala Ala Trp Val Gly Val Cys Glu Leu Ser
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Gly Arg Asp Ala Ala Gln Leu Ala Glu Glu Ala Gly Phe Pro Glu Val
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Ala Arg Met Val Arg Glu Ser His Gly Glu Thr Arg Ser Pro Glu Asn
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Arg Ser Pro Thr Pro Ser Leu Gln Tyr Cys Glu Asn Cys Asp Thr His
210                215                220
Phe Gln Asp Ser Asn His Arg Thr Ser Thr Ala His Leu Leu Ser Leu
225                230                235                240
Ser Gln Gly Pro Gln Pro Pro Asn Leu Pro Leu Gly Val Pro Ile Ser
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Ser Pro Gly Phe Lys Leu Leu Leu Arg Gly Gly Trp Glu Pro Gly Met
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Gly Leu Gly Pro Arg Gly Glu Gly Arg Ala Asn Pro Ile Pro Thr Val
275                280                285
Leu Lys Arg Asp Gln Glu Gly Leu Gly Tyr Arg Ser Ala Pro Gln Pro
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Arg Val Thr His Phe Pro Ala Trp Asp Thr Arg Ala Val Ala Gly Arg
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Glu Arg Pro Pro Arg Val Ala Thr Leu Ser Trp Arg Glu Glu Arg Arg
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Asn Leu Glu Phe
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&lt;210&gt; 3585

&lt;211&gt; 2782

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3585

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1740



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&lt;210&gt; 3586

&lt;211&gt; 663

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3586

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			20					25					30		
Arg	Ser	Cys	Trp	Arg	Lys	Trp	Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn
		35				40						45			
Met	Ile	Leu	Phe	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe
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Pro	Pro	Val	Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn									
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Leu	Pro	Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly									
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Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	Arg									
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Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	Ala	Val									
			165						170					175										
Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	Ala	Glu	Val									
		180						185					190											
Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	Gly	Thr	Pro	Val									
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His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	Val	Phe	Leu	His	Ala									
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Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	His	Asp	Glu	Leu	Lys	Pro									
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			245						250					255										
Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu									
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			325						330					335										
Pro	Tyr	Ser	Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg									
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Trp	Thr	Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu									
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			405							410				415										
Leu	Gly	Val	Phe	Thr	Leu	Gly																		

515	520	525
Thr Gly Leu Ser Pro Glu Ile Val His Phe Asn Leu Tyr Pro Gln Pro		
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Asp Arg Lys Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser		
580	585	590
Arg Phe Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val		
595	600	605
Gln Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
610	615	620
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp Pro		
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Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala His Pro		
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Leu Pro Ile Trp Thr Pro Ala		
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&lt;210&gt; 3587

&lt;211&gt; 3148

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3587

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&lt;210&gt; 3588

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3588

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Lys	Thr	Ile	Ala	Lys	Leu	Trp	Asp	Ser	Lys	Met	Phe	Ala	Glu	Ile	Met
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Asn	Asn	Leu	Thr	Val	Glu	Ile	Glu	Asn	Glu	Leu	Asn	Ile	Ile	His	Lys
			100					105						110	
Phe	Ile	Arg	Asp	Lys	Tyr	Ser	Lys	Arg	Phe	Pro	Glu	Leu	Glu	Ser	Leu
			115				120					125			
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			130			135					140				
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Asn	Ala	Thr	Ile	Met	Val	Val	Ser	Val	Thr	Ala	Ser	Thr	Thr	Gln	Gly
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<211> 675
<212> DNA
<213> Homo sapiens
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180
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<210> 3590

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3590

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	20						25					30			
Asp	Pro	Met	Ser	Pro	Phe	His	Leu	Ser	Ser	Val	Ile	Leu	Cys	Arg	Pro
	35					40					45				
Ser	Ala	Trp	Pro	Cys	Leu	Arg	Ser	Ser	Ser	Pro	Pro	Ala	Ala	Gln	Gly
	50				55					60					
Ser	Phe	Val	Ser	Ala	Gln	Glu	Gly	Pro	Tyr	Asn	Pro	Ser	Trp	Leu	Trp
	65				70				75				80		
Pro	Gly	Pro	Cys	Phe	Val	Ser	Glu	Leu	Gly	Gly	Pro	Ile	Pro	Lys	His
			85				90					95			
Trp	Leu	Gly	Asn	Ser	Tyr	Pro	Ile	Cys	Cys	Leu	Gly	Ser	Ala	Trp	Phe
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Phe	Thr	His	Ile	Ser											
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<210> 3591

<211> 669

<212> DNA

<213> Homo sapiens

<400> 3591

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<210> 3592

<211> 223

<212> PRT

<213> Homo sapiens

<400> 3592

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		20						25					30		
Lys	Gln	Val	Asn	Trp	Lys	Ala	Cys	Arg	Trp	Ser	Ser	Ser	Gly	Val	Ile
		35					40						45		
Pro	Asn	Glu	Lys	Ile	Arg	Asn	Ile	Gly	Ile	Ser	Ala	His	Ile	Asp	Ser
		50				55					60				
Gly	Lys	Thr	Thr	Leu	Thr	Glu	Arg	Val	Leu	Tyr	Tyr	Thr	Gly	Arg	Ile
65					70					75				80	
Ala	Lys	Met	His	Glu	Val	Lys	Gly	Lys	Asp	Gly	Val	Gly	Ala	Val	Met
				85					90					95	
Asp	Ser	Met	Glu	Leu	Glu	Arg	Gln	Arg	Gly	Ile	Thr	Ile	Gln	Ser	Ala
			100						105					110	
Ala	Thr	Tyr	Thr	Met	Trp	Lys	Asp	Val	Asn	Ile	Asn	Ile	Ile	Asp	Thr
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Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Glu	Arg	Ala	Leu	Arg	Val
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Leu	Asp	Gly	Ala	Val	Leu	Val	Leu	Cys	Ala	Val	Gly	Gly	Val	Gln	Cys
145					150					155				160	
Gln	Thr	Met	Thr	Val	Asn	Arg	Gln	Met	Lys	Arg	Tyr	Asn	Val	Pro	Phe
				165					170					175	
Leu	Thr	Phe	Ile	Asn	Lys	Leu	Asp	Arg	Met	Gly	Ser	Asn	Pro	Ala	Arg
			180					185					190		
Ala	Leu	Gln	Gln	Met	Arg	Ser	Lys	Leu	Asn	His	Asn	Ala	Ala	Phe	Met
		195					200					205			
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 <211> 1005  
 <212> DNA  
 <213> Homo sapiens

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 840  
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<210> 3594  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<400> 3594  
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 Arg Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp  
 35 40 45  
 Arg Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys

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Pro Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile
65              70              75              80
Glu Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp
      85              90              95
Glu Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu
      100             105             110
Asp Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu
      115             120             125
Gln Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp
      130             135             140
Glu Lys Asn Asp Arg Thr Ser Leu Asn Arg Lys Leu Asp Arg Asn Leu
145             150             155             160
Val Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu
      165             170             175
Pro Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu
      180             185             190
Arg Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu
      195             200             205
Gly Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met
      210             215             220
Arg Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu
225             230             235             240
Leu Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val
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Trp Val Thr Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu
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Ala Gln Val Arg Arg Phe Val Ser Asp Leu
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<210> 3595  
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 <212> DNA  
 <213> Homo sapiens

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1903

&lt;210&gt; 3596

&lt;211&gt; 496

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3596

Phe Gln Val Thr Arg Gly Asp Tyr Ala Pro Ile Leu Gln Lys Val Val

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Glu Gln Leu Glu Lys Ala Lys Ala Tyr Ala Ala Asn Ser His Gln Gly			
	20	25	30
Gln Met Leu Ala Gln Tyr Ile Glu Ser Phe Thr Gln Gly Ser Ile Glu			
	35	40	45
Ala His Lys Arg Gly Ser Arg Phe Trp Ile Gln Asp Lys Gly Pro Ile			
	50	55	60
Val Glu Ser Tyr Ile Gly Phe Ile Glu Ser Tyr Arg Asp Pro Phe Gly			
65	70	75	80
Ser Arg Gly Glu Phe Glu Gly Phe Val Ala Val Val Asn Lys Ala Met			
	85	90	95
Ser Ala Lys Phe Glu Arg Leu Val Ala Ser Ala Glu Gln Leu Leu Lys			
	100	105	110
Glu Leu Pro Trp Pro Pro Thr Phe Glu Lys Asp Lys Phe Leu Thr Pro			
	115	120	125
Asp Phe Thr Ser Leu Asp Val Leu Thr Phe Ala Gly Ser Gly Ile Pro			
	130	135	140
Ala Gly Ile Asn Ile Pro Asn Tyr Asp Asp Leu Arg Gln Thr Glu Gly			
145	150	155	160
Phe Lys Asn Val Ser Leu Gly Asn Val Leu Ala Val Ala Tyr Ala Thr			
	165	170	175
Gln Arg Glu Lys Leu Thr Phe Leu Glu Glu Asp Asp Lys Asp Leu Tyr			
	180	185	190
Ile Leu Trp Lys Gly Pro Ser Phe Asp Val Gln Val Gly Leu His Glu			
	195	200	205
Leu Leu Gly His Gly Ser Gly Lys Leu Phe Val Gln Asp Glu Lys Gly			
	210	215	220
Ala Phe Asn Phe Asp Gln Glu Thr Val Ile Asn Pro Glu Thr Gly Glu			
225	230	235	240
Gln Ile Gln Ser Trp Tyr Arg Ser Gly Glu Thr Trp Asp Ser Lys Phe			
	245	250	255
Ser Thr Ile Ala Ser Ser Tyr Glu Glu Cys Arg Ala Glu Ser Val Gly			
	260	265	270
Leu Tyr Leu Cys Leu His Pro Gln Val Leu Glu Ile Phe Gly Phe Glu			
	275	280	285
Gly Ala Asp Ala Glu Asp Val Ile Tyr Val Asn Trp Leu Asn Met Val			
	290	295	300
Arg Ala Gly Leu Leu Ala Leu Glu Phe Tyr Thr Pro Glu Ala Phe Asn			
305	310	315	320
Trp Arg Gln Ala His Met Gln Ala Arg Phe Val Ile Leu Arg Val Leu			
	325	330	335
Leu Glu Ala Gly Glu Gly Leu Val Thr Ile Thr Pro Thr Thr Gly Ser			
	340	345	350
Asp Gly Arg Pro Asp Ala Arg Val Arg Leu Asp Arg Ser Lys Ile Arg			
	355	360	365
Ser Val Gly Lys Pro Ala Leu Glu Arg Phe Leu Arg Arg Leu Gln Val			
	370	375	380
Leu Lys Ser Thr Gly Asp Val Ala Gly Gly Arg Ala Leu Tyr Glu Gly			
385	390	395	400
Tyr Ala Thr Val Thr Asp Ala Pro Pro Glu Cys Phe Leu Thr Leu Arg			
	405	410	415
Asp Thr Val Leu Leu Arg Lys Glu Ser Arg Lys Leu Ile Val Gln Pro			
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Asn Thr Arg Leu Glu Gly Asn Gly Ser Asp Val Gln Leu Leu Glu Tyr			

<210> 3598

<211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 3598

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      20             25             30
Asp Tyr Asn Lys Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu
      35             40             45
Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg
      50             55             60
Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys
65             70             75             80
His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala
      85             90             95
Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu
      100            105            110
Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
      115            120            125
Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
      130            135            140
Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
145            150            155

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<210> 3599  
 <211> 691  
 <212> DNA  
 <213> Homo sapiens

<400> 3599

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<210> 3600  
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<213> Homo sapiens

<400> 3600  
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Met Val Glu Val Arg Ser Trp Ser Gly Ser Leu Val Gly Trp Leu Ala  
35 40 45  
Pro Arg Pro Leu Ser Val Pro Ile Glu His Leu Leu Gly Ala Lys Asn  
50 55 60  
Cys Cys Arg His Gly Gly Gln Trp Val Arg Arg Ala Val Pro Ala Val  
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Leu Leu

<210> 3601  
<211> 2963  
<212> DNA  
<213> Homo sapiens

<400> 3601  
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<210> 3602

<211> 299

<212> PRT

<213> Homo sapiens

<400> 3602

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			20					25					30		
Glu	Ala	Arg	Glu	Leu	Met	Tyr	Ser	Gly	Ala	Leu	Leu	Phe	Phe	Ser	His
			35					40					45		
Gly	Gln	Gln	Asn	Ser	Ala	Ala	Asp	Leu	Ser	Met	Leu	Val	Leu	Glu	Ser
			50					55					60		
Leu	Glu	Lys	Ala	Glu	Val	Glu	Val	Ala	Asp	Glu	Leu	Leu	Glu	Asn	Leu
								70					75		80
Ala	Lys	Val	Phe	Ser	Leu	Met	Asp	Pro	Asn	Ser	Pro	Glu	Arg	Val	Thr
Phe	Val	Ser	Arg	Ala	Leu	Lys	Trp	Ser	Ser	Gly	Gly	Ser	Gly	Lys	Leu
Gly	His	Pro	Arg	Leu	His	Gln	Leu	Leu	Ala	Leu	Thr	Leu	Trp	Lys	Glu
Gln	Asn	Tyr	Cys	Glu	Ser	Arg	Tyr	His	Phe	Leu	His	Ser	Ala	Asp	Gly
Glu	Gly	Cys	Ala	Asn	Met	Leu	Val	Glu	Tyr	Ser	Thr	Ser	Arg	Gly	Phe
Arg	Ser	Glu	Val	Asp	Met	Phe	Val	Ala	Gln	Ala	Val	Leu	Gln	Phe	Leu
Cys	Leu	Lys	Asn	Lys	Ser	Ser	Ala	Ser	Val	Val	Phe	Thr	Thr	Tyr	Thr
Gln	Lys	His	Pro	Ser	Ile	Glu	Asp	Gly	Pro	Pro	Phe	Val	Glu	Pro	Leu

195	200	205
Leu Asn Phe Ile Trp Phe	Leu Leu Leu Ala Val Asp	Gly Gly Lys Leu
210	215	220
Thr Val Phe Thr Val Leu Cys Glu Gln Tyr Gln	Pro Ser Leu Arg Arg	
225	230	235
Asp Pro Met Tyr Asn Glu Tyr Leu Asp Arg Ile Gly Gln Leu Phe Phe		240
	245	250
Gly Val Pro Pro Lys Gln Thr Ser Ser Tyr Gly Gly Leu Leu Gly Asn		255
	260	265
Leu Leu Thr Ser Leu Met Gly Ser Ser Glu Gln Glu Asp Gly Glu Glu		270
	275	280
Ser Pro Ser Asp Gly Ser Pro Ile Glu Leu Asp		285
290	295	

&lt;210&gt; 3603

&lt;211&gt; 1082

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3603

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 tt  
 1082

<210> 3604  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 3604  
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 20 25 30  
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 35 40 45  
 Ala Gly Val Ser Pro Arg Gly Val Lys Arg Gln Arg Arg Ser Ser Ser  
 50 55 60  
 Gly Gly Ser Gln Glu Lys Arg Gly Arg Pro Ser Gln Glu Pro Pro Leu  
 65 70 75 80  
 Ala Pro Pro His Arg Arg Arg Arg Ser Arg Gln His Pro Gly Pro Leu  
 85 90 95  
 Pro Pro Thr Asn Ala Ala Pro Thr Val Pro Gly Pro Val Glu Pro Leu  
 100 105 110  
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 Arg Leu  
 145

<210> 3605  
 <211> 2004  
 <212> DNA  
 <213> Homo sapiens

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 420  
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840  
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1920  
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1980  
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2004

&lt;210&gt; 3606

<211> 324  
 <212> PRT  
 <213> Homo sapiens

<400> 3606

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Pro Arg Gly Val Gln Arg Val Glu Gly Lys Leu Arg Ala Ser Val Glu
 20           25           30
Lys Gly Asp Tyr Tyr Glu Ala His Gln Met Tyr Arg Thr Leu Phe Phe
 35           40           45
Arg Tyr Met Ser Gln Ser Lys His Thr Glu Ala Arg Glu Leu Met Tyr
 50           55           60
Ser Gly Ala Leu Leu Phe Phe Ser His Gly Gln Gln Asn Ser Ala Ala
 65           70           75           80
Asp Leu Ser Met Leu Val Leu Glu Ser Leu Glu Lys Ala Glu Val Glu
 85           90           95
Val Ala Asp Glu Leu Leu Glu Asn Leu Ala Lys Val Phe Ser Leu Met
 100          105          110
Asp Pro Asn Ser Pro Glu Arg Val Thr Phe Val Ser Arg Ala Leu Lys
 115          120          125
Trp Ser Ser Gly Gly Ser Gly Lys Leu Gly His Pro Arg Leu His Gln
 130          135          140
Leu Leu Ala Leu Thr Leu Trp Lys Glu Gln Asn Tyr Cys Glu Ser Arg
 145          150          155          160
Tyr His Phe Leu His Ser Ala Asp Gly Glu Gly Cys Ala Asn Met Leu
 165          170          175
Val Glu Tyr Ser Thr Ser Arg Gly Phe Arg Ser Glu Val Asp Met Phe
 180          185          190
Val Ala Gln Ala Val Leu Gln Phe Leu Cys Leu Lys Asn Lys Ser Ser
 195          200          205
Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro Ser Ile Glu
 210          215          220
Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile Trp Phe Leu
 225          230          235          240
Leu Leu Ala Val Asp Gly Gly Lys Leu Thr Val Phe Thr Val Leu Cys
 245          250          255
Glu Gln Tyr Gln Pro Ser Leu Arg Arg Asp Pro Met Tyr Asn Glu Tyr
 260          265          270
Leu Asp Arg Ile Gly Gln Leu Phe Phe Gly Val Pro Pro Lys Gln Thr
 275          280          285
Ser Ser Tyr Gly Gly Leu Leu Gly Asn Leu Leu Thr Ser Leu Met Gly
 290          295          300
Ser Ser Glu Gln Glu Asp Gly Glu Glu Ser Pro Ser Asp Gly Ser Pro
 305          310          315          320
Ile Glu Leu Asp

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<210> 3607  
 <211> 1726  
 <212> DNA  
 <213> Homo sapiens

<400> 3607

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accctgtgtg ctgggatatg cagctatgaa ggggaagggtg gaatgtgttc catccgtctc  
180  
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240  
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300  
gaattttgta aacatatgca tcgcatcaac agcctgactg gagccaatat aacggtatac  
360  
catacttttc acgatgaggt ggatgagtat cggcgacact ggtggcgctg caatgggccg  
420  
tgccagcaca ggccaccgta ttacggctat gtcaaacgag ctactaacag ggaaccctct  
480  
gctcatgact attggtgggc tgagcaccag aaaacctgtg gaggcactta cataaaaaatc  
540  
aaggaaccag agaattactc aaaaaaaggc aaaggaaagg caaaactagg aaaggaacca  
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660  
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720  
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cctagagtat catttgccaa ccaaaaggct ttcagagggtg tgaatggatc tccaaggata  
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1380  
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1620

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 1680  
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 1726

<210> 3608  
 <211> 436  
 <212> PRT  
 <213> Homo sapiens

<400> 3608  
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 20 25 30  
 Glu Val Lys Trp Ser Val Arg Met Thr Leu Cys Ala Gly Ile Cys Ser  
 35 40 45  
 Tyr Glu Gly Lys Gly Gly Met Cys Ser Ile Arg Leu Ser Glu Pro Leu  
 50 55 60  
 Leu Lys Leu Arg Pro Arg Lys Asp Leu Val Glu Thr Leu Leu His Glu  
 65 70 75 80  
 Met Ile His Ala Tyr Leu Phe Val Thr Asn Asn Asp Lys Asp Arg Glu  
 85 90 95  
 Gly His Gly Pro Glu Phe Cys Lys His Met His Arg Ile Asn Ser Leu  
 100 105 110  
 Thr Gly Ala Asn Ile Thr Val Tyr His Thr Phe His Asp Glu Val Asp  
 115 120 125  
 Glu Tyr Arg Arg His Trp Trp Arg Cys Asn Gly Pro Cys Gln His Arg  
 130 135 140  
 Pro Pro Tyr Tyr Gly Tyr Val Lys Arg Ala Thr Asn Arg Glu Pro Ser  
 145 150 155 160  
 Ala His Asp Tyr Trp Trp Ala Glu His Gln Lys Thr Cys Gly Gly Thr  
 165 170 175  
 Tyr Ile Lys Ile Lys Glu Pro Glu Asn Tyr Ser Lys Lys Gly Lys Gly  
 180 185 190  
 Lys Ala Lys Leu Gly Lys Glu Pro Val Leu Ala Ala Glu Asn Lys Asp  
 195 200 205  
 Lys Pro Asn Arg Gly Glu Ala Gln Leu Val Ile Pro Phe Ser Gly Lys  
 210 215 220  
 Gly Tyr Val Leu Gly Glu Thr Ser Asn Leu Pro Ser Pro Gly Lys Leu  
 225 230 235 240  
 Ile Thr Ser His Ala Ile Asn Lys Thr Gln Asp Leu Leu Asn Gln Asn  
 245 250 255  
 His Ser Ala Asn Ala Val Arg Pro Asn Ser Lys Ile Lys Val Lys Phe  
 260 265 270  
 Glu Gln Asn Gly Ser Ser Lys Asn Ser His Leu Val Ser Pro Ala Val  
 275 280 285  
 Ser Asn Ser His Gln Asn Val Leu Ser Asn Tyr Phe Pro Arg Val Ser  
 290 295 300  
 Phe Ala Asn Gln Lys Ala Phe Arg Gly Val Asn Gly Ser Pro Arg Ile  
 305 310 315 320  
 Ser Val Thr Val Gly Asn Ile Pro Lys Asn Ser Val Ser Ser Ser Ser  
 325 330 335  
 Gln Arg Arg Val Ser Ser Ser Lys Ile Ser Leu Arg Asn Ser Ser Lys

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          340          345          350
Val Thr Glu Ser Ala Ser Val Met Pro Ser Gln Asp Val Ser Gly Ser
          355          360          365
Glu Asp Thr Phe Pro Asn Lys Arg Pro Arg Leu Glu Asp Lys Thr Val
          370          375          380
Phe Asp Asn Phe Phe Ile Lys Lys Glu Gln Ile Lys Ser Ser Gly Asn
385          390          395          400
Asp Pro Lys Tyr Ser Thr Thr Thr Ala Gln Asn Ser Ser Ser Ser Ser
          405          410          415
Ser Gln Ser Lys Met Val Asn Cys Pro Val Cys Gln Asn Glu Val Leu
          420          425          430
Gly Val Ser Asp
          435

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&lt;210&gt; 3609

&lt;211&gt; 1286

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3609

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780
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960
tcctctgggc cctctccttc gtctgggaag gcaccagcat gagtcccaca caccagcct
1020

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 1286

<210> 3610

<211> 268

<212> PRT

<213> Homo sapiens

<400> 3610

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		20					25					30			
Glu	Pro	Gln	Asp	Leu	Glu	Ser	Thr	Asn	Leu	Leu	Glu	Ser	Glu	Ala	Pro
		35					40				45				
Arg	Asp	Tyr	Phe	Leu	Lys	Phe	Ala	Tyr	Ile	Val	Asp	Leu	Asp	Ser	Asp
50					55						60				
Thr	Ala	Asp	Lys	Phe	Leu	Gln	Leu	Xaa	Trp	Asn	Gln	Arg	Cys	Gln	Glu
65					70					75				80	
Gly	Ala	Val	Ser	Tyr	Gln	Xaa	Tyr	Pro	Leu	Ser	Pro	Thr	Arg	Phe	Thr
			85						90					95	
His	Cys	Glu	Gln	Val	Leu	Gly	Glu	Gly	Ala	Leu	Asp	Arg	Gly	Thr	Tyr
			100					105					110		
Tyr	Trp	Glu	Val	Glu	Ile	Ile	Glu	Gly	Trp	Val	Ser	Met	Gly	Val	Met
		115					120					125			
Ala	Ala	Asp	Phe	Ser	Pro	Gln	Glu	Pro	Tyr	Asp	Arg	Gly	Arg	Leu	Gly
		130				135					140				
Arg	Asn	Ala	His	Ser	Cys	Cys	Leu	Gln	Trp	Asn	Gly	Arg	Ser	Phe	Ser
145					150					155				160	
Val	Trp	Phe	His	Gly	Leu	Glu	Ala	Pro	Leu	Pro	His	Pro	Phe	Ser	Pro
			165						170					175	
Thr	Val	Gly	Val	Cys	Leu	Glu	Tyr	Ala	Asp	Arg	Ala	Leu	Ala	Phe	Tyr
			180					185					190		
Ala	Val	Arg	Asp	Gly	Lys	Met	Ser	Leu	Leu	Arg	Arg	Leu	Lys	Ala	Ser
		195					200					205			
Arg	Pro	Arg	Arg	Gly	Gly	Ile	Pro	Ala	Ser	Pro	Ile	Asp	Pro	Phe	Gln
		210				215						220			
Ser	Arg	Leu	Asp	Ser	His	Phe	Ala	Gly	Leu	Phe	Thr	His	Arg	Leu	Lys
225					230					235				240	
Pro	Ala	Phe	Phe	Leu	Glu	Ser	Val	Asp	Ala	His	Leu	Gln	Ile	Gly	Pro
			245						250					255	
Leu	Lys	Lys	Ser	Cys	Ile	Ser	Val	Leu	Lys	Arg	Arg				
			260						265						

<210> 3611

<211> 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3611

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240  
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660  
cccattgttc ggagaagaat aggaacagcc ttcaaaactgg atgaacagaa aatcctgccc  
720  
aaaggagagg aagctgaact ggaacgcctg gaacgagagt ttgccattca gtcccagatt  
780  
acggaggccg cccgccgcct agccagtgc cccaac  
816

&lt;210&gt; 3612

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3612

Tyr	Gly	Val	His	Tyr	Tyr	Ala	Val	Lys	Asp	Lys	Gln	Gly	Ile	Pro	Trp
1			5						10					15	
Trp	Leu	Gly	Leu	Ser	Tyr	Lys	Gly	Ile	Phe	Gln	Tyr	Asp	Tyr	His	Asp
	20							25				30			
Lys	Val	Lys	Pro	Arg	Lys	Ile	Phe	Gln	Trp	Arg	Gln	Leu	Glu	Asn	Leu
	35					40					45				
Tyr	Phe	Arg	Glu	Lys	Lys	Phe	Ser	Val	Glu	Val	His	Asp	Pro	Arg	Arg
	50					55					60				
Ala	Ser	Val	Thr	Arg	Arg	Thr	Phe	Gly	His	Ser	Gly	Ile	Ala	Val	His
65				70					75				80		
Thr	Trp	Tyr	Ala	Cys	Pro	Ala	Leu	Ile	Lys	Ser	Ile	Trp	Ala	Met	Ala
			85					90					95		
Ile	Ser	Gln	His	Gln	Phe	Tyr	Leu	Asp	Arg	Lys	Gln	Ser	Lys	Ser	Lys
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<210> 3614
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<212> PRT
<213> Homo sapiens
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&lt;400&gt; 3614

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      20             25             30
Gly Leu Gly Ile Ser Leu Asn Ser Lys Arg Arg Lys Glu Glu Thr Phe
      35             40             45
Pro Thr Arg Cys Gly Cys Asp Ala Ser Gln Gly Pro Gln Gly His Cys
      50             55             60
Pro Arg Ala His Arg Pro Pro Leu Thr Ala Thr Gly Ala Trp Ile Arg
65             70             75             80
Ser Tyr Ile Val Gln Ser Phe Arg Pro Leu Pro Trp Ser Thr Arg Thr
      85             90             95
Arg Ala Arg Ile Ser Gly Arg Ala His Thr His Ser Tyr Thr Arg Thr
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Gln Thr Arg Ser Glu Lys Ser Pro Pro Pro Pro
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&lt;210&gt; 3615

&lt;211&gt; 1388

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3615

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900

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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asp Asp Glu Asp Tyr Glu Arg Arg Arg Ser Glu Cys Val Ser Glu Met  
 50 55 60  
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 65 70 75 80  
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 85 90 95  
 Arg Ala Pro Glu Tyr Thr Glu Pro Leu Gly Gly Leu Gln Arg Ser Leu  
 100 105 110  
 Lys Ile Arg Ile Gln Val Ala Gly Ile Tyr Lys Gly Phe Cys Leu Asp  
 115 120 125  
 Val Ile Arg Asn Lys Tyr Glu Cys Glu Leu Gln Gly Ala Lys Gln His  
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 145 150 155 160  
 Gln Glu Arg Ile Gln Arg Leu Glu Glu Asp Arg Gln Ser Leu Asp Leu  
 165 170 175  
 Ser Ser Glu Trp Trp Asp Asp Lys Leu His Ala Arg Gly Ser Ser Arg  
 180 185 190  
 Ser Trp Asp Ser Leu Pro Pro Ser Lys Arg Lys Lys Ala Pro Leu Val  
 195 200 205  
 Ser Gly Pro Tyr Ile Val Tyr Met Leu Gln Glu Ile Gly Ile Leu Glu  
 210 215 220  
 Asp Trp Thr Ala Ile Lys Lys Ala Arg Ala Ala Val Ser Pro Gln Lys

225		230		235		240									
Arg	Lys	Ser	Asp	Asp	Arg	Arg	Thr	His	Arg	Pro	Leu	Arg	Val	Cys	Pro
		245		250		255									
Ala	Arg	Leu	Leu	Trp	Cys	Cys	Trp	Ala	Leu	Pro	Leu	His	Leu	Ala	Leu
		260		265		270									
Ala	Trp	Thr	Pro	Pro	Leu	Pro	Ser	Ser	Arg	Pro	Ala	Gln	Leu	Trp	Pro
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Trp	Ser														
	290														

<210> 3617  
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 <212> DNA  
 <213> Homo sapiens

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<210> 3618  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 3618  
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<210> 3619
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<212> DNA
<213> Homo sapiens
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240
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35 40 45  
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50 55 60  
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Thr Ala Ser Thr Pro Thr Thr Ser Cys Thr Ser Phe Met Thr Thr Cys  
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<210> 3621  
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<212> DNA  
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<211> 228

<212> PRT

<213> Homo sapiens

<400> 3622

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			20					25					30		
Glu	Ser	Gly	Phe	Asp	Pro	Asn	Ile	Arg	Asp	Ser	Arg	Gly	Arg	Thr	Gly
		35				40						45			
Leu	His	Leu	Ala	Ala	Ala	Arg	Gly	Asn	Val	Asp	Ile	Cys	Gln	Leu	Leu
		50				55					60				
His	Lys	Phe	Gly	Ala	Asp	Leu	Leu	Ala	Thr	Asp	Tyr	Gln	Gly	Asn	Thr
65				70					75					80	
Ala	Leu	His	Leu	Cys	Gly	His	Val	Asp	Thr	Ile	Gln	Phe	Leu	Val	Ser
			85					90					95		
Asn	Gly	Leu	Lys	Ile	Asp	Ile	Cys	Asn	His	Gln	Gly	Ala	Thr	Pro	Leu
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Val	Leu	Ala	Lys	Arg	Arg	Gly	Val	Asn	Lys	Asp	Val	Ile	Arg	Leu	Leu
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Glu	Ser	Leu	Glu	Glu	Gln	Glu	Val	Lys	Gly	Phe	Asn	Arg	Gly	Thr	His
		130				135					140				
Ser	Lys	Leu	Glu	Thr	Met	Gln	Thr	Ala	Glu	Ser	Glu	Ser	Ala	Met	Glu
145				150					155				160		
Ser	His	Ser	Leu	Leu	Asn	Pro	Asn	Leu	Gln	Gln	Gly	Glu	Gly	Val	Leu

165 170 175  
 Ser Ser Phe Arg Thr Thr Trp Gln Glu Phe Val Glu Asp Leu Gly Phe  
 180 185 190  
 Trp Arg Val Leu Leu Leu Ile Phe Val Ile Ala Leu Leu Ser Leu Gly  
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<210> 3623  
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 420  
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 480  
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<210> 3624  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 3624  
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 Arg Asp Ile Thr Lys Glu Glu Ile Ser Lys Phe Ser Lys Ala Glu Trp  
 35 40 45  
 Glu Lys Lys Arg Met Asp Lys Ala Ile Gly Tyr Ser Phe Ala Ile Val  
 50 55 60  
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<210> 3625
<211> 4799
<212> DNA
<213> Homo sapiens
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2700  
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<210> 3626

<211> 551

<212> PRT

<213> Homo sapiens

<400> 3626

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		20						25					30		
Trp	Gly	Pro	Ser	Ser	Ser	Leu	Met	Ser	Glu	Ile	Ala	Asp	Leu	Thr	Tyr
	35						40					45			
Asn	Val	Val	Ala	Phe	Ser	Glu	Ile	Met	Ser	Met	Ile	Trp	Lys	Arg	Leu
	50					55					60				
Asn	Asp	His	Gly	Lys	Asn	Trp	Arg	His	Val	Tyr	Lys	Ala	Met	Thr	Leu
65				70					75					80	
Met	Glu	Tyr	Leu	Ile	Lys	Thr	Gly	Ser	Glu	Arg	Val	Ser	Gln	Gln	Cys
			85					90					95		
Lys	Glu	Asn	Met	Tyr	Ala	Val	Gln	Thr	Leu	Lys	Asp	Phe	Gln	Tyr	Val
		100					105					110			
Asp	Arg	Asp	Gly	Lys	Asp	Gln	Gly	Val	Asn	Val	Arg	Glu	Lys	Ala	Lys
		115				120					125				
Gln	Leu	Val	Ala	Leu	Leu	Arg	Asp	Glu	Asp	Arg	Leu	Arg	Glu	Glu	Arg
	130					135					140				
Ala	His	Ala	Leu	Lys	Thr	Lys	Glu	Lys	Leu	Ala	Gln	Thr	Ala	Thr	Ala
145				150					155					160	
Ser	Ser	Ala	Ala	Val	Gly	Ser	Gly	Pro	Pro	Pro	Glu	Ala	Glu	Gln	Ala
			165					170					175		
Trp	Pro	Gln	Ser	Ser	Gly	Glu	Glu	Glu	Leu	Gln	Leu	Gln	Leu	Ala	Leu
		180					185				190				
Ala	Met	Ser	Lys	Glu	Glu	Ala	Asp	Gln	Glu	Glu	Arg	Ile	Arg	Arg	Gly
	195					200					205				
Asp	Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr
	210				215						220				
Gly	Gly	Lys	Glu	Glu	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	
225				230					235				240		
Ala	Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro
			245					250					255		
Met	Ala	Ala	Ala	Val	Pro	Thr	Ala	Ala	Pro	Thr	Ser	Asp	Pro	Trp	Gly

260 265 270  
 Gly Pro Pro Val Pro Pro Ala Ala Asp Pro Trp Gly Gly Pro Ala Pro  
 275 280 285  
 Thr Pro Ala Ser Gly Asp Pro Trp Arg Pro Ala Ala Pro Ala Gly Pro  
 290 295 300  
 Ser Val Asp Pro Trp Gly Gly Thr Pro Ala Pro Ala Ala Gly Glu Gly  
 305 310 315 320  
 Pro Thr Pro Asp Pro Trp Gly Ser Ser Asp Gly Gly Val Pro Val Ser  
 325 330 335  
 Gly Pro Ser Ala Ser Asp Pro Trp Thr Pro Ala Pro Ala Phe Ser Asp  
 340 345 350  
 Pro Trp Gly Gly Ser Pro Ala Lys Pro Ser Thr Asn Gly Thr Thr Thr  
 355 360 365  
 Ala Gly Gly Phe Asp Thr Glu Pro Asp Glu Phe Ser Asp Phe Asp Arg  
 370 375 380  
 Leu Arg Thr Ala Leu Pro Thr Ser Gly Ser Ser Ala Gly Glu Leu Glu  
 385 390 395 400  
 Leu Leu Ala Gly Glu Val Pro Ala Arg Ser Pro Gly Ala Phe Asp Met  
 405 410 415  
 Ser Gly Val Arg Gly Ser Leu Ala Glu Ala Val Gly Ser Pro Pro Pro  
 420 425 430  
 Ala Ala Thr Pro Thr Pro Thr Pro Thr Arg Lys Thr Pro Glu Ser  
 435 440 445  
 Phe Leu Gly Pro Asn Ala Ala Leu Val Asp Leu Asp Ser Leu Val Ser  
 450 455 460  
 Arg Pro Gly Pro Thr Pro Gly Ala Lys Ala Ser Asn Pro Phe Leu  
 465 470 475 480  
 Pro Gly Gly Gly Pro Ala Thr Gly Pro Ser Val Thr Asn Pro Phe Gln  
 485 490 495  
 Pro Ala Pro Pro Ala Thr Leu Thr Leu Asn Gln Leu Arg Leu Ser Pro  
 500 505 510  
 Val Pro Pro Val Pro Gly Ala Pro Pro Thr Tyr Ile Ser Pro Leu Gly  
 515 520 525  
 Gly Gly Pro Gly Leu Pro Pro Met Met Pro Pro Gly Pro Pro Ala Pro  
 530 535 540  
 Asn Thr Asn Pro Phe Leu Leu  
 545 550

&lt;210&gt; 3627

&lt;211&gt; 1760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3627

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 120  
 aaaccaaaca tcataaattt tgacaccagt ctgccgacat cacatacata cctaggtgct  
 180  
 gatatggaag aatttcatgg caggactttg cacgatgacg acagctgtca ggtgattcca  
 240  
 gttcttccac aagtgatgat gatcctgatt cccggacaga cattacctct tcagcttttt  
 300



caccctcaag aagtcagtat ggtgcggaat ttaattcaga aagatagaac ctttgctgtt  
360  
cttgcataca gcaatgtaca ggaaagggaa gcacagtttg gaacaacagc agagatatat  
420  
gcctatcgag aagaacagga ttttggaatt gagatagtga aagtgaagc aattggaaga  
480  
caaaggttca aagtccttga gctaagaaca cagtcagatg gaatccagca agctaaagtg  
540  
caaattcttc ccgaatgtgt gttgccttca accatgtctg cagttcaatt agaatccctc  
600  
aataagtgcc agatatttcc ttcaaacct gtctcaagag aagaccaatg ttcataataa  
660  
tggtggcaga aataccagaa gagaaagttt cattgtgcaa atctaacttc atggcctcgc  
720  
tggtgtatt ccttatatga tgctgagacc ttaatggaca gaatcaagaa acagctacgt  
780  
gaatgggatg aaaatctaaa agatgattct cttccttcaa atccaataga ttttcttac  
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agagtagctg cttgtcttcc tattgatgat gtattgagaa ttcagctcct taaaattggc  
900  
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&lt;210&gt; 3628

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3628

Gly Glu Gly Asp Gln Gln Asp Ala Ala His Asn Met Gly Asn His Leu  
 1 5 10 15  
 Pro Leu Leu Pro Ala Glu Ser Glu Glu Asp Glu Met Glu Val Glu  
 20 25 30  
 Asp Gln Asp Ser Lys Glu Ala Lys Lys Pro Asn Ile Ile Asn Phe Asp  
 35 40 45  
 Thr Ser Leu Pro Thr Ser His Thr Tyr Leu Gly Ala Asp Met Glu Glu  
 50 55 60  
 Phe His Gly Arg Thr Leu His Asp Asp Asp Ser Cys Gln Val Ile Pro  
 65 70 75 80  
 Val Leu Pro Gln Val Met Met Ile Leu Ile Pro Gly Gln Thr Leu Pro  
 85 90 95  
 Leu Gln Leu Phe His Pro Gln Glu Val Ser Met Val Arg Asn Leu Ile  
 100 105 110  
 Gln Lys Asp Arg Thr Phe Ala Val Leu Ala Tyr Ser Asn Val Gln Glu  
 115 120 125  
 Arg Glu Ala Gln Phe Gly Thr Thr Ala Glu Ile Tyr Ala Tyr Arg Glu  
 130 135 140  
 Glu Gln Asp Phe Gly Ile Glu Ile Val Lys Val Lys Ala Ile Gly Arg  
 145 150 155 160  
 Gln Arg Phe Lys Val Leu Glu Leu Arg Thr Gln Ser Asp Gly Ile Gln  
 165 170 175  
 Gln Ala Lys Val Gln Ile Leu Pro Glu Cys Val Leu Pro Ser Thr Met  
 180 185 190  
 Ser Ala Val Gln Leu Glu Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser  
 195 200 205  
 Lys Pro Val Ser Arg Glu Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys  
 210 215 220  
 Tyr Gln Lys Arg Lys Phe His Cys Ala Asn Leu Thr Ser Trp Pro Arg  
 225 230 235 240  
 Trp Leu Tyr Ser Leu Tyr Asp Ala Glu Thr Leu Met Asp Arg Ile Lys  
 245 250 255  
 Lys Gln Leu Arg Glu Trp Asp Glu Asn Leu Lys Asp Asp Ser Leu Pro  
 260 265 270  
 Ser Asn Pro Ile Asp Phe Ser Tyr Arg Val Ala Ala Cys Leu Pro Ile  
 275 280 285  
 Asp Asp Val Leu Arg Ile Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln  
 290 295 300  
 Arg Leu Arg Cys Glu Leu Asp Ile Met Asn Lys Cys Thr Ser Leu Cys  
 305 310 315 320  
 Cys Lys Gln Cys Gln Glu Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe  
 325 330 335  
 Ser Leu Ser Leu Cys Gly Pro Met Ala Ala Tyr Val Asn Pro His Gly  
 340 345 350  
 Tyr Val His Glu Thr Leu Thr Val Tyr Lys Ala Cys Asn Leu Asn Leu  
 355 360 365  
 Ile Gly Arg Pro Ser Thr Glu His Ser Trp Phe Pro Gly Tyr Ala Trp  
 370 375 380  
 Thr Val Ala Gln Cys Lys Ile Cys Ala Ser His Ile Gly Trp Lys Phe  
 385 390 395 400  
 Thr Ala Thr Lys Lys Asp Met Ser Pro Gln Lys Phe Trp Gly Leu Thr

	405		410		415
Arg Ser Ala Leu Leu Pro Thr Ile Pro Asp Thr Glu Asp Glu Ile Ser					
	420		425		430
Pro Asp Lys Val Ile Leu Cys Leu					
	435		440		

&lt;210&gt; 3629

&lt;211&gt; 695

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3629

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695

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&lt;210&gt; 3630

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3630

Thr Arg Pro Leu Ser Gly Leu Val Trp Val Ala Leu Leu Ala Leu Gly														
1		5				10				15				
His Ala Phe Leu Phe Thr Gly Gly Val Val Ser Ala Trp Asp Gln Val														
	20					25				30				
Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu														
	35					40				45				
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His														
	50					55				60				
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro														
65					70				75				80	
Ala Leu Leu Pro Gln Leu Ala Ala Asn Ala Val Leu Phe Leu Cys Gly														

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<400> 3632
Met Gln Tyr Leu Glu Lys Arg Lys Asn Pro Val Cys His Phe Val Thr
  1             5             10             15
Pro Leu Asp Gly Ser Val Asp Val Asp Glu His Arg Arg Pro Glu Ala

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 Ile Thr Thr Glu Gly Lys Tyr Trp Lys Ser Arg Ile Glu Ile Val Ile  
 35 40 45  
 Arg Glu Tyr His Lys Trp Arg Thr Tyr Phe Lys Lys Arg Leu Gln Gln  
 50 55 60  
 His Lys Asp Glu Asp Leu Ser Ser Leu Val Gln Asp Asp Asp Met Leu  
 65 70 75 80  
 Tyr Trp His Lys His Gly Asp Gly Trp Lys Thr Pro Val Pro Met Glu  
 85 90 95  
 Glu Asp Pro Leu Leu Asp Thr Asp Met Leu Met Ser Glu Phe Ser Asp  
 100 105 110  
 Thr Leu Phe Ser Thr Leu Ser Ser His Gln Pro Val Ala Trp Pro Asn  
 115 120 125  
 Pro Arg Glu Ile Ala His Leu Gly Asn Ala Asp Met Ile Gln Pro Gly  
 130 135 140  
 Leu Ile Pro Leu Gln Pro Asn Leu Asp Phe Met Asp Thr Phe Glu Pro  
 145 150 155 160  
 Phe Gln Asp Leu Phe Ser Ser Ser Arg Ser Ile Phe Gly Ser Met Leu  
 165 170 175  
 Pro Ala Ser Ala Ser Ala Pro Val Pro Asp Pro Asn Asn Pro Pro Ala  
 180 185 190  
 Gln Glu Ser Ile Leu Pro Thr Thr Ala Leu Pro Thr Val Ser Leu Pro  
 195 200 205  
 Asp Ser Leu Ile Ala Pro Pro Thr Ala Pro Ser Leu Ala Arg  
 210 215 220

&lt;210&gt; 3633

&lt;211&gt; 1570

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3633

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 120  
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 180  
 ctgtgtgaag atggcatttc tcaactgatta ttggaaaagc acaagagcca cgtgctggag  
 240  
 ccattgtcca gccttgccct ggaggagcag tgtctggctt tgtccctaga ttggtccact  
 300  
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 360  
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 420  
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 480  
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 660

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<210> 3634
<211> 277
<212> PRT
<213> Homo sapiens
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<400> 3634																
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Ala	His	Gln	Phe	Glu	Ala	Trp	Ile	Ala	Phe	Asn	Tyr	Trp	His	Pro		
		20						25					30			
Glu	Ile	Val	Tyr	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Arg	Gly	Trp	Asp		
		35					40					45				
Thr	Arg	Val	Pro	Gly	Lys	Phe	Leu	Phe	Thr	Ser	Xaa	Lys	Thr	His	His	
		50				55						60				
Xaa	Gly	Val	Cys	Ser	Ile	Gln	Ser	Ser	Pro	His	Arg	Glu	His	Ile	Leu	
65					70					75				80		
Ala	Thr	Gly	Ser	Tyr	Asp	Glu	His	Ile	Leu	Leu	Trp	Asp	Thr	Arg	Asn	
			85						90					95		
Met	Lys	Gln	Pro	Leu	Ala	Asp	Thr	Pro	Val	Gln	Gly	Gly	Val	Trp	Arg	
			100					105					110			
Ile	Lys	Trp	His	Pro	Phe	His	His	His	Leu	Leu	Leu	Ala	Ala	Cys	Met	

115 120 125  
 His Ser Gly Phe Lys Ile Leu Asn Cys Gln Lys Ala Met Glu Glu Arg  
 130 135 140  
 Gln Glu Ala Thr Val Leu Thr Ser His Thr Leu Pro Asp Ser Leu Val  
 145 150 155 160  
 Tyr Gly Ala Asp Trp Ser Trp Leu Leu Phe Arg Ser Leu Gln Arg Ala  
 165 170 175  
 Pro Ser Trp Ser Phe Pro Ser Asn Leu Gly Thr Lys Thr Ala Asp Leu  
 180 185 190  
 Lys Gly Ala Ser Glu Leu Pro Thr Pro Cys His Glu Cys Arg Glu Asp  
 195 200 205  
 Asn Asp Gly Glu Gly His Ala Arg Pro Gln Ser Gly Met Lys Pro Leu  
 210 215 220  
 Thr Glu Gly Met Arg Lys Asn Gly Thr Trp Leu Gln Ala Thr Ala Ala  
 225 230 235 240  
 Thr Thr Arg Asp Cys Gly Val Asn Pro Glu Glu Ala Asp Ser Ala Phe  
 245 250 255  
 Ser Leu Leu Ala Thr Cys Ser Phe Tyr Asp His Ala Leu His Leu Trp  
 260 265 270  
 Glu Trp Glu Gly Asn  
 275

&lt;210&gt; 3635

&lt;211&gt; 835

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3635

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 gttggagttg gagagcagct tcttgagggg gactatgcac gggttacagca agtggatcct  
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 180  
 cctctggcga tgccctcaagc tttgcctctg gcggcaggtc ccttgccctcc aggggtccatc  
 240  
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835

<210> 3636

<211> 278

<212> PRT

<213> Homo sapiens

<400> 3636

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20 25 30  
Ala Arg Leu Gln Gln Val Asp Pro Val Leu Leu Lys Asp Glu Pro Gln  
35 40 45  
Gln Thr Ala Ala Gln Met Gly Cys Ala Pro Ile Gln Pro Leu Ala Met  
50 55 60  
Pro Gln Ala Leu Pro Leu Ala Ala Gly Pro Leu Pro Pro Gly Ser Ile  
65 70 75 80  
Ala Asn Leu Thr Glu Leu Gln Gly Val Ile Val Gly Gln Pro Val Leu  
85 90 95  
Gly Gln Ala Gln Leu Ala Gly Leu Gly Gln Gly Ile Leu Thr Glu Thr  
100 105 110  
Gln Gln Gly Leu Met Val Ala Ser Pro Ala Gln Thr Leu Asn Asp Thr  
115 120 125  
Leu Asp Asp Ile Met Ala Ala Val Ser Gly Arg Ala Ser Ala Met Ser  
130 135 140  
Asn Thr Pro Thr His Ser Ile Ala Ala Ser Ile Ser Gln Pro Gln Thr  
145 150 155 160  
Pro Thr Pro Ser Pro Ile Ile Ser Pro Ser Ala Met Leu Pro Ile Tyr  
165 170 175  
Pro Ala Ile Asp Ile Asp Ala Gln Thr Glu Ser Asn His Asp Thr Ala  
180 185 190  
Leu Thr Leu Ala Cys Ala Gly Gly His Glu Glu Leu Val Gln Thr Leu  
195 200 205  
Leu Glu Arg Gly Ala Ser Ile Glu His Arg Asp Lys Lys Gly Phe Thr  
210 215 220  
Pro Leu Ile Leu Ala Ala Thr Ala Gly His Val Gly Val Val Glu Ile  
225 230 235 240  
Leu Leu Asp Asn Gly Ala Asp Ile Glu Ala Gln Ser Glu Arg Thr Lys  
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Asp Thr Pro Leu Ser Leu Ala Cys Ser Gly Gly Arg Gln Glu Val Val  
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Glu Leu Leu Leu Ala Arg  
275

<210> 3637

<211> 2128

<212> DNA

<213> Homo sapiens

<400> 3637

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120  
cctgccaacc cctgctcttc caggtcgggc cccgggggttc tgcggtgtt agggacagag  
180  
gcaaagaagg gcaggacggt ccggtttccc gtggatgttc ccgcccgaga aagacagcaa  
240  
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300  
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720  
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960  
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1080  
accaagagca gacagaggag aagatgggcc aaaggggctt ggagaggtca aaacatccac  
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1200  
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1260  
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1320  
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1680

tattatcact ttataaaaca tacattaagc ctaataaatg gaccaataag ccaaactatc  
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 1860  
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 1920  
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 1980  
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 2040  
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 2128

&lt;210&gt; 3638

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3638

Met	Ala	Ser	Ser	Leu	Thr	Cys	Thr	Gly	Val	Ile	Trp	Ala	Leu	Leu	Ser
1				5					10					15	
Phe	Leu	Cys	Ala	Ala	Thr	Ser	Cys	Val	Gly	Phe	Phe	Met	Pro	Tyr	Trp
			20					25					30		
Leu	Trp	Gly	Ser	Gln	Leu	Gly	Lys	Pro	Val	Ser	Phe	Gly	Thr	Phe	Arg
		35					40					45			
Arg	Cys	Ser	Tyr	Pro	Val	His	Asp	Glu	Ser	Arg	Gln	Met	Met	Val	Met
	50					55					60				
Val	Glu	Glu	Cys	Gly	Arg	Tyr	Ala	Ser	Phe	Gln	Gly	Ile	Pro	Ser	Ala
65					70					75				80	
Glu	Trp	Arg	Ile	Cys	Thr	Ile	Val	Thr	Gly	Leu	Gly	Cys	Gly	Leu	Leu
			85						90					95	
Leu	Leu	Val	Ala	Leu	Thr	Ala	Leu	Met	Gly	Cys	Cys	Val	Ser	Asp	Leu
		100						105					110		
Ile	Ser	Arg	Thr	Val	Gly	Arg	Val	Ala	Gly	Gly	Ile	Gln	Phe	Leu	Gly
	115						120					125			
Gly	Leu	Leu	Ile	Gly	Ala	Gly	Cys	Ala	Leu	Tyr	Pro	Leu	Gly	Trp	Asp
	130					135					140				
Ser	Glu	Glu	Val	Arg	Gln	Thr	Cys	Gly	Tyr	Thr	Ser	Gly	Gln	Phe	Asp
145					150					155				160	
Leu	Gly	Lys	Cys	Glu	Ile	Gly	Trp	Ala	Tyr	Tyr	Cys	Thr	Gly	Ala	Gly
			165						170					175	
Ala	Thr	Ala	Ala	Met	Leu	Leu	Cys	Thr	Trp	Leu	Ala	Cys	Phe	Ser	Gly
			180					185					190		
Lys	Lys	Gln	Lys	His	Tyr	Pro	Tyr								
		195					200								

&lt;210&gt; 3639

&lt;211&gt; 726

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 120  
 aagactaaca gtggttatct ctcagcggga ttataaatgt tttgggtttt tttttttttt  
 180  
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 240  
 aagcacatta atgtaggcag attatcaatg ttatgcattt cactgattgc atatctcttt  
 300  
 ttttatcaat ggtgaacatt gcaaatgatt gatacgtttt tcttaggaag tggcattgcc  
 360  
 acaaatgggt tttccaacac cagcagggcc tgagagtgtc atcaccatac actcttgccg  
 420  
 gcaataaaaa aatttcacct tttaatggat ttaaaaggga aaagtggggg tgttgggttc  
 480  
 tccagggcat ttctttcatt atgagtgaca tttttctgaa aggaacgtga tctcgttttc  
 540  
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 600  
 tgtgccttct ccctgctctt tctaggtcct gattctcacc tctgcctgtg taataaccct  
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 720  
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 726

<210> 3640  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 3640  
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 20 25 30  
 Ser Leu Leu Asn Pro Leu Lys Gly Glu Ile Phe Leu Leu Pro Ala Arg  
 35 40 45  
 Val Tyr Gly Asp Asp Thr Leu Arg Pro Cys Trp Cys Trp Lys Asn His  
 50 55 60  
 Leu Trp Gln Cys His Phe Leu Arg Lys Thr Tyr Gln Ser Phe Ala Met  
 65 70 75 80  
 Phe Thr Ile Asp Lys Lys Arg Asp Met Gln Ser Val Lys Cys Ile Thr  
 85 90 95  
 Leu Ile Ile Cys Leu His  
 100

<210> 3641  
 <211> 455  
 <212> DNA  
 <213> Homo sapiens

<400> 3641  
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 agtccccgag cagtcacgcg agccgggacc ttgccccgct ggaacgcaga agcggccgtg  
 180  
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 240  
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 300  
 ggaggtggcc gaagggaaga ggggtgggca ggggctgctc tgcaccctct agcagagcgg  
 360  
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 420  
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 455

<210> 3642

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3642

Met	Ala	Gln	Pro	Leu	Val	Leu	Ala	Pro	Ser	Arg	Arg	Pro	Gly	Gln	Leu
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Pro	Arg	Gly	Arg	Ala	Gly	Gly	Ala	Ala	Pro	Gly	Gly	Glu	Glu	Met	Ser
			20					25				30			
Gln	Ser	Pro	Glu	Glu	Ser	Arg	Ser	Ser	His	Ala	Ser	Arg	Asp	Leu	Ala
		35					40				45				
Pro	Leu	Glu	Arg	Arg	Ser	Gly	Arg	Gly	Ala	Arg	Asp	Ala	Arg	Ala	Leu
	50				55					60					
Thr	Ser	Trp	Ala	Pro	Val	Arg	Gly	Glu	Val	Arg	Lys	Lys	Thr	Pro	Ser
65				70				75					80		
Glu	Val	Thr	Val	Pro	Thr	Arg	Val	Asp	Ser	Pro	Arg	Pro	Asp	His	Ala
			85					90					95		
Arg	Arg	Trp	Pro	Lys	Gly	Arg	Gly	Trp	Gly	Arg	Gly	Cys	Ser	Ala	Pro
			100				105					110			
Ser	Ser	Arg	Ala	Ala	Ser	Leu	Gln	Val	Phe	Ala	Leu	Ala	Arg	Arg	Ser
		115				120					125				
Pro	Arg	Glu	Gln	Phe	Gly	Thr	Val	Arg	Ile	Gly	Phe	Arg	Glu	Pro	Ala
	130					135					140				
Phe	Lys	Thr	Arg												
145															

<210> 3643

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 3643

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180  
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240  
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360  
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420  
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480  
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780  
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1560  
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1620  
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1680

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 1920  
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 1980  
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 2040  
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 2100  
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 2160  
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 2220  
 aaaaaaaaaa aaaaaaaaaa aaa  
 2243

&lt;210&gt; 3644

&lt;211&gt; 560

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3644

Gly	Leu	His	Glu	Glu	Gly	Leu	Arg	Lys	Phe	Ser	Glu	Tyr	Leu	Cys	Lys
1			5						10					15	
Gln	Val	Ala	Ser	Lys	Ala	Glu	Glu	Asn	Leu	Leu	Met	Val	Leu	Gly	Thr
			20					25					30		
Asp	Met	Ser	Asp	Arg	Arg	Ala	Ala	Val	Ile	Phe	Ala	Asp	Thr	Leu	Thr
		35				40					45				
Leu	Leu	Phe	Glu	Gly	Ile	Ala	Arg	Ile	Val	Glu	Thr	His	Gln	Pro	Ile
	50				55					60					
Val	Glu	Thr	Tyr	Tyr	Gly	Pro	Gly	Arg	Leu	Tyr	Thr	Leu	Ile	Lys	Tyr
65				70					75					80	
Leu	Gln	Val	Glu	Cys	Asp	Arg	Gln	Val	Glu	Lys	Val	Val	Asp	Lys	Phe
			85					90					95		
Ile	Lys	Gln	Arg	Asp	Tyr	His	Gln	Gln	Phe	Arg	His	Val	Gln	Asn	Asn
			100					105				110			
Leu	Met	Arg	Asn	Ser	Thr	Thr	Glu	Lys	Ile	Glu	Pro	Arg	Glu	Leu	Asp
	115						120					125			
Pro	Ile	Leu	Thr	Glu	Val	Thr	Leu	Met	Asn	Ala	Arg	Ser	Glu	Leu	Tyr
	130					135					140				
Leu	Arg	Phe	Leu	Lys	Lys	Arg	Ile	Ser	Ser	Asp	Phe	Glu	Val	Gly	Asp
145				150					155					160	
Ser	Met	Ala	Ser	Glu	Glu	Val	Lys	Gln	Glu	His	Gln	Lys	Cys	Leu	Asp
			165					170					175		
Lys	Leu	Leu	Asn	Asn	Cys	Leu	Leu	Ser	Cys	Thr	Met	Gln	Glu	Leu	Ile
			180					185				190			
Gly	Leu	Tyr	Val	Thr	Met	Glu	Glu	Tyr	Phe	Met	Arg	Glu	Thr	Val	Asn
	195					200						205			
Lys	Ala	Val	Ala	Leu	Asp	Thr	Tyr	Glu	Lys	Gly	Gln	Leu	Thr	Ser	Ser

210	215	220
Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys Cys Ile Gly Arg Ala		
225	230	235
Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu Ala		240
	245	250
Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys Leu		255
	260	265
Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly Val		270
	275	280
Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys Phe		285
	290	295
Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe Leu		300
305	310	315
Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr Leu		320
	325	330
Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly Ile		335
	340	345
Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp Leu		350
	355	360
Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu Thr		365
	370	375
Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile Asn		380
385	390	395
Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn Asp		400
	405	410
Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu Glu		415
	420	425
Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr Asp		430
	435	440
Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu Lys		445
	450	455
Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe Asp		460
465	470	475
Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr		480
	485	490
Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile Leu		495
	500	505
Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn Ser		510
	515	520
Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val Leu		525
	530	535
Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg Leu		540
545	550	555
		560

&lt;210&gt; 3645

&lt;211&gt; 823

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3645

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60

ccagggtttt gtagatggat tcctcaaaaa ctcttttgag gtattgcctg ggcttctcag  
120

tcgggttgat ttctcatct tctatttgat gggctaactg ctctatggaa ggaagatctt  
 180  
 cctcctcctt ggaggctaag atttggcgta actctttcct gagatcaata aaacgatcgt  
 240  
 ggaacagggc caggcaccac ggctcggtga agtagctata gagatctgtg atcagggtttt  
 300  
 catcgtaccg agcacacagg ttgttgagga gttgctcgtg ctggccaaac aagcggatgt  
 360  
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 420  
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 480  
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 540  
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 600  
 ggatgagccg gtcaagatta gctggtggct cggtcacagg ctcaaggggt ggatcaaaga  
 660  
 gatgtagcat agctgctgcc agctgaaagc caatttcttt ggaactgaag ttgctggtgg  
 720  
 gcccatcatc ttgagtagta tctattggag aatttgggtga gggagccagc agctctgatg  
 780  
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 823

&lt;210&gt; 3646

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3646

Met	Asn	Gly	Pro	Thr	Ser	Asn	Phe	Ser	Ser	Lys	Glu	Ile	Gly	Phe	Gln
1				5					10					15	
Leu	Ala	Ala	Ala	Met	Leu	His	Leu	Phe	Asp	Pro	Thr	Leu	Glu	Pro	Val
			20					25					30		
Thr	Glu	Pro	Pro	Ala	Asn	Leu	Asp	Arg	Leu	Ile	Pro	Met	Tyr	Lys	Gly
		35				40						45			
Ala	Lys	Ile	Gln	Gly	Gly	Ile	Leu	Pro	Gly	Ser	Tyr	His	Tyr	Leu	His
	50				55					60					
Ile	Ala	Lys	Pro	Ala	Ile	Pro	Thr	Pro	Leu	Glu	Val	Gln	Met	Ala	Gln
65					70				75					80	
Pro	Asn	Tyr	Gly	Leu	Glu	Leu	Val	Thr	Gly	Ser	Ala	Lys	Asn	Gly	Thr
			85					90						95	
Tyr	Phe	Arg	Ile	His	Ile	Asn	Lys	Tyr	Lys	Met	Val	Glu	Thr	Ile	Thr
		100					105						110		
Cys	Leu	Ser	Arg	Glu	Pro	Phe	Pro	Ala	Ser	Asn	Tyr	Ile	Arg	Leu	Phe
		115					120					125			
Gly	Gln	His	Glu	Gln	Leu	Leu	Asn	Asn	Leu	Cys	Ala	Arg	Tyr	Asp	Glu
	130				135					140					
Asn	Leu	Ile	Thr	Asp	Leu	Tyr	Ser	Tyr	Phe	Thr	Glu	Pro	Trp	Cys	Leu
145					150					155				160	
Ala	Leu	Phe	His	Asp	Arg	Phe	Ile	Asp	Leu	Arg	Lys	Glu	Leu	Arg	Gln
			165					170						175	
Ile	Leu	Ala	Ser	Lys	Glu	Glu	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Leu



```

                180                185                190
Ala His Gln Ile Glu Asp Glu Glu Ile Asn Pro Thr Glu Lys Pro Arg
                195                200                205
Gln Tyr Leu Lys Arg Val Phe Glu Glu Ser Ile Tyr Lys Thr Leu Val
                210                215                220
Glu Arg Ser Thr Leu Asp Tyr Leu His Tyr Asn Arg Tyr His Leu Pro
225                230                235                240
Met Tyr Ala

```

<210> 3647  
 <211> 584  
 <212> DNA  
 <213> Homo sapiens

```

<400> 3647
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gcgcggatgc ctttgagcgc ggtgacttct cactgctat cgagccgctg gaggtcgccg
120
acgagggcac ctactcctgc cacctgcacc accattactg tggcctgcac gaacgccgcg
180
tcttcacact gacggtcgcc gaacccacg cggagccgcc cccccggggc tctccgggca
240
acggctccag ccacagcggc gcccaggcc caggtgaagg aggcctccct gggacccggg
300
aaggcgggag cccacccac cgggggttgc tctgcgccg ctgtcccttg cccgagggcc
360
gcggatccca gcgggnnggc cgtggcccgc gtcggggcgc aggtcttgc ggtacctgac
420
gccgtccga ccccgcttc cccgcagacc ccacactggc gcgcggccac aacgtcatca
480
atgtcatcgt ccccgagagc cgagccact tcttcagca gctgggctac gtgctggcca
540
cgctgtgct cttcatcctg ctactggtca ctgtcctcct ggcc
584

```

<210> 3648  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens

```

<400> 3648
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1          5          10          15
Ala Trp Leu Trp Ala Arg Met Pro Leu Ser Ala Val Thr Ser His Cys
20        25        30
Val Ser Ser Arg Trp Arg Ser Pro Thr Arg Ala Pro Thr Pro Ala Thr
35        40        45
Cys Thr Thr Ile Thr Val Ala Cys Thr Asn Ala Ala Ser Ser Thr
50        55        60

```

<210> 3649  
 <211> 648

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3649

```

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60
ggaagcatga tactgaaggc ttgtcactcc tgttttctact tccacacaga caagcatatt
120
tgctcattgt ttgctgtgct cccctttttt tttcaggttg ctatttctgc agatgtcaaa
180
gaagttctgt taactgatgg gaatgaaaag gccatcagaa atgtgcaaga catcatcaca
240
aggaatcaga aggctggtgt gtttaagacc cagaaaatat caagctgcgt tttacgatgg
300
gataatgaga cagatgtctc tcaactggaa ggacattttg acattgttat gtgtgctgac
360
tgctgttttc tggaccagta cagagccagc cttgttgatg caataaagag attactccag
420
ccagggggga aagcgatggt atttgcccca cgccgaggga atactttaaa ccagttttgc
480
aatctagctg aaaaagctgg tttctgtatc caaagacatg aaaattatga tgaacacatt
540
tcaaacttcc actccaagtt gaaaaaggaa aaccgggaca tatatgaaga aaaccttcac
600
taccgcctc tgcttatttt gaccaaacat ggatagaaga ttaagctt
648

```

&lt;210&gt; 3650

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3650

```

Met Ile Leu Lys Ala Cys His Ser Cys Phe His Phe His Thr Asp Lys
1           5           10           15
His Ile Cys Ser Leu Phe Ala Val Leu Pro Phe Phe Phe Gln Val Ala
20           25           30
Ile Ser Ala Asp Val Lys Glu Val Leu Leu Thr Asp Gly Asn Glu Lys
35           40           45
Ala Ile Arg Asn Val Gln Asp Ile Ile Thr Arg Asn Gln Lys Ala Gly
50           55           60
Val Phe Lys Thr Gln Lys Ile Ser Ser Cys Val Leu Arg Trp Asp Asn
65           70           75           80
Glu Thr Asp Val Ser Gln Leu Glu Gly His Phe Asp Ile Val Met Cys
85           90           95
Ala Asp Cys Leu Phe Leu Asp Gln Tyr Arg Ala Ser Leu Val Asp Ala
100          105          110
Ile Lys Arg Leu Leu Gln Pro Arg Gly Lys Ala Met Val Phe Ala Pro
115          120          125
Arg Arg Gly Asn Thr Leu Asn Gln Phe Cys Asn Leu Ala Glu Lys Ala
130          135          140
Gly Phe Cys Ile Gln Arg His Glu Asn Tyr Asp Glu His Ile Ser Asn
145          150          155          160
Phe His Ser Lys Leu Lys Lys Glu Asn Pro Asp Ile Tyr Glu Glu Asn

```

165 170 175  
 Leu His Tyr Pro Pro Leu Leu Ile Leu Thr Lys His Gly  
 180 185

<210> 3651

<211> 2469

<212> DNA

<213> Homo sapiens

<400> 3651

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 120  
 tttagaagggg ccactgtggt catcctgaac atgcccgaagg gaacagagtt tgggattgac  
 180  
 tataactcct gggaggtcgg gcccaagttc cggggcgctga agatgatccc tccaggcatc  
 240  
 cacttcctcc actacagctc tgtggacaag gctaattccga aggaagtagg ccctcgtagt  
 300  
 gggtttcttc ttagcctgca ccagcggggg ctgacagtgc tgcgctggag cacactcagg  
 360  
 gaagaggtag acctgtcccc agccccagag tctgaggtgg aggccatgag ggccaacctc  
 420  
 caggagctgg accagtctct ggggccttac ccatatgcc aacctgaaga gtggatctca  
 480  
 ctcaccaact tcacagcga agccacagtg gagaagctac agcccagaaa tcgacagatc  
 540  
 tgtgcctttt ccgatgtgct acctgtgctc tccatgaagc acaccaagga ccgctggggg  
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 660  
 ccagagatga agcccagagc cgggacagag atccgcttct cagagctgcc cagcagatg  
 720  
 ttcccagagg gtgccacgcc agctgagata accaagcaca gcatggacct gagctatgcc  
 780  
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 gacattgtct cccaagacaa ctctctcacc agcaccttac aggttttctt ttctctgccc  
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 1320

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 1380  
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 1980  
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 aaaaaaaaaa  
 2469

&lt;210&gt; 3652

&lt;211&gt; 384

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3652

Met	Ala	Ala	Val	Gln	Met	Asp	Pro	Glu	Leu	Ala	Lys	Arg	Leu	Phe	Phe
1				5					10					15	
Glu	Gly	Ala	Thr	Val	Val	Ile	Leu	Asn	Met	Pro	Lys	Gly	Thr	Glu	Phe
			20					25					30		
Gly	Ile	Asp	Tyr	Asn	Ser	Trp	Glu	Val	Gly	Pro	Lys	Phe	Arg	Gly	Val
		35					40					45			
Lys	Met	Ile	Pro	Pro	Gly	Ile	His	Phe	Leu	His	Tyr	Ser	Ser	Val	Asp

50					55						60					
Lys	Ala	Asn	Pro	Lys	Glu	Val	Gly	Pro	Arg	Met	Gly	Phe	Phe	Leu	Ser	
65					70					75					80	
Leu	His	Gln	Arg	Gly	Leu	Thr	Val	Leu	Arg	Trp	Ser	Thr	Leu	Arg	Glu	
				85					90					95		
Glu	Val	Asp	Leu	Ser	Pro	Ala	Pro	Glu	Ser	Glu	Val	Glu	Ala	Met	Arg	
			100					105					110			
Ala	Asn	Leu	Gln	Glu	Leu	Asp	Gln	Phe	Leu	Gly	Pro	Tyr	Pro	Tyr	Ala	
		115					120					125				
Thr	Leu	Lys	Lys	Trp	Ile	Ser	Leu	Thr	Asn	Phe	Ile	Ser	Glu	Ala	Thr	
	130				135						140					
Val	Glu	Lys	Leu	Gln	Pro	Glu	Asn	Arg	Gln	Ile	Cys	Ala	Phe	Ser	Asp	
145				150				155						160		
Val	Leu	Pro	Val	Leu	Ser	Met	Lys	His	Thr	Lys	Asp	Arg	Val	Gly	Gln	
			165					170					175			
Asn	Leu	Pro	Arg	Cys	Gly	Ile	Glu	Cys	Lys	Ser	Tyr	Gln	Glu	Gly	Leu	
		180					185					190				
Ala	Arg	Leu	Pro	Glu	Met	Lys	Pro	Arg	Ala	Gly	Thr	Glu	Ile	Arg	Phe	
	195						200					205				
Ser	Glu	Leu	Pro	Thr	Gln	Met	Phe	Pro	Glu	Gly	Ala	Thr	Pro	Ala	Glu	
	210				215						220					
Ile	Thr	Lys	His	Ser	Met	Asp	Leu	Ser	Tyr	Ala	Leu	Glu	Thr	Val	Leu	
225				230						235				240		
Ile	Lys	Gln	Phe	Pro	Ser	Ser	Pro	Gln	Asp	Val	Leu	Gly	Glu	Leu	Gln	
		245						250					255			
Phe	Ala	Phe	Val	Cys	Phe	Leu	Leu	Gly	Asn	Val	Tyr	Glu	Ala	Phe	Glu	
		260					265					270				
His	Trp	Lys	Arg	Leu	Leu	His	Leu	Leu	Cys	Arg	Ser	Glu	Ala	Ala	Met	
	275						280					285				
Met	Lys	His	His	Thr	Leu	Tyr	Ile	Asn	Leu	Met	Ser	Ile	Leu	Tyr	His	
	290				295					300						
Gln	Leu	Gly	Glu	Ile	Pro	Ala	Asp	Phe	Phe	Val	Asp	Ile	Val	Ser	Gln	
305				310						315				320		
Asp	Asn	Phe	Leu	Thr	Ser	Thr	Leu	Gln	Val	Phe	Phe	Ser	Ser	Ala	Cys	
		325						330						335		
Ser	Ile	Ala	Val	Asp	Ala	Thr	Leu	Arg	Lys	Lys	Ala	Glu	Lys	Phe	Gln	
		340					345					350				
Ala	His	Leu	Thr	Lys	Lys	Phe	Arg	Trp	Asp	Phe	Ala	Ala	Glu	Pro	Glu	
	355					360					365					
Asp	Cys	Ala	Pro	Val	Val	Val	Glu	Leu	Pro	Glu	Gly	Ile	Glu	Met	Gly	
370					375						380					

&lt;210&gt; 3653

&lt;211&gt; 283

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3653

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60

gcattataacc aatcagagct tcttttctgt ctgctgaaat ggaacgggtgc catcaggccg

120

tcttctccac tggagatgct ccttcagctc agcaggacgc tagctcggaa ctcagactgc

180

acatttttgc ggattgggag gagggccgac gccgtggccg gatagtctct ggagctgcct  
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 283

<210> 3654  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens

<400> 3654  
 Met Pro Gln Ala Ser Pro Gly Ala Trp Arg His Trp Arg Lys Cys Ile  
 1 5 10 15  
 Ile Pro Ile Arg Ala Ser Phe Ala Ala Glu Met Glu Arg Cys His  
 20 25 30  
 Gln Ala Val Phe Ser Thr Gly Asp Ala Pro Ser Ala Gln Gln Asp Ala  
 35 40 45  
 Ser Ser Glu Leu Arg Leu His Ile Phe Ala Asp Trp Glu Glu Gly Arg  
 50 55 60  
 Arg Arg Gly Arg Ile Val Ser Gly Ala Ala Phe Trp Gly Cys Leu Pro  
 65 70 75 80  
 Val Gly Ile Phe Ser Thr Pro Arg  
 85

<210> 3655  
 <211> 3477  
 <212> DNA  
 <213> Homo sapiens

<400> 3655  
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 120  
 gagtgagagg ttgctctggt gcagctggag gaagaacagg gaacctaggg ttggggagag  
 180  
 atgtatagag gaaaactccc ccaggcacac agcctccgct ctggaccaac gcaggcttca  
 240  
 gtgagtacac acaaaggaac tgatgtcaag gccctttcta tgaccttcc cattctagca  
 300  
 agacctccca cccagtcac cttgggatct acagccacat gaaatacaga cacatcgttc  
 360  
 cccaagtca ggccagtttt aggccattga gttatgggga aatgattaat gggatgaatg  
 420  
 aaaaacaaat aaaataaata aataaataaa tacactaaag ccttattagc caggcgtgat  
 480  
 cacatgccca acactcccct ccatcccagc actatgcaca gttcacggct catatgcaaa  
 540  
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 600  
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 660  
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 720

agtggaaagt gcggaacccc aatgagtagg gcacagaaag gagggcgagc agagacagca  
780  
agaggtcagg taagccaagg agcagcggag caggtcaatc agggaagttc tgggcacccct  
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1980  
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2100  
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2280  
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2340

gagaataaag aaggcctgga gctgctgaag actgctattg ggaaagctgg ctacactgat  
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 3240  
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 3420  
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 3477

&lt;210&gt; 3656

&lt;211&gt; 429

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3656

Met	Ala	Ser	Leu	Lys	Glu	Leu	Ala	Pro	Thr	Gly	Arg	Ile	Met	Asn	Ser
1				5					10				15		
Cys	Met	Ala	Ser	Leu	Phe	Pro	Ala	Trp	Glu	Pro	Pro	Leu	Ile	Thr	Leu
			20					25				30			
Lys	Ala	Gly	Thr	Gly	Ser	Met	Arg	Ser	Gly	Phe	Pro	Ala	Lys	Ser	Ala
		35					40				45				
Met	Trp	Arg	Tyr	Arg	Gly	Thr	Pro	Phe	Ser	Lys	Ala	Val	Glu	His	Ile
	50				55					60					
Asn	Lys	Thr	Ile	Ala	Pro	Ala	Leu	Val	Ser	Lys	Lys	Leu	Asn	Val	Thr



```

65          70          75          80
Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met Asp Gly Thr Glu
85          90          95
Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala
100        105        110
Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro Leu Tyr Arg His
115        120        125
Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu Pro Val Pro Ala
130        135        140
Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met
145        150        155        160
Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn Phe Arg Glu Ala
165        170        175
Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys
180        185        190
Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe
195        200        205
Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu Leu Leu Lys Thr
210        215        220
Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val Ile Gly Met Asp
225        230        235        240
Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr Asp Leu Asp Phe
245        250        255
Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala
260        265        270
Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val Val Ser Ile Glu
275        280        285
Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln Lys Phe Thr Ala
290        295        300
Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr Val Thr Asn Pro
305        310        315        320
Lys Arg Ile Ala Gln Ala Val Asn Glu Lys Ser Cys Asn Cys Leu Leu
325        330        335
Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser Leu Gln Ala Cys
340        345        350
Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val Ser His Arg Ser
355        360        365
Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val Val Gly Leu Cys
370        375        380
Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser Glu Arg Leu Ala
385        390        395        400
Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu Gly Ser Lys Ala
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Lys Phe Ala Gly Arg Asn Phe Arg Asn Pro Leu Ala Lys
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&lt;210&gt; 3657

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3657

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<211> 99

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<213> Homo sapiens

<400> 3658

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<211> 1025

<212> DNA

<213> Homo sapiens

<400> 3659

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<212> PRT

<213> Homo sapiens

<400> 3660

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Glu	Ile	Ser	Asp	Leu	Glu	Asn	Glu	Val	Glu	Asn	Lys	Thr	Ala	Gln	Ile
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Glu	Glu	His	Gln	Ser	Val	Asp	Ile	Ala	Thr	Leu	Glu	Asp	Glu	Ala	Gln
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	245	250
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	260	265
Ser Lys Val Arg Thr Leu Lys Lys Phe Ile Lys Leu Leu Gly Glu Ile		270
	275	280
Met Glu His Arg Phe Lys Thr Tyr Gln Gln Phe Arg Arg Cys Leu Thr		285
	290	295
Leu Arg Cys Lys Leu Tyr Phe Asp Asn Leu Leu Ser Gln Arg Ala Tyr		300
305	310	315
Cys Gly Lys Met Asn Phe Asp His Lys Asn Glu Thr Leu Ser Ile Ser		320
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&lt;210&gt; 3661

&lt;211&gt; 1117

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3661

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<211> 371

<212> PRT

<213> Homo sapiens

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Lys	Trp	Gly	Glu	Glu	Ala	Leu	Lys	Met	Asp	Leu	Asp	Asn	Asn	Phe	Tyr
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				180					185					190	
Val	His	Ser	Ser	Gln	Phe	Ser	Ser	Val	Ile	Met	His	Ser	Asn	Ala	Ile
				195					200				205		
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&lt;210&gt; 3668

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				85					90					95	
Leu	Val	Thr	Leu	Ser	Lys	Ala	Ala	Val	Ala	Leu	Lys	Met	Gly	Asp	Leu
			100					105					110		
Asp	Val	Tyr	Arg	Asn	Glu	Met	Lys	Ser	His	Pro	Glu	Met	Lys	Leu	Val
		115				120						125			
Cys	Gly	Phe	Ile	Leu	Glu	Pro	Arg	Leu	Leu	Ile	Gln	His	Arg	Lys	Gly
	130					135					140				
Gln	Ile	Val	Pro	Thr	Glu	Leu	Ala	Thr	His	Leu	Lys	Glu	Thr	Gln	Pro
145					150					155				160	
Gly	Leu	Leu	Val	Ala	Ser	Val	Leu	Gly	Leu	Gln	Lys	Asn	Ser	Lys	Ile
			165					170						175	
Gly	Ile	Glu	Glu	Ala	Asp	Ser	Phe	Phe	Lys	Val	Leu	Cys	Gly	Lys	Asp
			180				185						190		
Glu	Asp	Thr	Ile	Pro	Gln	Leu	Leu	Ile	Asp	Phe	Trp	Glu	Ala	Gln	Leu
	195					200						205			
Val	Ala	Cys	Leu	Pro	Asp	Val	Val	Leu	Gln	Glu	Leu	Phe	Phe	Lys	Leu
	210					215					220				
Thr	Ser	Gln	Tyr	Ile	Trp	Arg	Leu	Ser	Lys	Arg	Gln	Pro	Pro	Asp	Thr
225					230				235					240	
Thr	Pro	Leu	Arg	Thr	Ser	Glu	Asp	Leu	Ile	Asn	Ala	Cys	Ser	His	Tyr
			245					250						255	
Gly	Leu	Ile	Tyr	Pro	Trp	Val	His	Val	Val	Ile	Ser	Ser	Asp	Ser	Leu

	260		265		270										
Ala	Asp	Lys	Asn	Tyr	Thr	Glu	Asp	Leu	Ser	Lys	Leu	Gln	Ser	Leu	Ile
	275		280		285										
Cys	Gly	Pro	Ser	Phe	Asp	Ile	Ala	Ser	Ile	Ile	Pro	Phe	Leu	Glu	Pro
	290		295		300										
Leu	Ser	Glu	Asp	Thr	Ile	Ala	Gly	Leu	Ser	Val	His	Val	Leu	Cys	Arg
305			310		315									320	
Thr	Arg	Leu	Lys	Glu	Tyr	Glu	Gln	Cys	Ile	Asp	Ile	Leu	Leu	Glu	Arg
	325		330		335										
Cys	Pro	Glu	Ala	Val	Ile	Pro	Tyr	Ala	Asn	His	Glu	Leu	Lys	Glu	Glu
	340		345		350										
Asn	Arg	Thr	Leu	Trp	Trp	Lys	Lys	Leu	Leu	Pro	Glu	Leu	Cys	Gln	Arg
	355		360		365										
Ile	Lys	Cys	Gly	Gly	Glu	Lys	Tyr	Gln	Leu	Tyr	Leu	Ser	Ser	Leu	Lys
	370		375		380										
Ala															
385															

&lt;210&gt; 3671

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3671

```

nntacagcta agattcattt catcacgtttg atgcttagct gaaaaattac aataaattct
60
ccaatgaaat tatgtatctt tatttaatga aaatgcctgc tgcgtaccaa ggtatgtact
120
agggcattctg gggtaagtaa aaacaaacac atagagcctg cctggagaag ctcatggtct
180
gatggaaaga taagcaagaa gagttaattt ctaatcaata tgataaaaag gtcagagagc
240
agtttctgaa aaacatgttt ttgagttgag tcctgaaaga caaggagatg ttagtaaagc
300
agagaagggg gaattcattc tagaaagatc agacaatgtg tgggaagggc agagtctgaa
360
aagagcatgc cccatttgga gaagcatcaa gaagcccacg cgtagaagc accggcccca
420
tgagacaaag acacagctag agagattgac taggccatgt cggaatgtcc tcttatttta
480
tacatacata agcatataga tacatatagc caaagttacc tttttaatga tcttttttac
540
ccagtgtatt ctggaggtcg aatggtcaca tatgaacatc tccgagaggt tgtgtttggc
600
aaaagtgaag atgagcatta tcccctttgg aaatcagtca ttggagggat gatggctggt
660
gttattggcc agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa
720
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca tgcatttgca
780
aaaatcttag ctgaaggagg aatacgaggg ctttgggcag gctgggta
828

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&lt;210&gt; 3672

<211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 3672  
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 Tyr Ser Gln Ser Tyr Leu Phe Asn Asp Leu Phe Tyr Pro Val Tyr Ser  
 20 25 30  
 Gly Gly Arg Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly  
 35 40 45  
 Lys Ser Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly  
 50 55 60  
 Met Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu  
 65 70 75 80  
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly Lys  
 85 90 95  
 Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile Leu Ala  
 100 105 110  
 Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val  
 115 120

<210> 3673  
 <211> 1052  
 <212> DNA  
 <213> Homo sapiens

<400> 3673  
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 gttcattctg ggagcgctgc tgggtggcat tattatgcat gtataaagtc attcagtgat  
 120  
 gagcagtggc acagcttcaa tgatcaacat gtcagcagga taacacaaga ggacattaag  
 180  
 aaaacacatg gtggatcttc aggaagcaga ggatattatt ctagtgtttt cgcaagtcc  
 240  
 acaaatgcat atatgctgat ctatagactg aaggatccag ccagaaatgc aaaatttcta  
 300  
 gaagtggatg aatacccaga acatattaaa aacttgggtgc agaaagagag agagttggaa  
 360  
 gaacaagaaa agagacaacg agaaattgag cgcaatacat gcaagataaa attattctgt  
 420  
 ttgcataccta caaaacaagt aatgatggaa aataaattgg aggttcataa ggataagaca  
 480  
 ttaaaggaag cagtagaaat ggcttataag atgatggatt tagaagaggt aatacccctg  
 540  
 gattgctgtc gccttggttaa atatgatgag tttcatgatt atctagaacg gtcatatgaa  
 600  
 ggagaagaag atacaccaat ggggcttcta ctagggtggcg tcaagtcaac atatatgttt  
 660  
 gatctgctgt tggagacgag aaagcctgat cagggttttcc aatcttataa acctggaggg  
 720  
 gagccatttt acaccatttt tagttgggtct gtacttagaa ttttcctgag aaagggtttt  
 780

tttttattgt agcaatgaac ataatttaca ttttgtatat ggtcttaca tgtagaataa  
 840  
 ttttgacagg ttgagaagta ctcagcacca gcttggaatt aagttctaga ttacttgcaa  
 900  
 agagttgtgt acataatttt aaaaacaaca aaaaacaaca aagcttctag cttacgggtct  
 960  
 tcagtggggtt ttttcttctc cagtgggcgg tactgaatca ttctggatgc tgtcaatccc  
 1020  
 taaagttatc aattgctctc ttaggaagat ct  
 1052

<210> 3674

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3674

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1				5					10					15	
Phe	Ser	Val	Met	Val	His	Ser	Gly	Ser	Ala	Ala	Gly	Gly	His	Tyr	Tyr
			20					25					30		
Ala	Cys	Ile	Lys	Ser	Phe	Ser	Asp	Glu	Gln	Trp	Tyr	Ser	Phe	Asn	Asp
		35					40					45			
Gln	His	Val	Ser	Arg	Ile	Thr	Gln	Glu	Asp	Ile	Lys	Lys	Thr	His	Gly
	50					55					60				
Gly	Ser	Ser	Gly	Ser	Arg	Gly	Tyr	Tyr	Ser	Ser	Ala	Phe	Ala	Ser	Ser
65				70					75					80	
Thr	Asn	Ala	Tyr	Met	Leu	Ile	Tyr	Arg	Leu	Lys	Asp	Pro	Ala	Arg	Asn
			85						90					95	
Ala	Lys	Phe	Leu	Glu	Val	Asp	Glu	Tyr	Pro	Glu	His	Ile	Lys	Asn	Leu
			100					105					110		
Val	Gln	Lys	Glu	Arg	Glu	Leu	Glu	Gln	Glu	Lys	Arg	Gln	Arg	Glu	
		115					120				125				
Ile	Glu	Arg	Asn	Thr	Cys	Lys	Ile	Lys	Leu	Phe	Cys	Leu	His	Pro	Thr
	130					135					140				
Lys	Gln	Val	Met	Met	Glu	Asn	Lys	Leu	Glu	Val	His	Lys	Asp	Lys	Thr
145					150				155					160	
Leu	Lys	Glu	Ala	Val	Glu	Met	Ala	Tyr	Lys	Met	Met	Asp	Leu	Glu	Glu
			165						170				175		
Val	Ile	Pro	Leu	Asp	Cys	Cys	Arg	Leu	Val	Lys	Tyr	Asp	Glu	Phe	His
			180					185					190		
Asp	Tyr	Leu	Glu	Arg	Ser	Tyr	Glu	Gly	Glu	Glu	Asp	Thr	Pro	Met	Gly
	195						200				205				
Leu	Leu	Leu	Gly	Gly	Val	Lys	Ser	Thr	Tyr	Met	Phe	Asp	Leu	Leu	Leu
	210					215					220				
Glu	Thr	Arg	Lys	Pro	Asp	Gln	Val	Phe	Gln	Ser	Tyr	Lys	Pro	Gly	Gly
225				230					235				240		
Glu	Pro	Phe	Tyr	Thr	Ile	Phe	Ser	Trp	Ser	Val	Leu	Arg	Ile	Phe	Leu
			245						250				255		
Arg	Lys	Val	Phe	Phe	Leu	Leu									
			260												

<210> 3675

<211> 837

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3675

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nntccggaga tgtgaagaag gggggcgagc ggacaggaag atgaaggag caaagctgcc
60
cgcccgggga caggcgtcta ggtgaacaag aaaatgaccg aagaaacaca cccagacgat
120
gacagctata ttgtgcgtgt caaggctgtg gttatgacca gagatgactc cagcggggga
180
tggttcccac aggaaggagg cgggatcagt cgcgtcgggg tctgtaaggt catgcacccc
240
gaaggcaatg gacgaagcgg ctttctcatc catggtgaac gacagaaaga caaactgggtg
300
gtattggaat gctatgtaag aaaggacttg gtctacacca aagccaatcc aacgtttcat
360
cactggaagg tcgataatag gaagtttga cttactttcc aaagccctgc tgatgccga
420
gcctttgaca ggggagtaag gaaagcaatc gaagacctta tagaagaagt agaaaatgat
480
tctggcgggc ccagaaggct cctggcctac ccactgtcct cctgtaatca gagggccagg
540
gtgtacagct gccactgaaa aggaaaggga tctgtgacct ctggagccct gggtcggttt
600
aggccttggt ctatgggtaa gtgagtagta ggcattgtgt tacatctgat cgtggcctgg
660
agggcccttg ggcagtcagt tctcatggtg ggcttgacta gagtccacag atgcaaacac
720
aaaaattctc cactgcagca catccaggta tcaaatacaga gggttaaaga agccatagac
780
agggccctgt gaagaaagaa atatcaagca aggcattgta ataccaaatt cagatct
837

```

&lt;210&gt; 3676

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3676

```

Met Thr Glu Glu Thr His Pro Asp Asp Asp Ser Tyr Ile Val Arg Val
1           5           10           15
Lys Ala Val Val Met Thr Arg Asp Asp Ser Ser Gly Gly Trp Phe Pro
20           25           30
Gln Glu Gly Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His
35           40           45
Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln
50           55           60
Lys Asp Lys Leu Val Val Leu Glu Cys Tyr Val Arg Lys Asp Leu Val
65           70           75           80
Tyr Thr Lys Ala Asn Pro Thr Phe His His Trp Lys Val Asp Asn Arg
85           90           95
Lys Phe Gly Leu Thr Phe Gln Ser Pro Ala Asp Ala Arg Ala Phe Asp
100          105          110
Arg Gly Val Arg Lys Ala Ile Glu Asp Leu Ile Glu Glu Val Glu Asn

```

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      115      120      125
Asp Ser Gly Gly Pro Arg Arg Leu Leu Ala Tyr Pro Leu Ser Ser Cys
      130      135      140
Asn Gln Arg Pro Arg Val Tyr Ser Cys His
145      150

```

<210> 3677  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

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<400> 3677
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ttcatgccaa agctcgtcaa gaatctccta ggcgagatgc ctctgtgggt ctgccagagt
120
tgccgaaaga gcatggagga agatgaaagg cagacaggtc gagaacatgc agtggcgatc
180
tccttgtcac acacatcctg caaatcacag tcttgtggag atgactctca ttcgtcctcg
240
tcttctcct catcctcctc atcctcgtcc tcctcttctt gccctgggaa ctcgaggagac
300
tgggataccta gctcgttcct gtcggcacat aagctctcgg gcctctggaa ttccccacat
360
tccagtgggg ccattgccagg cagctctctt gggagtcttc ctaccatccc tggcgcgc
418

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<210> 3678  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

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<400> 3678
Xaa Glu Glu Gly Pro Ser Gln Asn Gly Leu Val Leu Gln Gly Glu Lys
 1      5      10      15
Leu Pro Pro Asp Phe Met Pro Lys Leu Val Lys Asn Leu Leu Gly Glu
      20      25      30
Met Pro Leu Trp Val Cys Gln Ser Cys Arg Lys Ser Met Glu Glu Asp
      35      40      45
Glu Arg Gln Thr Gly Arg Glu His Ala Val Ala Ile Ser Leu Ser His
      50      55      60
Thr Ser Cys Lys Ser Gln Ser Cys Gly Asp Asp Ser His Ser Ser Ser
      65      70      75      80
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Pro Gly
      85      90      95
Asn Ser Gly Asp Trp Asp Pro Ser Ser Phe Leu Ser Ala His Lys Leu
      100      105      110
Ser Gly Leu Trp Asn Ser Pro His Ser Ser Gly Ala Met Pro Gly Ser
      115      120      125
Ser Leu Gly Ser Pro Pro Thr Ile Pro Gly Ala
      130      135

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<210> 3679  
 <211> 567

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3679

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 60  
 cgcctcaggc agctgctccc catgcttctt cagggaaaca gtatcttcac tgcccctaag  
 120  
 gagatcgag agatcaaggc ccagctggag acagccctga agtggaggaa ctatgaggtg  
 180  
 aagctgcggc tgctgctgca cctggaggaa ctgcagatgg agcatgatat ccggcactat  
 240  
 gacctggagt cggtgcccat gacctgggac cctgtggacc agaaccacag gctgctcacg  
 300  
 ctggagggtc ctggagtgc tgagagccgc ccctcagtgc tacggggcga ccacctgttt  
 360  
 gcccttttgt cctcggagac acaccaggag gaccccatca catataaggg ctttgtgcac  
 420  
 aaggtggaat tggaccgtgt caagctgagc tttccatga gcctcctgag ccgctttgtg  
 480  
 gatgggctga ctttcaaggt gaactttacc ttcaaccgcc agccgctgag agtccagcac  
 540  
 cgtgcctggg agttgacagg gcgctgg  
 567

&lt;210&gt; 3680

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3680

Arg	Val	Lys	Gly	Tyr	Asp	Leu	Glu	Leu	Ser	Met	Ala	Leu	Gly	Thr	Tyr
1				5					10					15	
Tyr	Pro	Pro	Pro	Arg	Leu	Arg	Gln	Leu	Leu	Pro	Met	Leu	Leu	Gln	Gly
			20				25						30		
Thr	Ser	Ile	Phe	Thr	Ala	Pro	Lys	Glu	Ile	Ala	Glu	Ile	Lys	Ala	Gln
		35				40					45				
Leu	Glu	Thr	Ala	Leu	Lys	Trp	Arg	Asn	Tyr	Glu	Val	Lys	Leu	Arg	Leu
	50				55					60					
Leu	Leu	His	Leu	Glu	Glu	Leu	Gln	Met	Glu	His	Asp	Ile	Arg	His	Tyr
65				70					75					80	
Asp	Leu	Glu	Ser	Val	Pro	Met	Thr	Trp	Asp	Pro	Val	Asp	Gln	Asn	Pro
			85					90					95		
Arg	Leu	Leu	Thr	Leu	Glu	Val	Pro	Gly	Val	Thr	Glu	Ser	Arg	Pro	Ser
			100				105						110		
Val	Leu	Arg	Gly	Asp	His	Leu	Phe	Ala	Leu	Leu	Ser	Ser	Glu	Thr	His
	115					120					125				
Gln	Glu	Asp	Pro	Ile	Thr	Tyr	Lys	Gly	Phe	Val	His	Lys	Val	Glu	Leu
	130				135					140					
Asp	Arg	Val	Lys	Leu	Ser	Phe	Ser	Met	Ser	Leu	Leu	Ser	Arg	Phe	Val
145				150					155					160	
Asp	Gly	Leu	Thr	Phe	Lys	Val	Asn	Phe	Thr	Phe	Asn	Arg	Gln	Pro	Leu
			165				170						175		
Arg	Val	Gln	His	Arg	Ala	Trp	Glu	Leu	Thr	Gly	Arg	Trp			

180

185

<210> 3681  
 <211> 788  
 <212> DNA  
 <213> Homo sapiens

<400> 3681  
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 120  
 gagaccggga ggcagagctt cagcagctgc gggacagcct ggggctgagc atggagcagc  
 180  
 gggcgaggagg tcgcctgcga ggccgctggc caggcctgag cctctgccac catggccatt  
 240  
 gtgcagactc tgccagtgcc actggagcct gctcctgaag ctgccactgc ccacaagct  
 300  
 ccagtcattg gtagtgtgag cagccttacc tcaggccggc cctgtcccgg ggggcccagct  
 360  
 cctccccgcc accacggccc tcttgggccc accttcttcc gccagcagga tggcctgcta  
 420  
 cgggggtggct atgaggcaca ggagccgctg tgcccagctg tgcccctag gaaggctgtc  
 480  
 cctgtcacca gcttcaccta catcaatgag gacttccgga cagagtcacc cccagccca  
 540  
 agcagtgatg ttgaggatgc ccgagagcag cgggcacaca atgcccacct ccgcgcccca  
 600  
 ccaccaaagc tcatccctgt ctctggaaag ctggagaaga acatagagaa gatcctgatc  
 660  
 cgcccaacag ccttcaagcc agtgcctgcc aaacctcgag gggctccgtc cctgcctagc  
 720  
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 780  
 gggggccc  
 788

<210> 3682  
 <211> 185  
 <212> PRT  
 <213> Homo sapiens

<400> 3682  
 Met Ala Ile Val Gln Thr Leu Pro Val Pro Leu Glu Pro Ala Pro Glu  
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 Ala Ala Thr Ala Pro Gln Ala Pro Val Met Gly Ser Val Ser Ser Leu  
 20 25 30  
 Ile Ser Gly Arg Pro Cys Pro Gly Gly Pro Ala Pro Pro Arg His His  
 35 40 45  
 Gly Pro Pro Gly Pro Thr Phe Phe Arg Gln Gln Asp Gly Leu Leu Arg  
 50 55 60  
 Gly Gly Tyr Glu Ala Gln Glu Pro Leu Cys Pro Ala Val Pro Pro Arg  
 65 70 75 80  
 Lys Ala Val Pro Val Thr Ser Phe Thr Tyr Ile Asn Glu Asp Phe Arg



<400> 3683  
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60  
t g c t g t t t a c a t g c c g g t g a g g t c c c c g g c g c t c c g a a c c c c t c c g a g c c c g g c t c c c  
120  
c g a g g g t g a a g c c c g c c g g c c c g c g a a c t g g a c t g g t g g a t c t c t c t c a g a c c t g g g g c c c c  
180  
g g a c t c c g a t c t c c g c c g t c t c c g c c a c c a t c a g g g c g g g a t c c g g c t c t g g t g t t t g a  
240  
g g a g g g g g t g t g g t g t a g g g a a g g a a t c c g t c c c t c t c c a c c t t t t t c g c c t t c g g g  
300  
g c t t c a g a c t c a g g g a a c t c g t c a t g g c t t t c t t g a t g a a g a a g a a a t t c a a a t t c  
360  
c a a a c t a c t t t c a c c c t g g a g g a g c t g a c t g c g g t t c c c t t c g t g a a c g g g t c c t c t t c  
420  
t g c a a g g t c c g g c t g c t g g a t g g a g g g g a t t t g t c a g c t t g t c g t c a a g g a g g a g g t a  
480  
c a g g a g a a c t g t g t g c g g t g g c g a a a g a g g t t c a c c t t c g t g t g t a a g a t g a g t g c t a a c  
540  
c c g g c c a c c g g c c t g c t g g a c c c c t g t g t c t t c c g t g t g t c t g t g c g c a a g g a g c t g a a a  
600  
g g c g g g a a g g c t t a t t c c a a g c t g g g c t t c g c t g a c t t g a a c c t g g c c g a g t t t g c g g g c  
660  
t c g g g c t c c a c g g t g c g c t g c t g c c t g c t c g a g g g a t a t g a c a c g a a g a a c a c t c g c c a g  
720  
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780  
a a g a c g c c a c c a t c g a c t g c c a g t c c a t c t c c a t c c c a g g c c a g g a t t c c t c c c t g c a g  
840  
c t g a c g t g t a a g g t g g t g g g a c c a g c a g t g g g g g c a g c a g c a c c a a c t c c t g a c t g g g  
900  
t c c c g g c c c c c a a g g c t c g g c c c a c t a t t c t c a g c t c a g g g c t g c c a g a g g a a c c c g a c  
960  
c a g a a c c t g t c c a g c c c t g a g g a g t g t t c c a c t c t g g c c a c t c c c g c a a c t c a g c t a t  
1020

gccagccagc agtccaagat ctccggctac agcacagagc actcgcactc ctccagcctc  
1080  
tcagacctga cgcaccgccg caacacgtcc accagcagca gcgcctctgg gggccttggc  
1140  
atgaccgtgg agggccctga gggcagtga cgggagcacc ggcccccgga gaagccgccg  
1200  
cggccacccc ggccccgca tctgtccgat cgctctttca ggcggaagaa ggactcgggtg  
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<211> 384

<212> PRT

<213> Homo sapiens

<400> 3684

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&lt;211&gt; 1293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3685

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<211> 504

<212> PRT

<213> Homo sapiens

<400> 3690

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&lt;210&gt; 3691

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3691

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 <213> Homo sapiens

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&lt;210&gt; 3695

&lt;211&gt; 1615

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3695

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&lt;210&gt; 3696

&lt;211&gt; 146

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3696

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Cys	Asn	Ser	Trp	Ser	Ser	Pro	Gln	Leu	Gln	Ser	Ser	Leu	Pro	Glu	Pro
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His	Asp	Arg	Pro	Leu	Ala	Leu	Pro	Leu	Ser	Asp	Ser	Gln	Ile	Gln	Trp
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Phe	Tyr	Gln	Ala	Leu	Asn	Leu	Ser	Leu	Pro	Leu	Pro	Asn	Phe	His	Ala
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&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3697

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&lt;210&gt; 3698

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3698

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 65 70 75 80  
 Gly His Cys Leu Phe Tyr Tyr Lys Asp Ser Arg Glu Glu Ser Val Leu  
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3702

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Cys	Gly	Lys	Cys	Phe	Gly	Gly	Ser	Gly	Asp	Leu	Arg	Arg	His	Val	Arg
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Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys	Glu	Ile	Cys	Asn	Lys	Cys
			100					105					110		
Phe	Thr	Arg	Ser	Ala	Val	Leu	Arg	Arg	His	Lys	Lys	Met	His	Cys	Lys
		115					120					125			
Ala	Gly	Asp	Glu	Ser	Pro	Asp	Val	Leu	Glu	Glu	Leu	Ser	Gln	Ala	Ile
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Glu	Thr	Ser	Asp	Leu	Glu	Lys	Ser	Gln	Ser	Ser	Asp	Ser	Phe	Ser	Gln
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<210> 3704

<211> 619

<212> PRT

<213> Homo sapiens

<400> 3704

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Leu	His	Leu	Leu	Lys	Ser	Ser	Cys	Ala	Pro	Ser	Val	Gln	Met	Lys	Ile
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Lys	Glu	Leu	Tyr	Arg	Arg	Arg	Phe	Pro	Arg	Lys	Thr	Leu	Gly	Pro	Ser
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Asp	Leu	Ser	Leu	Leu	Ser	Leu	Pro	Pro	Gly	Thr	Ser	Pro	Val	Gly	Ser
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Pro	Gly	Pro	Leu	Ala	Pro	Ile	Pro	Pro	Thr	Leu	Leu	Ala	Pro	Gly	Thr
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Leu	Leu	Gly	Pro	Lys	Arg	Glu	Val	Asp	Met	His	Pro	Pro	Leu	Pro	Gln
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Tyr	Gly	Glu	Leu	Ile	Arg	Pro	Thr	Thr	Leu	Ala	Ser	Thr	Ser	Ser	Gln
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Tyr	Thr	Ile	Gln	Val	Gln	Leu	Arg	Phe	Cys	Leu	Cys	Glu	Thr	Ser	Cys
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Pro	Gln	Glu	Asp	Tyr	Phe	Pro	Pro	Asn	Leu	Phe	Val	Lys	Val	Asn	Gly
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Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met Cys Pro Leu
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Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr Cys Ala His
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Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn Glu Lys Lys
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Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro Tyr Glu Ser
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Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys Pro Met Lys
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Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Gly Tyr Gly Leu
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Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val Thr Ser Ala
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Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr Ser Gly His
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          485          490          495
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Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu Asp Glu Gln
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Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro Ser His Phe
545          550          555          560
Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys Ser Ala Thr
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Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala Pro Gly Gly
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Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly Pro Ser Leu
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Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp
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&lt;210&gt; 3705

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3705

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<210> 3708

<211> 106

<212> PRT

<213> Homo sapiens

<400> 3708

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			20					25					30		
Glu	Asn	Ala	Phe	Asp	Asn	Ile	Gln	Leu	Pro	Tyr	Met	Ile	Lys	Thr	Leu
		35					40					45			
Lys	Lys	Leu	Gly	Ile	Glu	Gly	Met	Tyr	Leu	Asn	Val	Ile	Lys	Ala	Val
		50				55					60				
Tyr	Asp	Arg	Pro	Xaa	Val	Ser	Ile	Ile	Leu	Asn	Gly	Glu	Asn	Leu	Gln
65					70					75				80	
Glu	Leu	Gln	Thr	Phe	Gly	Leu	Arg	Ser	Gly	Thr	Gln	Gln	Gly	Cys	Pro
				85					90					95	
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<210> 3709

<211> 3768

<212> DNA

<213> Homo sapiens

<400> 3709

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3768

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<211> 70

<212> PRT

<213> Homo sapiens

<400> 3710

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		20					25					30			
Cys	Asp	Val	Ile	Leu	Val	Ala	Gly	Asp	Arg	Arg	Ile	Pro	Ala	His	Arg
		35					40					45			
Leu	Val	Leu	Ser	Ser	Val	Ser	Asp	Tyr	Phe	Ala	Ala	Met	Phe	Thr	Asn
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<210> 3711

<211> 1366

<212> DNA

<213> Homo sapiens

<400> 3711

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<210> 3712

<211> 368

<212> PRT

<213> Homo sapiens

<400> 3712

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Leu	Gly	Arg	Gly	Phe	Asn	Thr	Gly	Val	Ile	Leu	Leu	Arg	Leu	Asp	Arg
			35				40					45			
Leu	Arg	Gln	Ala	Gly	Trp	Glu	Gln	Met	Trp	Arg	Leu	Thr	Ala	Arg	Arg
	50					55					60				
Glu	Leu	Leu	Ser	Leu	Pro	Ala	Ala	Ser	Leu	Ala	Asp	Gln	Asp	Ile	Phe
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Asn	Ala	Val	Ile	Lys	Glu	His	Pro	Gly	Leu	Val	Gln	Arg	Leu	Pro	Cys
				85					90					95	
Val	Trp	Asn	Val	Gln	Leu	Ser	Asp	His	Thr	Leu	Ala	Glu	Arg	Cys	Tyr
			100					105					110		
Ser	Glu	Ala	Ser	Asp	Leu	Lys	Val	Ile	His	Trp	Asn	Ser	Pro	Lys	Lys
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Leu	Arg	Val	Lys	Asn	Lys	His	Val	Glu	Phe	Phe	Arg	Asn	Phe	Tyr	Leu
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Thr	Phe	Leu	Glu	Tyr	Asp	Gly	Asn	Leu	Leu	Arg	Arg	Glu	Leu	Phe	Val
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Cys	Pro	Ser	Gln	Pro	Pro	Pro	Gly	Ala	Glu	Gln	Leu	Gln	Gln	Ala	Leu
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Leu	Thr	Val	His	Arg	Val	His	Val	Thr	Phe	Leu	Pro	His	Glu	Pro	Pro
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Pro	Pro	Arg	Pro	His	Asp	Val	Thr	Leu	Val	Ala	Gln	Leu	Ser	Met	Asp
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Arg	Leu	Gln	Met	Leu	Glu	Ala	Leu	Cys	Arg	His	Trp	Pro	Gly	Pro	Met

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Ser	Leu	Ala	Leu	Tyr	Leu	Thr	Asp	Ala	Glu	Ala	Gln	Gln	Phe	Leu	His
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Phe	Val	Glu	Ala	Ser	Pro	Val	Leu	Ala	Ala	Arg	Gln	Asp	Val	Ala	Tyr
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His	Val	Val	Tyr	Arg	Glu	Gly	Pro	Leu	Tyr	Pro	Val	Asn	Gln	Leu	Arg
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Asn	Val	Ala	Leu	Ala	Gln	Ala	Leu	Thr	Pro	Tyr	Val	Phe	Leu	Ser	Asp
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Ile	Asp	Phe	Leu	Pro	Ala	Tyr	Ser	Leu	Tyr	Asp	Tyr	Leu	Arg	Ala	Ser
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Ile	Glu	Gln	Leu	Gly	Leu	Gly	Ser	Arg	Arg	Lys	Ala	Ala	Leu	Val	Val
			325					330					335		
Pro	Ala	Phe	Glu	Thr	Leu	Arg	Tyr	Arg	Phe	Ser	Phe	Pro	His	Ser	Lys
			340					345					350		
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&lt;210&gt; 3713

&lt;211&gt; 1719

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3713

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&lt;210&gt; 3714

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3714

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Thr	Pro	Val	Gln	Asp	Glu	Arg	Asp	Ser	Gly	Ser	Asp	Gly	Glu	Asp
			20				25					30		
Val	Asn	Glu	Gln	His	Ser	Gly	Ser	Asp	Thr	Gly	Ser	Val	Glu	Arg
			35				40					45		
Ser	Glu	Asn	Glu	Thr	Ser	Asp	Arg	Glu	Asp	Gly	Pro	Pro	Lys	Gly
			50				55				60			
His	Val	Thr	Asp	Ser	Glu	Asn	Asp	Glu	Pro	Leu	Asn	Leu	Asn	Ala
						70				75				80
Asp	Ser	Glu	Ser	Glu	Glu	Leu	His	Arg	Gln	Lys	Asp	Ser	Asp	Ser
						85				90				95
Ser	Glu	Glu	Arg	Ala	Glu	Pro	Pro	Ala	Ser	Asp	Ser	Glu	Asn	Glu
						100				105			110	
Val	Asn	Gln	His	Gly	Ser	Asp	Ser	Glu	Ser	Glu	Glu	Thr	Arg	Lys
						115				120			125	
Pro	Gly	Ser	Asp	Ser	Glu	Asn	Glu	Glu	Leu	Leu	Asn	Gly	His	Ala
						130				135			140	
Asp	Ser	Glu	Asn	Glu	Asp	Val	Gly	Lys	His	Pro	Ala	Ser	Asp	Ser
														Glu

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His Gln Ala Ser Asp Ser Glu Asn Glu Glu Pro Pro Lys Pro Arg Met
          195          200          205
Ser Asp Ser Glu Ser Glu Glu Leu Pro Lys Pro Gln Val Ser Asp Ser
          210          215          220
Glu Ser Glu Glu Pro Pro Arg His Gln Ala Ser Asp Ser Glu Asn Glu
225          230          235          240
Glu Leu Pro Lys Pro Arg Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro
          245          250          255
Arg His Gln Ala Ser Asp Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg
          260          265          270
Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro Arg Asn Gln Ala Ser Asp
          275          280          285
Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg Val Ser Asp Ser Glu Ser
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Glu Gly Pro Gln Lys Gly Pro Ala Ser Asp Ser Glu Thr Glu Asp Ala
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Ser Arg His Lys Gln Lys Pro Glu Ser Asp Asp Asp Ser Asp Arg Glu
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Ser His Met Asp Arg Lys Lys Phe His Ser Ser Asp Ser Glu Glu Glu
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Glu His Lys Lys Gln Lys Met Asp Ser Asp Glu Asp Glu Lys Glu Gly
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Glu Glu Glu Lys Val Ala Lys Arg Lys Ala Ala Val Leu Ser Asp Ser
385          390          395          400
Glu Asp Glu Glu Lys Ala Ser Ala Lys Lys Ser Arg Val Val Ser Asp
          405          410          415
Ala Asp Asp Ser Asp Ser Asp Ala Val Ser Asp Lys Ser Gly Lys Arg
          420          425          430
Glu Lys Thr Ile Ala Ser Asp Ser Glu Glu Glu Ala Gly Lys Glu Leu
          435          440          445
Ser Asp Lys Lys Asn Glu Glu Lys Asp Leu Phe Gly Ser Asp Ser Glu
          450          455          460
Ser Gly Asn Glu Glu Glu Asn Leu Ile Ala Asp Ile Phe Gly Glu Ser
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Gly Asp Glu Glu Glu Glu Glu Phe
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&lt;210&gt; 3715

&lt;211&gt; 288

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3715

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120

cacttggaga aacatcgaaa ggacaaagcc cacaaacgct atctgcta at gagcattgac  
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 cagaggaaaa agatgctcaa aaacctccgt aacaccaact atgatgtctt tgagaagata  
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 <213> Homo sapiens

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 35 40 45  
 Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys Lys  
 50 55 60  
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 540  
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 660



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 720  
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 780  
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 900  
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&lt;210&gt; 3718

&lt;211&gt; 374

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3718

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Gly	Ile	Leu	Leu	Glu	Pro	Cys	Ser	Asp	Arg	Gly	Asp	Ser	Glu	Asp	Gly
			20					25					30		
Cys	Leu	Glu	Arg	Glu	Glu	Tyr	Leu	Leu	Phe	Asp	Ser	Asp	Lys	Leu	Ser
			35				40					45			
His	Leu	Ile	Leu	Asp	Ser	Ser	Ser	Lys	Ile	Cys	Asp	Leu	Asn	Ala	Asn
			50				55				60				
Thr	Glu	Ser	Glu	Val	Pro	Gly	Gly	Gln	Ser	Val	Gly	Val	Gln	Gly	Glu
65				70					75					80	
Ala	Ala	Cys	Val	Ser	Ile	Pro	His	Leu	Asp	Leu	Lys	Asn	Val	Ser	Asp
			85					90					95		
Gly	Asp	Lys	Trp	Glu	Glu	Pro	Phe	Pro	Ala	Phe	Lys	Ser	Trp	Gln	Glu
			100					105					110		
Asp	Ser	Glu	Ser	Gly	Glu	Ala	Gln	Leu	Ser	Pro	Gln	Ala	Gly	Arg	Met
			115				120					125			
Asn	His	His	Pro	Leu	Glu	Glu	Asp	Cys	Pro	Pro	Val	Leu	Ser	His	Arg

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 165 170 175  
 Ser Phe Ser Ser Lys Asp Glu Lys Arg Glu Asp Arg Thr Pro Tyr Gln  
 180 185 190  
 Leu Val Lys Lys Leu Gln Lys Lys Ile Arg Gln Phe Glu Glu Gln Phe  
 195 200 205  
 Glu Arg Glu Arg Asn Ser Lys Pro Ser Tyr Ser Asp Ile Ala Ala Asn  
 210 215 220  
 Pro Lys Val Leu Lys Trp Met Thr Glu Leu Thr Lys Leu Arg Lys Gln  
 225 230 235 240  
 Ile Lys Asp Ala Lys His Lys Asn Ser Asp Gly Glu Phe Val Pro Gln  
 245 250 255  
 Thr Arg Pro Arg Ser Asn Thr Leu Pro Lys Ser Phe Gly Ser Ser Leu  
 260 265 270  
 Asp His Glu Asp Glu Glu Asn Glu Asp Glu Pro Lys Val Ile Gln Lys  
 275 280 285  
 Glu Lys Lys Pro Ser Lys Glu Ala Thr Leu Glu Leu Ile Leu Lys Arg  
 290 295 300  
 Leu Lys Glu Lys Arg Ile Glu Arg Cys Leu Pro Glu Asp Ile Lys Lys  
 305 310 315 320  
 Met Thr Lys Asp His Leu Val Glu Glu Lys Ala Ser Leu Gln Lys Ser  
 325 330 335  
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 340 345 350  
 Arg His Ile Val Lys Pro Leu Tyr Asp Arg Tyr Arg Leu Val Lys Gln  
 355 360 365  
 Met Leu Thr Arg Ala Ser  
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&lt;210&gt; 3719

&lt;211&gt; 422

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3719

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 35 40 45  
 Val Cys Phe Asp Asp Phe Phe Pro Ile Ser Gln Val Arg Leu Trp Ala  
 50 55 60  
 Leu Gln Leu Ile Met Val Ser Thr Pro Ser Leu Leu Val Val Leu His  
 65 70 75 80  
 Val Ala Tyr His Glu Gly Arg Glu Lys Arg His Arg Lys Lys Leu Tyr  
 85 90 95  
 Val Ser Pro Gly Thr Met Asp Gly Gly Leu Trp Tyr Ala Tyr Leu Ile  
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2869

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 4728

&lt;210&gt; 3722

&lt;211&gt; 1216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3722

Ser	Glu	Lys	Glu	Lys	Glu	Glu	Leu	Glu	Arg	Leu	Gln	Lys	Glu	Glu	Glu
1				5					10					15	
Glu	Arg	Lys	Lys	Arg	Leu	Gln	Leu	Tyr	Val	Phe	Val	Met	Arg	Cys	Ile
			20					25					30		
Ala	Tyr	Pro	Phe	Asn	Ala	Lys	Gln	Pro	Thr	Asp	Met	Ala	Arg	Arg	Gln
			35				40					45			
Gln	Lys	Ile	Ser	Lys	Gln	Gln	Leu	Gln	Thr	Val	Lys	Asp	Arg	Phe	Gln
		50				55					60				
Ala	Phe	Leu	Asn	Gly	Glu	Thr	Gln	Ile	Met	Ala	Asp	Glu	Ala	Phe	Met
65					70				75					80	
Asn	Ala	Val	Gln	Ser	Tyr	Tyr	Glu	Val	Phe	Leu	Lys	Ser	Asp	Arg	Val
			85					90					95		
Ala	Arg	Met	Val	Gln	Ser	Gly	Gly	Cys	Ser	Ala	Asn	Asp	Ser	Arg	Glu
			100					105					110		
Val	Phe	Lys	Lys	His	Ile	Glu	Lys	Arg	Val	Arg	Ser	Leu	Pro	Glu	Ile
			115				120					125			
Asp	Gly	Leu	Ser	Lys	Glu	Thr	Val	Leu	Ser	Ser	Trp	Met	Ala	Lys	Phe
	130					135					140				
Asp	Ala	Ile	Tyr	Arg	Gly	Glu	Glu	Asp	Pro	Arg	Lys	Gln	Gln	Ala	Arg
145					150				155					160	
Met	Thr	Ala	Ser	Ala	Ala	Ser	Glu	Leu	Ile	Leu	Ser	Lys	Glu	Gln	Leu

2871

595					600					605					
Gly	Trp	Phe	Ser	Pro	Gly	Gln	Val	Phe	Val	Leu	Asp	Glu	Tyr	Cys	Ala
610					615					620					
Arg	Asn	Gly	Val	Arg	Gly	Cys	His	Arg	His	Leu	Cys	Tyr	Leu	Arg	Asp
625					630					635					
Leu	Leu	Glu	Arg	Ala	Glu	Asn	Gly	Ala	Met	Ile	Asp	Pro	Thr	Leu	Leu
645					650					655					
His	Tyr	Ser	Phe	Ala	Phe	Cys	Ala	Ser	His	Val	His	Gly	Asn	Arg	Pro
660					665					670					
Asp	Gly	Ile	Gly	Thr	Val	Thr	Val	Glu	Glu	Lys	Glu	Arg	Phe	Glu	Glu
675					680					685					
Ile	Lys	Glu	Arg	Leu	Arg	Val	Leu	Leu	Glu	Asn	Gln	Ile	Thr	His	Phe
690					695					700					
Arg	Tyr	Cys	Phe	Pro	Phe	Gly	Arg	Pro	Glu	Gly	Ala	Leu	Lys	Ala	Thr
705					710					715					
Leu	Ser	Leu	Leu	Glu	Arg	Val	Leu	Met	Lys	Asp	Ile	Val	Thr	Pro	Val
725					730					735					
Pro	Gln	Glu	Glu	Val	Lys	Thr	Val	Ile	Arg	Lys	Cys	Leu	Glu	Gln	Ala
740					745					750					
Ala	Leu	Val	Asn	Tyr	Ser	Arg	Leu	Ser	Glu	Tyr	Ala	Lys	Ile	Glu	Glu
755					760					765					
Asn	Gln	Lys	Asp	Ala	Glu	Asn	Val	Gly	Arg	Leu	Ile	Thr	Pro	Ala	Lys
770					775					780					
Lys	Leu	Glu	Asp	Thr	Ile	Arg	Leu	Ala	Glu	Leu	Val	Ile	Glu	Val	Leu
785					790					795					
Gln	Gln	Asn	Glu	Glu	His	His	Ala	Glu	Pro	His	Val	Asp	Lys	Gly	Glu
805					810					815					
Ala	Phe	Ala	Trp	Trp	Ser	Asp	Leu	Met	Val	Glu	His	Ala	Glu	Thr	Phe
820					825					830					
Leu	Ser	Leu	Phe	Ala	Val	Asp	Met	Asp	Ala	Ala	Leu	Glu	Val	Gln	Pro
835					840					845					
Pro	Asp	Thr	Trp	Asp	Ser	Phe	Pro	Leu	Phe	Gln	Leu	Leu	Asn	Asp	Phe
850					855					860					
Leu	Arg	Thr	Asp	Tyr	Asn	Leu	Cys	Asn	Gly	Lys	Phe	His	Lys	His	Leu
865					870					875					
Gln	Asp	Leu	Phe	Ala	Pro	Leu	Val	Val	Arg	Tyr	Val	Asp	Leu	Met	Glu
885					890					895					
Ser	Ser	Ile	Ala	Gln	Ser	Ile	His	Arg	Gly	Phe	Glu	Arg	Glu	Ser	Trp
900					905					910					
Glu	Pro	Val	Asn	Asn	Gly	Ser	Gly	Thr	Ser	Glu	Asp	Leu	Phe	Trp	Lys
915					920					925					
Leu	Asp	Ala	Leu	Gln	Thr	Phe	Ile	Arg	Asp	Leu	His	Trp	Pro	Glu	Glu
930					935					940					
Glu	Phe	Gly	Lys	His	Leu	Glu	Gln	Arg	Leu	Lys	Leu	Met	Ala	Ser	Asp
945					950					955					
Met	Ile	Glu	Ser	Cys	Val	Lys	Arg	Thr	Arg	Ile	Ala	Phe	Glu	Val	Lys
965					970					975					
Leu	Gln	Lys	Thr	Ser	Arg	Ser	Thr	Asp	Phe	Arg	Val	Pro	Gln	Ser	Ile
980					985					990					
Cys	Thr	Met	Phe	Asn	Val	Met	Val	Asp	Ala	Lys	Ala	Gln	Ser	Thr	Lys
995					1000					1005					
Leu	Cys	Ser	Met	Glu	Met	Gly	Gln	Glu	Phe	Ala	Lys	Met	Trp	His	Gln
1010					1015					1020					
Tyr	His	Ser	Lys	Ile	Asp	Glu	Leu	Ile	Glu	Glu	Thr	Val	Lys	Glu	Met



1025                      1030                      1035                      1040  
 Ile Thr Leu Leu Val Ala Lys Phe Val Thr Ile Leu Glu Gly Val Leu  
                                  1045                      1050                      1055  
 Ala Lys Leu Ser Arg Tyr Asp Glu Gly Thr Leu Phe Ser Ser Phe Leu  
                                  1060                      1065                      1070  
 Ser Phe Thr Val Lys Ala Ala Ser Lys Tyr Val Asp Val Pro Lys Pro  
                                  1075                      1080                      1085  
 Gly Met Asp Val Ala Asp Ala Tyr Val Thr Phe Val Arg His Ser Gln  
                                  1090                      1095                      1100  
 Asp Val Leu Arg Asp Lys Val Asn Glu Glu Met Tyr Ile Glu Arg Leu  
 1105                      1110                      1115                      1120  
 Phe Asp Gln Trp Tyr Asn Ser Ser Met Asn Val Ile Cys Thr Trp Leu  
                                  1125                      1130                      1135  
 Thr Asp Arg Met Asp Leu Gln Leu His Ile Tyr Gln Leu Lys Thr Leu  
                                  1140                      1145                      1150  
 Ile Arg Met Val Lys Lys Thr Tyr Arg Asp Phe Arg Leu Gln Gly Val  
                                  1155                      1160                      1165  
 Leu Asp Ser Thr Leu Asn Ser Lys Thr Tyr Glu Thr Ile Arg Asn Arg  
                                  1170                      1175                      1180  
 Leu Thr Val Glu Glu Ala Thr Ala Ser Val Ser Glu Gly Gly Gly Leu  
 1185                      1190                      1195                      1200  
 Gln Gly Ile Ser Met Lys Asp Ser Asp Glu Glu Asp Glu Glu Asp Asp  
                                  1205                      1210                      1215

&lt;210&gt; 3723

&lt;211&gt; 830

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3723

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 60  
 tgtgtcaaca ccaccgggca tttggtgaag atcattgact ttggcctggc acggagggtat  
 120  
 aaccccaacg agaagctgaa ggtgaacttt gggaccccag agttcctgtc acctgagggtg  
 180  
 gtgaattatg accaaatctc cgataagaca gacatgtgga gtatgggggt gatcacctac  
 240  
 atgctgctga gcggcctctc ccccttctctg ggagatgatg acacagagac cctaaacaac  
 300  
 gttctatctg gcaactggta ctttgatgaa gagacctttg aggccgtatc agacgaggcc  
 360  
 aaagactttg tctccaacct catcgtaag gaccagaggg cccggatgaa cgctgcccag  
 420  
 tgtctcgccc atccctggct caacaacctg gcggagaaag ccaaacgctg taaccgacgc  
 480  
 cttaagtccc agatcttgct taagaaatac ctcatgaaga ggcgctggaa gaaaaacttc  
 540  
 attgctgtca gcgctgcca ccgcttcaag aagatcagca gctcgggggc actgatggct  
 600  
 ctgggggtct gagccctggg cgcagctgaa gcctggacgc agccacacag tggccggggc  
 660  
 tgaagccaca cagcccagaa ggccagaaaa ggcagccaga tccccagggc agcctcgtaa  
 720

ggacaaggct gtgccaggct gggaggctcg gggctcccca cgccccatg cagtgaccgc  
 780  
 ttccccgatg tgagccgcct cggagtgtgg cctggatcca tcctgctagc  
 830

<210> 3724  
 <211> 203  
 <212> PRT  
 <213> Homo sapiens

<400> 3724  
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 Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu Val Lys Ile Ile  
 20 25 30  
 Asp Phe Gly Leu Ala Arg Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val  
 35 40 45  
 Asn Phe Gly Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp  
 50 55 60  
 Gln Ile Ser Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr  
 65 70 75 80  
 Met Leu Leu Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu  
 85 90 95  
 Thr Leu Asn Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr  
 100 105 110  
 Phe Glu Ala Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile  
 115 120 125  
 Val Lys Asp Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His  
 130 135 140  
 Pro Trp Leu Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg  
 145 150 155 160  
 Leu Lys Ser Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp  
 165 170 175  
 Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg Phe Lys Lys Ile  
 180 185 190  
 Ser Ser Ser Gly Ala Leu Met Ala Leu Gly Val  
 195 200

<210> 3725  
 <211> 1244  
 <212> DNA  
 <213> Homo sapiens

<400> 3725  
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 tctgctcatg gcttatcagt cttgaatctg cgggatggaa gagagctgga ttccagatct  
 120  
 gaccatcttc acttttgttt tcaggccttt aaaattgtgc cctacaacac agagaccctt  
 180  
 gataaactgc taaccgaatc cctgaagaac aatatccctg caagcggact gcacctcttt  
 240  
 ggaatcaacc agctggaaga agaagatatg atgacaaatc agagggatga agagctgccc  
 300

accctgttgc attttgcgc gaagtatgga ctgaagaacc tcaactgcctt gttgctcacc  
 360  
 tgcccaggag ccctgcaggc gtacagcgtg gccacaagc atggccacta ccccaacacc  
 420  
 atcgcctgaga aacacggctt cagggacctg cggcagttca tcgacgagta tgtggaaacg  
 480  
 gtggacatgc tcaagagtca cattaaagag gaactgatgc acggggagga ggctgatgct  
 540  
 gtgtacgagt ccatggccca cctttccaca gacctgctta tgaaatgctc gctcaacccc  
 600  
 ggctgtgacg aggatctcta tgagtccatg gctgcctttg tcccagctgc cactgaagac  
 660  
 ctctatgttg aaatgcttca ggccagtaca tctaaccctaa tccctggaga tggtttctct  
 720  
 cggggccacta aggactctat gatccgcaag tttttagaag gcaacagcat gggaatgacc  
 780  
 aatctggaga gagatcagtg ccatcttggc caggaagaag atgtttatca cacggtggat  
 840  
 gacgatgagg ccttttctgt ggacttggcc agcaggcccc ctgtcccagt gccagacca  
 900  
 gagaccactg ctctggtgc tcaccagctg cctgacaacg aaccatacat ttttaaaggc  
 960  
 aagtatggca gggaatgatg tccaactggc tctttggagc ttctcaacag ggatttcctg  
 1020  
 gatgacctgg ctttttgaac cattgctcag agactatccc cttctaaatg gtcttcaccc  
 1080  
 agccctacga gacagggttc atatcctggg gccagattct ggagctagaa taggagtaat  
 1140  
 gaccagagtc agtgctggcc ttcctggaag tatttacgca cagttgcaaa ggcaggtaaa  
 1200  
 caagaccctt gatatatattt tatctcctga accccttcac gcgt  
 1244

&lt;210&gt; 3726

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3726

Xaa	Ile	His	Val	Ser	Gly	Lys	Asp	Ile	Thr	Arg	Lys	Pro	Glu	Ile	Ser
1				5					10					15	
Gly	His	Val	Ile	Ser	Ala	His	Gly	Leu	Ser	Val	Leu	Asn	Leu	Arg	Asp
		20						25					30		
Gly	Arg	Glu	Leu	Asp	Phe	Arg	Ser	Asp	His	Leu	His	Phe	Cys	Phe	Gln
	35						40					45			
Ala	Phe	Lys	Ile	Val	Pro	Tyr	Asn	Thr	Glu	Thr	Leu	Asp	Lys	Leu	Leu
	50					55					60				
Thr	Glu	Ser	Leu	Lys	Asn	Asn	Ile	Pro	Ala	Ser	Gly	Leu	His	Leu	Phe
65				70					75					80	
Gly	Ile	Asn	Gln	Leu	Glu	Glu	Glu	Asp	Met	Met	Thr	Asn	Gln	Arg	Asp
		85						90					95		
Glu	Glu	Leu	Pro	Thr	Leu	Leu	His	Phe	Ala	Ala	Lys	Tyr	Gly	Leu	Lys
		100					105						110		
Asn	Leu	Thr	Ala	Leu	Leu	Leu	Thr	Cys	Pro	Gly	Ala	Leu	Gln	Ala	Tyr

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      115              120              125
Ser Val Ala Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys
      130              135              140
His Gly Phe Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr
      145              150              155              160
Val Asp Met Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu
      165              170              175
Glu Ala Asp Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu
      180              185              190
Leu Met Lys Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu
      195              200              205
Ser Met Ala Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu
      210              215              220
Met Leu Gln Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser
      225              230              235              240
Arg Ala Thr Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser
      245              250              255
Met Gly Met Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu
      260              265              270
Glu Asp Val Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp
      275              280              285
Leu Ala Ser Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala
      290              295              300
Pro Gly Ala His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Gly
      305              310              315              320
Lys Tyr Gly Arg Glu
      325

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&lt;210&gt; 3727

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3727

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cggattcgag tcattcaagaa gaaaaagggtc attatgaaga agcgggaagaa gctaactcta
60
actcgcccca cccactggt gactgccggg ccccttgtga ccccaactcc agcaggggacc
120
ctcgaccccg ctgagaaaca agaaacaggc tgcctcctt tgggtctgga gtccttgcga
180
gtttcagata gccggcttga ggcattccagc agccagtcct ttggtcttgg accacaccga
240
ggacggctca acattcagtc aggcctggag gacggcgatc tatatgatgg agcctgggtgt
300
gctgaggagc aggacgccga tccatggttt caggtggacg ctgggcaccc caccgcttc
360
tcgggtgtta tcacacaggg caggaactct gtctggaggt atgactgggt cacatcatac
420
aaggtccagt tcagcaatga cagtcggacc tgggtgggaa gtaggaacca cagcagtggg
480
atggacgcag tatttctctg caattcagac ccagaaactc cagtgtgaa cctcctgccg
540
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600

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ccttgccctcc gggcagagat cctggcctgc  
630

<210> 3728  
<211> 210  
<212> PRT  
<213> Homo sapiens

<400> 3728  
Arg Ile Arg Val Ile Lys Lys Lys Lys Val Ile Met Lys Lys Arg Lys  
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Lys Leu Thr Leu Thr Arg Pro Thr Pro Leu Val Thr Ala Gly Pro Leu  
20 25 30  
Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln Glu  
35 40 45  
Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp Ser  
50 55 60  
Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His Arg  
65 70 75 80  
Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr Asp  
85 90 95  
Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln Val  
100 105 110  
Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly Arg  
115 120 125  
Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln Phe  
130 135 140  
Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser Gly  
145 150 155 160  
Met Asp Ala Val Phe Pro Ala Asn Ser Asp Pro Glu Thr Pro Val Leu  
165 170 175  
Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe Ile Arg Leu Leu Pro  
180 185 190  
Gln Thr Trp Leu Gln Gly Gly Ala Pro Cys Leu Arg Ala Glu Ile Leu  
195 200 205  
Ala Cys  
210

<210> 3729  
<211> 1552  
<212> DNA  
<213> Homo sapiens

<400> 3729  
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cctcctccgc gcctcgcggc atggagtaga aagggaccgc ggaagcccga aagcgaaggc  
120  
atcaagttat cagcagatgt caaaccattt gtccccagat ttgccgggct caatgtggca  
180  
tggttagagt cctcagaagc atgtgtcttc cccagctctg cagccacata ctatccgttt  
240  
gttcaggaac caccagtgc agagcagaaa atatatactg aagacatggc ctttggagct  
300

tcaacttttc cacctcagta tttatcttct gagataactc ttcattccata tgcctattct  
 360  
 ccttataccc ttgactccac acagaatgtt tactcagtgc ctggctccca gtatctttat  
 420  
 aaccaacca gttgttacgc aggttttcaa acagtgaagc atcgaaatga gaacacatgc  
 480  
 cctctccac aagaaatgaa agctctgttt aagaagaaaa cctatgatga gaaaaaacg  
 540  
 tatgatcagc aaaagtttga cagtgaagg gctgatggaa ctatatcatc tgagataaaa  
 600  
 tcagctagag gttcacatca tttgtccatt tacgctgaga atagtttgaa atcagatggt  
 660  
 taccataagc gaacagacag gaaatccaga atcattgcaa aaaatgtatc tacctccaaa  
 720  
 cctgagtttg aatttaccac actggacttt cctgaactgc aagggtgcaga gaacaatatg  
 780  
 tcagagatac agaagcaacc caagtgggga cctgtccact ctgtctctac cgacatttct  
 840  
 cttctaagag aagtagtaaa accagctgca gtgttatcaa agggtgaaat agtggtgaaa  
 900  
 aataacccaa atgaatctgt aactgctaata gccgctacca attctccttc atgtacaaga  
 960  
 gagttatctt ggacaccaat gggttatggt gttcgacaga cattatctac agaactgtca  
 1020  
 gcagccccta aaaatgttac ttctatgata aacttaaaga ccattgcttc atcagcagat  
 1080  
 cctaaaaatg ttagtatacc atcttctgaa gctttatctt cggatccttc ctacaacaaa  
 1140  
 gaaaaacaca ttattcatcc taccctaaaag tctaaagcat cacaaggtag tgaccttgaa  
 1200  
 caaatgaag cctcaagaaa gaataagaaa aagaaagaaa aatctacatc aaaatatgaa  
 1260  
 gtcctgacag ttcaagagcc tccaaggatt gaagatgccg aggaatttcc caacctggca  
 1320  
 gttgcatctg aaagaagaga cagaatagag acaccgaaat ttcaatctaa gcagcagcca  
 1380  
 caggataatt ttaaaaataa tgtaaagaag agccagcttc cagtgcagtt ggacttgggg  
 1440  
 ggcagctga cagccctgga gaagaagcag cactctcagc atgcaaagca gtcctccaaa  
 1500  
 ccagtggtag tctcagttgg agcagtgcca gtcctttcca aagaatgtgc ac  
 1552

&lt;210&gt; 3730

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3730

Met Ala Phe Gly Ala Ser Thr Phe Pro Pro Gln Tyr Leu Ser Ser Glu  
 1 5 10 15  
 Ile Thr Leu His Pro Tyr Ala Tyr Ser Pro Tyr Thr Leu Asp Ser Thr  
 20 25 30  
 Gln Asn Val Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro

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      35      40      45
Ser Cys Tyr Arg Gly Phe Gln Thr Val Lys His Arg Asn Glu Asn Thr
  50      55      60
Cys Pro Leu Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Tyr
  65      70      75      80
Asp Glu Lys Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala
      85      90      95
Asp Gly Thr Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His
      100      105      110
Leu Ser Ile Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys
      115      120      125
Arg Thr Asp Arg Lys Ser Arg Ile Ile Ala Lys Asn Val Ser Thr Ser
      130      135      140
Lys Pro Glu Phe Glu Phe Thr Thr Leu Asp Phe Pro Glu Leu Gln Gly
  145      150      155      160
Ala Glu Asn Asn Met Ser Glu Ile Gln Lys Gln Pro Lys Trp Gly Pro
      165      170      175
Val His Ser Val Ser Thr Asp Ile Ser Leu Leu Arg Glu Val Val Lys
      180      185      190
Pro Ala Ala Val Leu Ser Lys Gly Glu Ile Val Val Lys Asn Asn Pro
      195      200      205
Asn Glu Ser Val Thr Ala Asn Ala Ala Thr Asn Ser Pro Ser Cys Thr
      210      215      220
Arg Glu Leu Ser Trp Thr Pro Met Gly Tyr Val Val Arg Gln Thr Leu
  225      230      235      240
Ser Thr Glu Leu Ser Ala Ala Pro Lys Asn Val Thr Ser Met Ile Asn
      245      250      255
Leu Lys Thr Ile Ala Ser Ser Ala Asp Pro Lys Asn Val Ser Ile Pro
      260      265      270
Ser Ser Glu Ala Leu Ser Ser Asp Pro Ser Tyr Asn Lys Glu Lys His
      275      280      285
Ile Ile His Pro Thr Gln Lys Ser Lys Ala Ser Gln Gly Ser Asp Leu
      290      295      300
Glu Gln Asn Glu Ala Ser Arg Lys Asn Lys Lys Lys Lys Glu Lys Ser
  305      310      315      320
Thr Ser Lys Tyr Glu Val Leu Thr Val Gln Glu Pro Pro Arg Ile Glu
      325      330      335
Asp Ala Glu Glu Phe Pro Asn Leu Ala Val Ala Ser Glu Arg Arg Asp
      340      345      350
Arg Ile Glu Thr Pro Lys Phe Gln Ser Lys Gln Gln Pro Gln Asp Asn
      355      360      365
Phe Lys Asn Asn Val Lys Lys Ser Gln Leu Pro Val Gln Leu Asp Leu
      370      375      380
Gly Gly Met Leu Thr Ala Leu Glu Lys Lys Gln His Ser Gln His Ala
  385      390      395      400
Lys Gln Ser Ser Lys Pro Val Val Val Ser Val Gly Ala Val Pro Val
      405      410      415
Leu Ser Lys Glu Cys Ala
      420

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&lt;210&gt; 3731

&lt;211&gt; 1704

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 3731  
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120  
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420  
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1560



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 1704

<210> 3732  
 <211> 281  
 <212> PRT  
 <213> Homo sapiens

<400> 3732  
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 Cys Trp Ala Ser Leu Asn Gln Leu Asp Ser His Val Leu Leu Cys Phe  
 20 25 30  
 Glu Gly Ile Thr Asp Ala Ser Ser Cys Ala Val Leu Leu Pro Ala Ser  
 35 40 45  
 Leu Phe Val Asn Ser His Pro Gly Ile Asp Arg Pro Gly Met Leu Cys  
 50 55 60  
 Ser Phe Arg Ile Pro Gly Ala Trp Ser Cys Ala Trp Ser Leu Asn Ile  
 65 70 75 80  
 Gln Ala Asn Asn Cys Phe Ser Thr Gly Leu Ser Arg Arg Val Leu Leu  
 85 90 95  
 Thr Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp  
 100 105 110  
 Val Leu Ala Gln Gln Phe Ala Leu Met Ala Pro Leu Leu Phe Asn Gly  
 115 120 125  
 Cys Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln  
 130 135 140  
 Gly Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr  
 145 150 155 160  
 Ser Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met  
 165 170 175  
 Ala Gly Lys Ile Lys Leu Trp Asp Leu Arg Thr Thr Lys Cys Val Arg  
 180 185 190  
 Gln Tyr Glu Gly His Val Asn Glu Tyr Ala Tyr Leu Pro Leu His Val  
 195 200 205  
 His Glu Glu Glu Gly Ile Leu Val Ala Val Gly Gln Asp Cys Tyr Thr  
 210 215 220  
 Arg Ile Trp Ser Leu His Asp Ala Arg Leu Leu Arg Thr Ile Pro Ser  
 225 230 235 240  
 Pro Tyr Pro Ala Ser Lys Ala Asp Ile Pro Ser Val Ala Phe Ser Ser  
 245 250 255  
 Arg Leu Gly Gly Ser Arg Gly Ala Pro Gly Leu Leu Met Ala Val Gly  
 260 265 270  
 Gln Asp Leu Tyr Cys Tyr Ser Tyr Ser  
 275 280

<210> 3733  
 <211> 515  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 3733

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 120  
 tcctcagtgc gggagaggga gacgccgggg gcangtccat gcctcccgcg gcgtgggtgg  
 180  
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 240  
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 300  
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 360  
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 420  
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 480  
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 515

&lt;210&gt; 3734

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3734

Xaa	Gly	Arg	Ala	Val	Arg	Arg	Val	Thr	Ala	Gly	Thr	Arg	Pro	Gly	Trp
1				5					10					15	
Val	Ser	Gly	Ser	Arg	Tyr	Arg	Arg	Gly	Arg	Arg	Arg	Gly	Arg	Leu	Lys
			20					25					30		
Gly	Lys	Asp	Pro	Gly	Ser	Ala	Pro	Ser	Ser	Val	Arg	Glu	Arg	Glu	Thr
		35					40				45				
Pro	Gly	Ala	Xaa	Pro	Cys	Leu	Pro	Arg	Arg	Gly	Trp	Cys	Val	Pro	Gly
	50					55					60				
Asp	Val	Arg	Ser	Ser	Pro	Pro	Leu	Pro	Gly	Trp	Cys	Ala	Leu	Ser	Asp
65					70				75					80	
Val	Arg	Ser	Arg	Gly	Arg	Ser	Cys	Pro	Ser	Ala	Pro	Lys	Ala	Ala	Gly
				85					90				95		
Gly	Leu	Arg	Ala	Trp	Gly	Arg	Gly	Ser	Gly	Ala	Ala	Arg	Ala	Pro	Ala
			100				105						110		
Pro	Ala	Pro	Ser	Pro	Ser	Ser	Gly	Xaa	Ser	Pro	Ser	Ser	Arg	Thr	Pro
		115					120					125			
Arg	Asp	Trp	Ser	Ala	Ser	Arg	Cys	Trp	Thr	Trp	Ser	Gly	Ala	Ala	Thr
	130					135					140				
Ala	Pro	Thr	Pro	Phe	Ser	Pro	Ala	Gln	Gln	Pro	Pro	Ser	Ser	His	Asp
145					150					155					160
Gly	Leu	Ser	Leu	Asp	Pro	Ser	Gln	Leu	Glu	Pro					
				165						170					

&lt;210&gt; 3735

&lt;211&gt; 2512

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 3735  
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120  
tgatcactga acccatccct gacatccgaa accagtatcc agagcacata agcaacatca  
180  
tctccctcct ccaggacctt gtaagtgtct tccctgccag ctctgtgcag gaaacttcca  
240  
tgctggtttc cctcctgcc aacctcttta atgctctgag agcctctggt gttgacatag  
300  
aagaggaaac ggagaagaac ctggaaaagg tacagactat cattgaacat ctgcaggaaa  
360  
agaggcgaga gggcactttg agagtggata cctacactct agtgcagcct gaggcagaag  
420  
accatgttga gagctaccga accatgccca tttaccctac ctacaatgaa gtgcacttgg  
480  
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540  
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600  
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660  
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720  
acaaggtgca gtttgacaca aaaccactga agtttgttcg ctggcagaat tccaaacgat  
780  
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840  
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caactgcata ctttgaggcc tacaggcacg tcctggaagg actccaggag gtccaggagg  
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1560

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 1920  
 aagctgacct gattcaagca gaccgggtga ttgaggagga agaggtggtg aggccccagg  
 1980  
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 2160  
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 2280  
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 2340  
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 2400  
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<210> 3736

<211> 155

<212> PRT

<213> Homo sapiens

<400> 3736

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Ser	Gly	Arg	Pro	Ser	Ala	Thr	Gln	Lys	Lys	Lys	Met	Lys	Lys	Arg	Val
			20					25					30		
Lys	Asp	Glu	Leu	Arg	Lys	Leu	Asn	Thr	Met	Pro	Ala	Ala	Glu	Ala	Asn
		35				40						45			
Glu	Ile	Glu	Asp	Val	Trp	His	Leu	Asp	Leu	Ser	Ser	Arg	Trp	Gln	Leu
	50					55				60					
Tyr	Arg	Leu	Trp	Leu	Gln	Leu	Tyr	Gln	Ala	Asp	Thr	Pro	Pro	Gly	Lys
65				70					75					80	
Ile	Leu	Ser	Tyr	Glu	Arg	Gln	Tyr	Arg	Thr	Ser	Ala	Glu	Arg	Met	Ala
			85					90						95	
Glu	Leu	Arg	Leu	Gln	Glu	Asp	Leu	His	Ile	Leu	Lys	Asp	Ala	Gln	Val
		100						105						110	
Val	Gly	Met	Thr	Thr	Thr	Gly	Ala	Ala	Lys	Tyr	Arg	Gln	Ile	Leu	Gln

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      115              120              125
Lys Val Glu Pro Arg Ile Val Ile Val Glu Glu Ala Ala Glu Val Leu
      130              135              140
Glu Ala His Thr Ile Ala Thr Leu Ser Lys Ala
145              150              155

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<210> 3737  
 <211> 1046  
 <212> DNA  
 <213> Homo sapiens

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<400> 3737
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120
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180
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240
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360
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420
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540
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720
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780
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900
ccttaccatc ccatctggac cggcagggcc accgatgagg agccgctggg gcttcccaag
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1046

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<210> 3738  
 <211> 348  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 3738

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 Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln  
 20 25 30  
 Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile  
 35 40 45  
 Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg  
 50 55 60  
 Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala  
 65 70 75 80  
 Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Gly Ala Leu  
 85 90 95  
 Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe  
 100 105 110  
 His Gly Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu  
 115 120 125  
 Gln Glu Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr  
 130 135 140  
 Leu Tyr Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe  
 145 150 155 160  
 Arg Asp Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile  
 165 170 175  
 Ser Ser Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg  
 180 185 190  
 Leu Leu Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe  
 195 200 205  
 Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu  
 210 215 220  
 Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr  
 225 230 235 240  
 Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro  
 245 250 255  
 Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro  
 260 265 270  
 Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala  
 275 280 285  
 Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro  
 290 295 300  
 Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys  
 305 310 315 320  
 Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly  
 325 330 335  
 Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg  
 340 345

&lt;210&gt; 3739

&lt;211&gt; 1252

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3739

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 60

acaccctca gccagctgtt cttggaggtc ctgcccctgg gacttgtccg gctcatccag  
 120  
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 180  
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 240  
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 300  
 aggtttctga actgctgttt gttctctgcc aactgggggc gcaatttctc gttgatttct  
 360  
 agaatgttca tctctgcctt ctcgctggac aaagggcccg ctgataccac catgctgacg  
 420  
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 480  
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 540  
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 600  
 gtaaccgtct tgateccatag gctcacattt gatcccaact ggcggctgct tcttggcatt  
 660  
 aactttggat tccaaccag taaatcttag caagatctga gtttctccag gtatgatatt  
 720  
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 900  
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 960  
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 1020  
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 1080  
 gcgcgcgcgc gcctcggccc agctcctggc gccgcagatc gcccgctccc cgttcccaaa  
 1140  
 agccccgcgc tcgctcagaa gctcgggcag cctcgcgacc ctcacctacc cctcccaata  
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 1252

&lt;210&gt; 3740

&lt;211&gt; 139

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3740

Met Gly Lys Phe Leu His Gln Gly Leu Gly Glu Ser Thr Gly Ser Pro  
 1 5 10 15  
 Gly Gln Trp Glu Ser Ala Ala Pro Pro Val Trp Arg Pro Arg Ala His  
 20 25 30  
 Ser Thr Glu Ala Pro Gly His Pro Gln Glu Asp Gly Lys Gly Gln Leu  
 35 40 45  
 Ala Gly Glu Ser Pro Gly His Arg Glu Pro Ser Pro Gly Ser Lys Gln

```

      50              55              60
Asp Leu Pro Ser Asp Cys Leu Arg Asn Ala Gly Trp Thr Ser Arg Asn
65              70              75              80
Phe Pro Phe Thr Gly Gln Pro Ala Ala Ala Pro Pro Arg Leu Gly Pro
      85              90              95
Ala Pro Gly Ala Ala Asp Arg Pro Ser Arg Val Pro Lys Ser Pro Ala
      100             105             110
Leu Ala Gln Lys Leu Gly Gln Pro Arg Asp Pro His Leu Pro Leu Pro
      115             120             125
Ile Ser Pro Leu Ser Gln Pro Pro Pro Ser Pro
      130             135

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<210> 3741  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

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<400> 3741
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gtcgtgtcca ctgtggggat ccacgtcctg actaaccttg tgttcctaga aatccctcac
120
cggcagatcg gtgcctcctg aatcccaccc aaaattccca ctgggaatgt gttcctgaaa
180
gagctgcccc ggcttgagaa agcctctttt cagaccaaac ttcgtattca aagctcaaaa
240
agaactgcac acaattagga cagtcataca agatgctgcc cctaactctg ccacaatctg
300
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420
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562

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<210> 3742  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

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<400> 3742
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Ala Glu Ala Ala Glu Met Asn Pro Val Cys Glu Arg Arg Ala Leu Ser
      20              25              30
Pro Ala Arg Ala Cys Ser Pro Arg Gly Trp Gly Leu Trp Ser Phe Gln
      35              40              45
Ser Cys Ser Leu Arg Ile Pro Ser Gln Gly His Phe Ala Leu Gly Ser
      50              55              60
Pro Ala Ser Leu Leu Ala Asp Cys Gly Arg Ile Arg Gly Ser Ile Leu

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65              70              75              80
Tyr Asp Cys Pro Asn Cys Val Gln Phe Phe Leu Ser Phe Glu Tyr Glu
              85              90              95
Val Trp Ser Glu Lys Arg Leu Ser Gln Ala Trp Ala Ala Leu Ser Gly
              100              105              110
Thr His Ser Gln Trp Glu Phe Trp Val Gly Phe Arg Arg His Arg Ser
              115              120              125
Ala Gly Glu Gly Phe Leu Gly Thr Gln Gly
              130              135

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&lt;210&gt; 3743

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3743

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&lt;210&gt; 3744

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3744

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              20              25              30
Asn Met Ala Glu Thr His Lys Ala Met Ile Leu Gln Leu Asn Pro Ser
              35              40              45
Glu Asn Cys Thr Trp Thr Ile Glu Arg Pro Glu Asn Lys Ser Ile Arg
              50              55              60
Ile Ile Phe Ser Tyr Val Gln Leu Asp Pro Asp Gly Ser Cys Glu Ser
65              70              75              80
Glu Asn Ile Lys Val Phe Asp Gly Thr Ser Ser Asn Gly Pro Leu Leu
              85              90              95
Gly Gln Val Cys Ser Lys Asn Asp Tyr Val Pro Val Phe Glu Ser Ser
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Ser Ser Thr Leu Thr Phe Gln Ile Val Thr Asp Ser Ala Arg Ile Gln

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120

125

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<213> Homo sapiens

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<210> 3746  
<211> 102  
<212> PRT  
<213> Homo sapiens

<400> 3746  
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35 40 45  
Arg Thr Gln Pro Cys Ser Pro Arg Ser Cys Ser His Ser His Gly Ile  
50 55 60  
Ala Trp Ser Asp Ala Ala Ser Ala Pro Asp Ala Ser Arg Cys Arg Cys  
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Gln Ala Cys Gln Ala Lys Pro Arg Phe Ser Gly Ala Ala Gly Gly Gly  
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Arg His Val Trp Ala Asp  
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<211> 800  
<212> DNA  
<213> Homo sapiens

<400> 3747  
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&lt;210&gt; 3748

&lt;211&gt; 138

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3748

Met	Gln	Met	Arg	Phe	Asp	Gly	Arg	Leu	Gly	Phe	Pro	Gly	Gly	Phe	Val
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Asp	Thr	Gln	Asp	Arg	Ser	Leu	Glu	Asp	Gly	Leu	Asn	Arg	Glu	Leu	Arg
		20						25					30		
Glu	Glu	Leu	Gly	Glu	Ala	Ala	Ala	Ala	Phe	Arg	Val	Glu	Arg	Thr	Asp
		35					40						45		
Tyr	Arg	Ser	Ser	His	Val	Gly	Val	Arg	Ala	Thr	Arg	Cys	Gly	Pro	Leu
	50					55					60				
Leu	Cys	Gln	Ala	Ser	Asp	Ala	Arg	Gly	Ala	Val	Gly	Cys	Gly	Gly	Arg
65					70					75				80	
Arg	Asn	Thr	Arg	Gln	Gly	Pro	Arg	Ala	Gly	Gly	Gly	Thr	Ser	Leu	Gly
				85					90					95	
Leu	Cys	Pro	Phe	Pro	Asn	Phe	Leu	Phe	Ser	Gln	Ser	Phe	Leu	Ser	Pro
		100						105					110		
Lys	Lys	Ala	Ser	Leu	Glu	Lys	Ser	Leu	Cys	Pro	Ser	Asp	Leu	Ala	Leu
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Ser	Pro	Ala	Phe	Leu	Val	Glu	Leu	Gly	Ser						
		130						135							

&lt;210&gt; 3749

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3749

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 420  
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 480  
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 648

&lt;210&gt; 3750

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3750

Arg	Ala	Pro	Trp	Glu	Asp	Pro	Ala	Lys	Trp	Val	Met	Asp	Thr	Tyr	Pro
1				5					10					15	
Trp	Ala	Ala	Ser	Pro	Gln	Gln	His	Glu	Trp	Pro	Pro	Leu	Leu	Gln	Leu
		20					25						30		
Arg	Pro	Glu	Asp	Val	Gly	Phe	Asp	Gly	Tyr	Ser	Met	Pro	Arg	Glu	Gly
		35				40					45				
Ser	Thr	Ser	Lys	Gln	Met	Pro	Pro	Ser	Asp	Ala	Glu	Gly	Asp	Pro	Leu
		50			55					60					
Met	Asn	Met	Leu	Met	Arg	Leu	Gln	Glu	Ala	Ala	Asn	Tyr	Ser	Ser	Pro
65					70				75					80	
Gln	Ser	Tyr	Asp	Ser	Asp	Ser	Asn	Ser	Asn	Ser	His	His	Asp	Asp	Ile
			85				90						95		
Leu	Asp	Ser	Ser	Leu	Glu	Ser	Thr	Leu							
			100					105							

&lt;210&gt; 3751

&lt;211&gt; 554

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3751

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<210> 3752

<211> 66

<212> PRT

<213> Homo sapiens

<400> 3752

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Pro	His	His	Gly	Pro	Gly	Pro	Ala	Ala	Ala	Arg	Gly	Ser	Val	Ala	Pro
			20					25					30		
Ser	Gly	Ala	Lys	Gly	Val	Ser	Tyr	Thr	Gln	Gly	Gln	Ser	Pro	Glu	Pro
			35				40					45			
Arg	Thr	Arg	Glu	Val	Phe	Leu	Leu	Arg	Gly	Pro	Pro	Gly	Pro	Ala	Phe
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Pro	Gly														
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<210> 3753

<211> 1426

<212> DNA

<213> Homo sapiens

<400> 3753

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 1020  
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 1080  
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 aaaaagtcca tgtccacctg agataagagc tgttggtggg attggggggg ccacatgcga  
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<210> 3754

<211> 261

<212> PRT

<213> Homo sapiens

<400> 3754

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Ser	Ala	Thr	Glu	Ser	Leu	Pro	Thr	Leu	Glu	Leu	Leu	Ser	Gln	Val	Asp
			20						25				30		
Met	Asp	Cys	Arg	Val	His	Met	Arg	Pro	Ile	Gly	Leu	Thr	Trp	Val	Leu
		35					40					45			
Gln	Leu	Thr	Leu	Ala	Trp	Ile	Leu	Leu	Glu	Ala	Cys	Gly	Gly	Ser	Arg
	50					55					60				
Pro	Leu	Gln	Ala	Arg	Ser	Gln	Gln	His	His	Gly	Leu	Ala	Ala	Asp	Leu
65				70						75				80	
Gly	Lys	Gly	Lys	Leu	His	Leu	Ala	Gly	Pro	Cys	Cys	Pro	Ser	Glu	Met

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<211> 3149
<212> DNA
<213> Homo sapiens
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720

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 3149

&lt;210&gt; 3756

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3756

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Asp	Asp	Asp	Ser	Ala	Pro	Ser	Thr	Ser	Asn	Ser	Gln	Ser	Asp	Leu	Phe
			20					25					30		
Ser	Glu	Glu	Thr	Thr	Ser	Asp	Asn	Asn	Asn	Thr	Ser	Ile	Thr	Thr	Pro
			35				40					45			
Thr	Leu	Ser	Pro	Ser	Gln	Gln	Pro	Leu	Pro	Thr	Glu	Leu	Asn	Val	Thr
			50			55					60				
Ser	Pro	Ser	Lys	Glu	Glu	Cys	Gly	Pro	Cys	Thr	Asp	Thr	Ala	His	Val
65				70					75					80	
Ser	Leu	Ile	Thr	Pro	Thr	Lys	Arg	Ser	Cys	Gly	Thr	Asp	Ser	Gln	Ser
			85					90						95	
Glu	Asn	Glu	Ala	Ser	Pro	Val	Lys	Arg	Pro	Arg	Leu	Leu	Glu	Asn	Thr
			100				105						110		
Glu	Arg	Ser	Glu	Glu	Thr	Ser	Arg	Ser	Lys	Gln	Lys	Ser	Arg	Arg	Arg
			115			120						125			
Cys	Phe	Gln	Cys	Gln	Thr	Lys	Leu	Glu	Leu	Val	Gln	Gln	Glu	Leu	Gly
			130			135					140				
Ser	Cys	Arg	Cys	Gly	Tyr	Val	Phe	Cys	Met	Leu	His	Arg	Leu	Pro	Glu

145		150		155		160									
Gln	His	Asp	Cys	Thr	Phe	Asp	His	Met	Gly	Arg	Gly	Arg	Glu	Glu	Ala
					165					170				175	
Ile	Met	Lys	Met	Val	Lys	Leu	Asp	Arg	Lys	Val	Gly	Arg	Ser	Cys	Gln
			180					185					190		
Arg	Ile	Gly	Glu	Gly	Cys	Ser									
			195												

<210> 3757  
 <211> 1046  
 <212> DNA  
 <213> Homo sapiens

<400> 3757  
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 120  
 ccgggcctca ggttcgacaa catccaggga gatgcagtta aagacttgat gtttcgcttt  
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 300  
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<213> Homo sapiens

<400> 3758

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Gly Lys Ser Gly Leu Leu Thr Ser His Thr Thr Asp Ser Leu Gln Leu
      35           40           45
Trp Phe Val Arg Leu Ala Leu Leu Val Lys Leu Gly Leu Phe Gln Asn
      50           55           60
Ala Glu Met Glu Phe Glu Pro Phe Gly Asn Leu Asp Gln Pro Asp Leu
65           70           75           80
Tyr Ser Glu Tyr Tyr Pro His Val Tyr Pro Gly Arg Arg Gly Ser Met
      85           90           95
Val Pro Phe Ser Met Arg Ile Leu His Ala Glu Leu Gln Gln Tyr Leu
      100          105          110
Gly Asn Pro Gln Glu Ser Leu Asp Arg Leu His Lys Val Lys Thr Val
      115          120          125
Cys Ser Lys Val Gly Gly Ala Val Ile Leu Pro Cys His Gly Glu Asn
      130          135          140
Met Pro Ser Thr Pro Ser Pro Gln Asp Met Pro Val Leu Phe Pro Ala
145          150          155          160
Arg Pro Ala Pro Cys Thr Ile Ala Ala Ser Ala Phe Arg Arg Leu Gly
      165          170          175
Asp Pro Gly Leu Cys Gly Leu Val Val Val Ala Leu Ala Glu Ile Phe
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Phe Arg Asp Gly Lys Ser Phe
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<210> 3759

<211> 830

<212> DNA

<213> Homo sapiens

<400> 3759

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<212> PRT  
<213> Homo sapiens

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Cys Asp Arg Glu Leu Tyr Pro Gly Glu Pro Arg Leu His Leu Ser Ala  
35 40 45  
Pro Gly Pro Ala Ser His Gln Asp Gln Pro Glu Trp Gln Glu Asp Met  
50 55 60  
Gly Arg Thr Gly Gly Gly Gly Cys Gly His Pro Ser Phe Asn Gln Met  
65 70 75 80  
Leu Asp Val Lys Gly Pro Ile Pro Val Lys Arg Gly Gly Gln Ala Leu  
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Phe Val Leu Leu  
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<210> 3761  
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<212> DNA  
<213> Homo sapiens

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<400> 3763  
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 <211> 288  
 <212> PRT  
 <213> Homo sapiens

<400> 3764

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			20					25					30		
Ser	Pro	Arg	Cys	Ala	Ala	Thr	Met	Ala	Ser	Ser	Asp	Glu	Asp	Gly	Thr
		35				40					45				
Asn	Gly	Gly	Ala	Ser	Glu	Ala	Gly	Glu	Asp	Arg	Glu	Ala	Pro	Gly	Lys
	50				55					60					
Arg	Arg	Arg	Leu	Gly	Phe	Leu	Ala	Thr	Ala	Trp	Leu	Thr	Phe	Tyr	Asp
65					70					75					80
Ile	Ala	Met	Thr	Ala	Gly	Trp	Leu	Val	Leu	Ala	Ile	Ala	Met	Val	Arg
			85						90					95	
Phe	Tyr	Met	Glu	Lys	Gly	Thr	His	Arg	Gly	Leu	Tyr	Lys	Ser	Ile	Gln
			100				105						110		
Lys	Thr	Leu	Lys	Phe	Phe	Gln	Thr	Phe	Ala	Leu	Leu	Glu	Ile	Val	His
		115				120						125			
Cys	Leu	Ile	Gly	Ile	Val	Pro	Thr	Ser	Val	Ile	Val	Thr	Gly	Val	Gln
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Val	Ser	Ser	Arg	Ile	Phe	Met	Val	Trp	Leu	Ile	Thr	His	Ser	Ile	Lys
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Pro	Ile	Gln	Asn	Glu	Glu	Ser	Val	Val	Leu	Phe	Leu	Val	Ala	Trp	Thr
			165						170					175	
Val	Thr	Glu	Ile	Thr	Arg	Tyr	Ser	Phe	Tyr	Thr	Phe	Ser	Leu	Leu	Asp
			180					185					190		
His	Leu	Pro	Tyr	Phe	Ile	Lys	Trp	Ala	Arg	Tyr	Asn	Phe	Phe	Ile	Ile
		195				200					205				
Leu	Tyr	Pro	Val	Gly	Val	Ala	Gly	Glu	Leu	Leu	Thr	Ile	Tyr	Ala	Ala
	210					215					220				
Leu	Pro	Tyr	Val	Lys	Lys	Thr	Gly	Met	Phe	Ser	Ile	Arg	Leu	Pro	Asn
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<210> 3765
<211> 2764
<212> DNA
<213> Homo sapiens
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2764

&lt;210&gt; 3766



&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3766

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          20           25           30
Arg Arg Arg Arg Gly Pro Ile Gly Arg Val Asn Met Asp Leu Glu Asn
 35           40           45
Lys Val Lys Lys Met Gly Leu Gly His Glu Gln Gly Phe Gly Ala Pro
 50           55           60
Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe Glu Leu His Phe Trp
65           70           75           80
Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln Glu Glu His Asp Val
          85           90           95
Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly Lys Leu Phe Glu Asp
          100          105          110
Thr Lys Tyr Thr Thr Leu Ile Ala Lys Leu Lys Ser Asp Gly Ile Pro
          115          120          125
Met Tyr Lys Arg Asn Val Met Ile Leu Thr Asn Pro Val Ala Ala Lys
          130          135          140
Lys Asn Val Ser Ile Asn Thr Val Thr Tyr Glu Trp Ala Pro Pro Val
145          150          155          160
Gln Asn Gln Ala Leu Ala Arg Gln Tyr Met Gln Met Leu Pro Lys Glu
          165          170          175
Lys Gln Pro Val Ala Gly Ser Glu Gly Ala Gln Tyr Arg Lys Lys Gln
          180          185          190
Leu Ala Lys Gln Leu Pro Ala His Asp Gln Asp Pro Ser Lys Cys His
          195          200          205
Glu Leu Ser Pro Arg Glu Val Lys Glu Met Glu Gln Phe Val Lys Lys
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Tyr Lys Ser Glu Ala Leu Gly Val Gly Asp Val Lys Leu Pro Cys Glu
225          230          235          240
Met Asp Ala Gln Gly Pro Lys Gln Met Asn Ile Pro Gly Gly Asp Arg
          245          250          255
Ser Thr Pro Ala Ala Val Gly Ala Met Glu Asp Lys Ser Ala Glu His
          260          265          270
Lys Arg Thr Gln Tyr Ser Cys Tyr Cys Cys Lys Leu Ser Met Lys Glu
          275          280          285
Gly Asp Pro Ala Ile Tyr Ala Glu Arg Ala Gly Tyr Asp Lys Leu Trp
          290          295          300
His Pro Ala Cys Phe Val Cys Ser Thr Cys His Glu Leu Leu Val Asp
305          310          315          320
Met Ile Tyr Phe Trp Lys Asn Glu Lys Leu Tyr Cys Gly Arg His Tyr
          325          330          335
Cys Asp Ser Glu Lys Pro Arg Cys Ala Gly Cys Asp Glu Leu Ile Phe
          340          345          350
Ser Asn Glu Tyr Thr Gln Ala Glu Asn Gln Asn Trp His Leu Lys His
          355          360          365
Phe Cys Cys Phe Asp Cys Asp Ser Ile Leu Ala Gly Glu Ile Tyr Val
          370          375          380
Met Val Asn Asp Lys Pro Val Cys Lys Pro Cys Tyr Val Lys Asn His

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Arg Val Thr Tyr Asn Asn Phe Ser Trp His Ala Ser Thr Glu Cys Phe
              420              425              430
Leu Cys Ser Cys Cys Ser Lys Cys Leu Ile Gly Gln Lys Phe Met Pro
              435              440              445
Val Glu Gly Met Val Phe Cys Ser Val Glu Cys Lys Lys Arg Met Ser
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&lt;210&gt; 3767

&lt;211&gt; 2439

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3767

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1140

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<211> 379

<212> PRT

<213> Homo sapiens

<400> 3768

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			20					25					30			
Ser	Cys	Arg	Asn	Trp	Arg	Ala	Ala	Val	Asp	Leu	Cys	Gly	Arg	Leu	Leu	
		35					40					45				
Thr	Ala	His	Gly	Gln	Gly	Tyr	Gly	Lys	Ser	Gly	Leu	Leu	Thr	Ser	His	
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Thr	Thr	Asp	Ser	Leu	Gln	Leu	Trp	Phe	Val	Arg	Leu	Ala	Leu	Leu	Val	
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Lys	Leu	Gly	Leu	Phe	Gln	Asn	Ala	Glu	Met	Glu	Phe	Glu	Pro	Phe	Gly	
				85					90						95	
Asn	Leu	Asp	Gln	Pro	Asp	Leu	Tyr	Tyr	Glu	Tyr	Tyr	Pro	His	Val	Tyr	
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Pro	Gly	Arg	Arg	Gly	Ser	Met	Val	Pro	Phe	Ser	Met	Arg	Ile	Leu	His	
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Ala	Glu	Leu	Gln	Gln	Tyr	Leu	Gly	Asn	Pro	Gln	Glu	Ser	Leu	Asp	Arg	
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Leu	His	Lys	Val	Lys	Thr	Val	Cys	Ser	Lys	Ile	Leu	Ala	Asn	Leu	Glu	
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Val	Glu	Ala	Tyr	His	Ser	Val	Ile	Lys	Tyr	Tyr	Pro	Glu	Gln	Glu	Pro	
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Gln	Leu	Leu	Ser	Gly	Ile	Gly	Arg	Ile	Ser	Leu	Gln	Ile	Gly	Asp	Ile	
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Lys	Thr	Ala	Glu	Lys	Tyr	Phe	Gln	Asp	Val	Glu	Lys	Val	Thr	Gln	Lys	
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Ala	Val	Cys	Leu	Leu	Tyr	Leu	Gly	Lys	Leu	Lys	Asp	Ser	Leu	Arg	Gln	
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<211> 447

<212> PRT

<213> Homo sapiens

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Ser	Gly	Asp	Ser	Gly	Ser	Asp	Tyr	Leu	Phe	Pro	Glu	Ala	Ser	Glu	Glu
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Ser	Ser	Asp	Thr	Ala	Leu	Pro	Pro	Pro	Val	Pro	Pro	Pro	Lys	Ser	Glu
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Arg	Ser	Ala	Lys	Pro	Leu	Ser	Thr	Ser	Pro	Ser	Ile	Pro	Pro	Arg	Thr
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Val	Lys	Pro	Ala	Arg	Gln	Gln	Thr	Arg	Ser	Pro	Ser	Pro	Thr	Leu	Ser
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&lt;210&gt; 3771

&lt;211&gt; 1514

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3771

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 3772

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Gln	Lys	Arg	Pro	Ser	Glu	Ala	Gln	Ser	Val	Ile	Leu	Arg	Arg	Tyr	Phe
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<211> 678

<212> PRT

<213> Homo sapiens

<400> 3774

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Arg	Tyr	Asp	Asp	Leu	Cys	Leu	Pro	Trp	Ala	Thr	Ala	Gly	Ala	Val	Arg
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Trp	Trp	Thr	Cys	Arg	Gly	Gly	His	Thr	Gln	Gly	Trp	Gln	Ile	Val	Ala
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Gly	Lys	Ser	Thr	Ile	Thr	Val	Ile	Ala	Glu	Asp	Ile	Ser	Gly	Asn	Asn
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Gly	Tyr	Val	Glu	Leu	Ser	Phe	Arg	Ala	Arg	Lys	Leu	Asp	Asp	Lys	Asp
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Leu Asp Tyr Ile Met Gly Gly Cys Gln Ile Ser Phe Thr Val Ala Ile
      420              425              430
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Tyr Ile Ser Pro Arg Gln Pro Asn His Tyr Leu Gln Ala Leu Arg Ala
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Pro Leu Arg Cys Pro Arg Gly Glu Pro Ala Leu Arg Asp Ile Val Gln
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Phe Val Pro Phe Arg Glu Leu Lys Asn Ala Ser Pro Ala Ala Leu Ala
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&lt;211&gt; 549

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3775

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 <212> PRT  
 <213> Homo sapiens

<400> 3778

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&lt;210&gt; 3780

&lt;211&gt; 530

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3780

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His Ser Leu Ser Ser Pro Gln Arg Lys Gln Ser Pro Pro Arg His Arg			
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Ser Pro Met Arg Glu Lys Gly Arg His Asp His Glu Arg Thr Ser Gln			
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Ser His Asp Arg Arg His Glu Gly Arg Glu Asp Thr Arg Gly Lys Arg			
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Asp Arg Glu Lys Asp Ser Arg Glu Glu Arg Glu Tyr Glu Gln Asp Gln			
305	310	315	320
Ser Ser Ser Arg Asp His Arg Asp Asp Arg Glu Pro Arg Asp Gly Arg			
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Asp Arg Arg Asp Ala Arg Asp Thr Arg Asp Arg Arg Glu Leu Arg Asp			
340	345	350	
Ser Arg Asp Met Arg Asp Ser Arg Glu Met Arg Asp Tyr Ser Arg Asp			
355	360	365	
Thr Lys Glu Ser Arg Asp Pro Arg Asp Ser Arg Ser Thr Arg Asp Ala			
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His Asp Tyr Arg Asp Arg Glu Gly Arg Asp Thr His Arg Lys Glu Asp			
385	390	395	400
Thr Tyr Pro Glu Glu Ser Arg Ser Tyr Gly Arg Asn His Leu Arg Glu			
405	410	415	
Glu Ser Ser Arg Thr Glu Ile Arg Asn Glu Ser Arg Asn Glu Ser Arg			
420	425	430	
Ser Glu Ile Arg Asn Asp Arg Met Gly Arg Ser Arg Gly Arg Val Pro			

435                      440                      445  
 Glu Leu Pro Glu Lys Gly Ser Arg Gly Ser Arg Gly Ser Gln Ile Asp  
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 Ser His Ser Ser Asn Ser Asn Tyr His Asp Ser Trp Glu Thr Arg Ser  
 465                      470                      475                      480  
 Ser Tyr Pro Glu Arg Asp Arg Tyr Pro Glu Arg Asp Asn Arg Asp Gln  
 485                      490                      495  
 Ala Arg Asp Ser Ser Phe Glu Arg Arg His Gly Glu Arg Asp Arg Arg  
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 Lys Glu  
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&lt;210&gt; 3781

&lt;211&gt; 1364

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3781

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 1364

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 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 3782  
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 Asp Leu Gln Asp Ser Ser Glu Leu His Pro Glu Phe Ala Lys Cys His  
 35 40 45  
 Val Pro Trp Thr Pro Arg Phe Ala Tyr Gly Val Phe Tyr Ala Asp Pro  
 50 55 60  
 Cys Thr Gly Gly Asp Ser Tyr His Pro His Glu Gln Ser Ser Pro Pro  
 65 70 75 80  
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<210> 3783  
 <211> 4137  
 <212> DNA  
 <213> Homo sapiens

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2040



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<210> 3784

<211> 804

<212> PRT

<213> Homo sapiens

<400> 3784

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Ile	Gln	Arg	Phe	Glu	Ser	Val	His	Pro	Asn	Ile	Tyr	Ser	Ile	Tyr	Glu
		20						25					30		
Leu	Leu	Glu	Arg	Val	Glu	Glu	Pro	Val	Leu	Gln	Asn	Gln	Ile	Arg	Glu
		35					40					45			
His	Val	Ile	Ala	Ile	Glu	Asp	Ala	Phe	Val	Asn	Ser	Gln	Glu	Trp	Thr
	50				55				60						
Leu	Ser	Arg	Ser	Val	Pro	Glu	Leu	Lys	Val	Gly	Ile	Val	Gly	Asn	Leu
65				70					75					80	
Ala	Ser	Gly	Lys	Ser	Ala	Leu	Val	His	Arg	Tyr	Leu	Thr	Gly	Thr	Tyr
			85					90					95		
Val	Gln	Glu	Glu	Ser	Pro	Glu	Gly	Gly	Arg	Phe	Lys	Lys	Glu	Ile	Val
		100					105						110		
Val	Asp	Gly	Gln	Ser	Tyr	Leu	Leu	Leu	Ile	Arg	Asp	Glu	Gly	Gly	Pro
	115					120					125				
Pro	Glu	Ala	Gln	Phe	Ala	Met	Trp	Val	Asp	Ala	Val	Ile	Phe	Val	Phe
	130					135					140				
Ser	Leu	Glu	Asp	Glu	Ile	Ser	Phe	Gln	Thr	Val	Tyr	His	Tyr	Tyr	Ser
145					150					155				160	
Arg	Met	Ala	Asn	Tyr	Arg	Asn	Thr	Ser	Glu	Ile	Pro	Leu	Val	Leu	Val
			165					170						175	
Gly	Thr	Gln	Asp	Ala	Ile	Ser	Ser	Ala	Asn	Pro	Arg	Val	Ile	Asp	Asp
		180						185					190		
Ala	Arg	Ala	Arg	Lys	Leu	Ser	Asn	Asp	Leu	Lys	Arg	Cys	Thr	Tyr	Tyr
	195					200					205				
Glu	Thr	Cys	Ala	Thr	Tyr	Gly	Leu	Asn	Val	Glu	Arg	Val	Phe	Gln	Asp
	210					215						220			
Val	Ala	Gln	Lys	Ile	Val	Ala	Thr	Arg	Lys	Lys	Gln	Gln	Leu	Ser	Ile
225					230					235				240	
Gly	Pro	Cys	Lys	Ser	Leu	Pro	Asn	Ser	Pro	Ser	His	Ser	Ser	Val	Cys

2931

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Asp Glu Asp Leu Arg Thr Ala Ile Leu Leu Leu Ala His Gly Ser Arg
   690              695              700
Asp Glu Val Asn Glu Thr Cys Gly Glu Gly Asp Gly Arg Thr Ala Leu
705              710              715              720
His Leu Ala Cys Arg Lys Gly Asn Val Val Leu Ala Gln Leu Leu Ile
              725              730              735
Trp Tyr Gly Val Asp Val Thr Ala Arg Asp Ala His Gly Asn Thr Ala
              740              745              750
Leu Ala Tyr Ala Arg Gln Ala Ser Ser Gln Glu Cys Ile Asp Val Leu
              755              760              765
Leu Gln Tyr Gly Cys Pro Asp Glu Arg Phe Val Leu Met Ala Thr Pro
              770              775              780
Asn Leu Ser Arg Arg Asn Asn Asn Arg Asn Asn Ser Ser Gly Arg Val
785              790              795              800
Pro Thr Ile Ile

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&lt;210&gt; 3785

&lt;211&gt; 1901

<212> DNA<sup>1</sup>

&lt;213&gt; Homo sapiens

&lt;400&gt; 3785

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&lt;210&gt; 3786

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3786

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Val	Trp	Glu	Gly	Gln	Leu	Gln	Ser	Leu	Val	Leu	Ser	Glu	Tyr	Ala	Ser
			20					25					30		
Thr	Glu	Met	Ser	Leu	His	Ala	Leu	Tyr	Met	His	Gln	Leu	His	Lys	Gln
		35					40					45			
Gln	Ala	Gln	Ala	Glu	Pro	Glu	Arg	His	Val	Trp	His	Arg	Arg	Glu	Ser
		50				55				60					
Asp	Glu	Ser	Gly	Glu	Ser	Ala	Pro	Asp	Glu	Gly	Gly	Glu	Gly	Ala	Arg
65					70				75					80	
Ala	Pro	Gln	Ser	Ile	Pro	Arg	Ser	Ala	Ser	Tyr	Pro	Cys	Ala	Ala	Pro
				85				90					95		
Arg	Pro	Gly	Ala	Pro	Glu	Thr	Thr	Ala	Leu	His	Gly	Gly	Phe	Gln	Arg

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Arg Tyr Gly Gly Ile Thr Asp Pro Gly Thr Val Pro Arg Val Pro Ser
          115          120          125
His Phe Ser Arg Leu Pro Leu Gly Gly Trp Ala Glu Asp Gly Gln Ser
          130          135          140
Ala Ser Arg His Pro Glu Pro Val Pro Glu Glu Gly Ser Glu Asp Glu
145          150          155          160
Leu Pro Pro Gln Val His Lys Val
          165

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&lt;210&gt; 3787

&lt;211&gt; 717

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3787

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717

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&lt;210&gt; 3788

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3788

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Cys Ala Ser Ile Lys Leu Arg His Gly Ser Arg Ala Ala Pro Pro Gly
          20          25          30
Pro Trp Gly Ala Lys Cys Ser Trp Arg Gln Val Ala Lys Gly Glu His
          35          40          45
Leu Gly Gln Thr Pro Gly Phe Ser Ser Arg Leu Pro His Leu Pro Ala

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50		55		60	
Ser	Leu	Leu	Ser	Trp	Leu
65		70		75	
Ala	Ala	Val	Ile	Thr	His
		85		90	
Ala	Val	Leu	Val	His	Met
		100		105	
Leu					

&lt;210&gt; 3789

&lt;211&gt; 4341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3789

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 <212> PRT  
 <213> Homo sapiens

<400> 3790  
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 Leu Gln Val Leu Lys Ala Gln Ser Glu Asp Pro Leu Pro Glu Leu His  
 35 40 45  
 Glu Asp Leu His Asn Glu Lys Glu Leu Ile Lys Glu Leu Glu Gln Ser  
 50 55 60  
 Leu Ala Ser Trp Thr Gln Asn Leu Lys Glu Leu Gln Thr Met Lys Ala  
 65 70 75 80  
 Asp Leu Thr Arg His Val Leu Val Glu Asp Val Met Val Leu Lys Glu  
 85 90 95  
 Gln Ile Glu His Leu His Arg Gln Trp Glu Asp Leu Cys Leu Arg Val  
 100 105 110  
 Ala Ile Arg Lys Gln Glu Ile Glu Asp Arg Leu Asn Thr Trp Val Val  
 115 120 125  
 Phe Asn Glu Lys Asn Lys Glu Leu Cys Ala Trp Leu Val Gln Met Glu  
 130 135 140  
 Asn Lys Val Leu Gln Thr Val Asp Ile Ser Ile Glu Glu Met Ile Glu  
 145 150 155 160  
 Lys Leu Gln Lys Asp Cys Met Glu Glu Ile Asn Leu Phe Ser Glu Asn  
 165 170 175  
 Lys Leu Gln Leu Lys Gln Met Gly Asp Gln Leu Ile Lys Ala Ser Asn  
 180 185 190  
 Lys Ser Arg Ala Ala Glu Ile Asp Asp Lys Leu Asn Lys Ile Asn Asp  
 195 200 205  
 Arg Trp Gln His Leu Phe Asp Val Ile Gly Ser Arg Val Lys Lys Leu  
 210 215 220  
 Lys Glu Thr Phe Ala Phe Ile Gln Gln Leu Asp Lys Asn Met Ser Asn  
 225 230 235 240  
 Leu Arg Thr Trp Leu Ala Arg Ile Glu Ser Glu Leu Ser Lys Pro Val  
 245 250 255  
 Val Tyr Asp Val Cys Asp Asp Gln Glu Ile Gln Lys Arg Leu Ala Glu  
 260 265 270  
 Gln Gln Asp Leu Gln Arg Asp Ile Glu Gln His Ser Ala Gly Val Glu  
 275 280 285  
 Ser Val Phe Asn Ile Cys Asp Val Leu Leu His Asp Ser Asp Ala Cys  
 290 295 300  
 Ala Asn Glu Thr Glu Cys Asp Ser Ile Gln Gln Thr Thr Arg Ser Leu  
 305 310 315 320  
 Asp Arg Arg Trp Arg Asn Ile Cys Ala Met Ser Met Glu Arg Arg Met  
 325 330 335  
 Lys Ile Glu Glu Thr Trp Arg Leu Trp Gln Lys Phe Leu Asp Asp Tyr  
 340 345 350  
 Ser Arg Phe Glu Asp Trp Leu Lys Ser Ala Glu Arg Thr Ala Ala Cys  
 355 360 365  
 Pro Asn Ser Ser Glu Val Leu Tyr Thr Ser Ala Lys Glu Glu Leu Lys

370		375		380
Arg Phe Glu Ala Phe Gln Arg Gln Ile His Glu Arg Leu Thr Gln Leu				
385		390		395
Glu Leu Ile Asn Lys Gln Tyr Arg Arg Leu Ala Arg Glu Asn Arg Thr				400
	405		410	415
Asp Thr Ala Ser Arg Leu Lys Gln Met Val His Glu Gly Asn Gln Arg				
	420		425	430
Trp Asp Asn Leu Gln Arg Arg Val Thr Ala Val Leu Arg Arg Leu Arg				
	435		440	445
His Phe Thr Asn Gln Arg Glu Phe Glu Gly Thr Arg Glu Ser Ile				
	450		455	460
Leu Val Trp Leu Thr Glu Met Asp Leu Gln Leu Thr Asn Val Glu His				
	465		470	475
Phe Ser Glu Ser Asp Ala Asp Asp Lys Met Arg Gln Leu Asn Gly Phe				
	485		490	495
Gln Gln Glu Ile Thr Leu Asn Thr Asn Lys Ile Asp Gln Leu Ile Val				
	500		505	510
Phe Gly Glu Gln Leu Ile Gln Lys Ser Glu Pro Leu Asp Ala Val Leu				
	515		520	525
Ile Glu Asp Glu Leu Glu Glu Leu His Arg Tyr Cys Gln Glu Val Phe				
	530		535	540
Gly Arg Val Ser Arg Phe His Arg Arg Leu Thr Ser Cys Thr Pro Gly				
	545		550	555
Leu Glu Asp Glu Lys Glu Ala Ser Glu Asn Glu Thr Asp Met Glu Asp				
	565		570	575
Pro Arg Glu Ile Gln Thr Asp Ser Trp Arg Lys Arg Gly Glu Ser Glu				
	580		585	590
Glu Pro Ser Ser Pro Gln Ser Leu Cys His Leu Val Ala Pro Gly His				
	595		600	605
Glu Arg Ser Gly Cys Glu Thr Pro Val Ser Val Asp Ser Ile Pro Leu				
	610		615	620
Glu Trp Asp His Thr Gly Asp Val Gly Gly Ser Ser Ser His Glu Glu				
	625		630	635
Asp Glu Glu Gly Pro Tyr Tyr Ser Ala Leu Ser Gly Lys Ser Ile Ser				
	645		650	655
Asp Gly His Ser Trp His Val Pro Asp Ser Pro Ser Cys Pro Glu His				
	660		665	670
His Tyr Lys Gln Met Glu Gly Asp Arg Asn Val Pro Pro Val Pro Pro				
	675		680	685
Ala Ser Ser Thr Pro Tyr Lys Pro Pro Tyr Gly Lys Leu Leu Leu Pro				
	690		695	700
Pro Gly Thr Asp Gly Gly Lys Glu Gly Pro Arg Val Leu Asn Gly Asn				
	705		710	715
Pro Gln Gln Glu Asp Gly Gly Leu Ala Gly Ile Thr Glu Gln Gln Ser				
	725		730	735
Gly Ala Phe Asp Arg Trp Glu Met Ile Gln Ala Gln Glu Leu His Asn				
	740		745	750
Lys Leu Lys Ile Lys Gln Asn Leu Gln Gln Leu Asn Ser Asp Ile Ser				
	755		760	765
Ala Ile Thr Thr Trp Leu Lys Lys Thr Glu Ala Glu Leu Glu Met Leu				
	770		775	780
Lys Met Ala Lys Pro Pro Ser Asp Ile Gln Glu Ile Glu Leu Arg Val				
	785		790	795
Lys Arg Leu Gln Glu Ile Leu Lys Ala Phe Asp Thr Tyr Lys Ala Leu				800

805 810 815  
 Val Val Ser Val Asn Val Ser Ser Lys Glu Phe Leu Gln Thr Glu Ser  
 820 825 830  
 Pro Glu Ser Thr Glu Leu Gln Ser Arg Leu Arg Gln Leu Ser Leu Leu  
 835 840 845  
 Trp Glu Ala Ala Gln Gly Ala Val Asp Ser Trp Arg Gly Gly Leu Arg  
 850 855 860  
 Gln Ser Leu Met Gln Cys Gln Asp Phe His Gln Leu Ser Gln Asn Leu  
 865 870 875 880  
 Leu Leu Trp Leu Ala Ser Ala Lys Asn Arg Arg Gln Lys Ala His Val  
 885 890 895  
 Thr Asp Pro Lys Ala Asp Pro Arg Ala Leu Leu Glu Cys Arg Arg Glu  
 900 905 910  
 Leu Met Gln Leu Glu Lys Glu Leu Val Glu Arg Gln Pro Gln Val Asp  
 915 920 925  
 Met Leu Gln Glu Ile Ser Asn Ser Leu Leu Ile Lys Gly His Gly Glu  
 930 935 940  
 Asp Cys Ile Glu Ala Glu Glu Lys Val His Val Ile Glu Lys Lys Leu  
 945 950 955 960  
 Lys Gln Leu Arg Glu Gln Val Ser Gln Asp Leu Met Ala Leu Gln Gly  
 965 970 975  
 Thr Gln Asn Pro Ala Ser Pro Leu Pro Ser Phe Asp Glu Val Asp Ser  
 980 985 990  
 Gly Asp Gln Pro Pro Ala Thr Ser Val Pro Ala Pro Arg Ala Lys Gln  
 995 1000 1005  
 Phe Arg Ala Val Arg Thr Thr Glu Gly Glu Glu Glu Thr Glu Ser Arg  
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 Val Pro Gly Ser Thr Arg Pro Gln Arg Ser Phe Leu Ser Arg Val Val  
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 Arg Ala Ala Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Leu  
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 Ala Cys Leu Leu Pro Ser Ser Glu Glu Asp Tyr Ser Cys Thr Gln Ala  
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 Pro Pro Pro Thr  
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&lt;210&gt; 3791

&lt;211&gt; 1011

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3791

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&lt;210&gt; 3792

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3792

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Ala	Leu	Ser	Met	Gly	Gly	Lys	Val	Pro	Val	Ser	Glu	Gly	Leu	Glu	His
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Ser	Asp	Leu	Pro	Asp	Gly	Thr	Gly	Glu	Phe	Leu	Asp	Ala	Trp	Leu	Met
		50				55					60				
Leu	Val	Glu	Lys	Met	Val	Asn	Pro	Thr	Thr	Val	Leu	Glu	Ser	Pro	His
					70					75				80	
Ser	Leu	Pro	Ala	Lys	Leu	Pro	Gly	Gly	Val	Gln	Asn	Phe	Pro	Gln	Phe
				85				90						95	
Ser	Ala	Leu	Arg	Phe	Leu	Val	Val	Thr	Gln	Lys	Ala	Ala	Phe	Thr	Cys
			100					105						110	
Ile	Lys	Asn	Leu	Trp	Asn	Arg	Lys	Pro	Leu	Lys	Val	Tyr	Gly	Gly	Arg
		115					120						125		
Met	Ala	Glu	Ser	Met	Leu	Ala	Ile	Leu	Cys	His	Ile	Leu	Arg	Gly	Glu
		130				135					140				
Pro	Val	Ile	Arg	Glu	Arg	Leu	Ser	Lys	Glu	Lys	Glu	Gly	Ser	Arg	Gly
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Glu	Glu	Asp	Thr	Gly	Gln	Glu	Glu	Gly	Gly	Ser	Arg	Arg	Glu	Pro	Gln
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Val	Asn	Gln	Gln	Gln	Leu	Gln	Gln	Leu	Met	Asp	Met	Gly	Phe	Thr	Arg



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3795

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&lt;210&gt; 3796

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3796

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Val Asp Arg Glu Arg Phe Cys Arg Trp Ala Gly Leu Pro Arg Gln Gly
          50           55           60
Phe Pro Ile Ile Phe His Gly Val Met Gly Lys Asp Glu Arg Glu Gly
          65           70           75           80
Asn Ser Pro Ser Phe Phe Asn Pro Glu Glu Ala Ala Thr Val Thr Ser
          85           90           95
Tyr Leu Lys Leu Leu Leu Ala Pro Ser Ser Lys Lys Gly Lys Ala Arg
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Leu Ser Pro Arg Ser Val Gly Val Ile Ser Pro Tyr Arg Lys Gln Val
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Glu Lys Ile Arg Tyr Cys Ile Thr Lys Leu Asp Arg Glu Leu Arg Gly
          130          135          140
Leu Asp Asp Ile Lys Asp Leu Lys Val Gly Ser Val Glu Glu Phe Gln
          145          150          155          160
Gly Gln Glu Arg Ser Val Ile Leu Ile Ser Thr Val Arg Ser Ser Gln
          165          170          175
Ser Phe Val Gln Leu Asp Leu Asp Phe Asn Leu Gly Phe Leu Lys Asn
          180          185          190
Pro Lys Arg Phe Asn Val Ala Val Thr Arg Ala Lys Ala Leu Leu Ile
          195          200          205
Ile Val Gly Asn Pro Leu Leu Leu Gly His Asp Pro Asp Trp Lys Val
          210          215          220
Phe Leu Glu Phe Cys Lys Glu Asn Gly Gly Tyr Thr Gly Cys Pro Phe
          225          230          235          240
Pro Ala Lys Leu Asp Leu Gln Gln Gly Gln Asn Leu Leu Gln Gly Leu
          245          250          255
Ser Lys Leu Ser Pro Ser Thr Ser Gly Pro His Ser His Asp Tyr Leu
          260          265          270
Pro Gln Glu Arg Glu Gly Glu Gly Gly Leu Ser Leu Gln Val Glu Pro
          275          280          285
Glu Trp Arg Asn Glu Leu
          290

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&lt;210&gt; 3797

&lt;211&gt; 1970

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3797

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<210> 3798

<211> 473

<212> PRT

<213> Homo sapiens

<400> 3798

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		20						25					30		
His	Trp	Trp	Ser	Glu	Arg	Thr	His	Lys	Asn	Leu	Ser	Asp	Met	Glu	Asn
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Glu	Phe	Tyr	Tyr	Arg	Tyr	Pro	Ser	Phe	Gln	Asp	Val	His	Val	Met	Val
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Phe	Val	Gly	Phe	Gly	Phe	Leu	Met	Thr	Phe	Leu	Gln	Arg	Tyr	Gly	Phe
65					70					75				80	
Ser	Ala	Val	Gly	Phe	Asn	Phe	Leu	Leu	Ala	Ala	Phe	Gly	Ile	Gln	Trp
			85						90					95	
Ala	Leu	Leu	Met	Gln	Gly	Trp	Phe	His	Phe	Leu	Gln	Asp	Arg	Tyr	Ile
			100					105					110		
Val	Val	Gly	Val	Glu	Asn	Leu	Ile	Asn	Ala	Asp	Phe	Cys	Val	Ala	Ser
		115					120					125			
Val	Cys	Val	Ala	Phe	Gly	Ala	Val	Leu	Gly	Lys	Val	Ser	Pro	Ile	Gln
		130				135					140				
Leu	Leu	Ile	Met	Thr	Phe	Phe	Gln	Val	Thr	Leu	Phe	Ala	Val	Asn	Glu
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Phe	Ile	Leu	Leu	Asn	Leu	Leu	Lys	Val	Lys	Asp	Ala	Gly	Gly	Ser	Met
			165						170					175	
Thr	Ile	His	Thr	Phe	Gly	Ala	Tyr	Phe	Gly	Leu	Thr	Val	Thr	Arg	Ile
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Leu	Tyr	Arg	Arg	Asn	Leu	Glu	Gln	Ser	Lys	Glu	Arg	Gln	Asn	Ser	Val
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Tyr	Gln	Ser	Asp	Leu	Phe	Ala	Met	Ile	Gly	Thr	Leu	Phe	Leu	Trp	Met
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His	Arg	Ala	Ala	Ile	Asn	Thr	Tyr	Cys	Ser	Leu	Ala	Ala	Cys	Val	Leu
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Thr	Ser	Val	Ala	Ile	Ser	Ser	Ala	Leu	His	Lys	Lys	Gly	Lys	Leu	Asp
		260						265					270		
Met	Val	His	Ile	Gln	Asn	Ala	Thr	Leu	Ala	Gly	Gly	Val	Ala	Val	Gly
		275					280					285			
Thr	Ala	Ala	Glu	Met	Met	Leu	Met	Pro	Tyr	Gly	Ala	Leu	Ile	Ile	Gly
		290				295					300				
Phe	Val	Cys	Gly	Ile	Ile	Ser	Thr	Leu	Gly	Phe	Val	Tyr	Leu	Thr	Pro
305					310					315				320	
Phe	Leu	Glu	Ser	Arg	Leu	His	Ile	Gln	Asp	Thr	Cys	Gly	Ile	Asn	Asn

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          325          330          335
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Gly Lys Phe Gln Ile Tyr Gly Leu Leu Val Thr Leu Ala Met Ala Leu
385          390          395          400
Met Gly Gly Ile Ile Val Gly Leu Ile Leu Arg Leu Pro Phe Trp Gly
          405          410          415
Gln Pro Ser Asp Glu Asn Cys Phe Glu Asp Ala Val Tyr Trp Glu Met
          420          425          430
Pro Glu Gly Asn Ser Thr Val Tyr Ile Pro Glu Asp Pro Thr Phe Lys
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Pro Ser Gly Pro Ser Val Pro Ser Val Pro Met Val Ser Pro Leu Pro
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Met Ala Ser Ser Val Pro Leu Val Pro
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<210> 3799  
 <211> 210  
 <212> DNA  
 <213> Homo sapiens

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120
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210

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<210> 3800  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

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<400> 3800
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Ile Thr Glu Arg Ser Lys Gln Lys Ala Arg Arg Arg Thr Arg Ser Ser
20     25     30
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
35     40     45
Ser Ser Ser Ser Ser Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr
50     55     60
Lys Asp Lys Arg Arg Lys
65      70

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<210> 3801  
 <211> 4070

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3801

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gctgggcccgc gggcagcgtc gcctcacgcg gagcagagct gagctgaagc gggacccgga  
120  
gcccagcag cgcgcccat ggcaatcaaa tttctggaag tcatcaagcc cttctgtgtc  
180  
atcctgcccg aaattcagaa gccagagagg aagattcagt ttaaggagaa agtgctgtgg  
240  
accgctatca ccctctttat cttcttagtg tgctgccaga ttccctgtt tgggatcatg  
300  
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&lt;210&gt; 3802

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3802

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			20					25					30		
Leu	Trp	Thr	Ala	Ile	Thr	Leu	Phe	Ile	Phe	Leu	Val	Cys	Cys	Gln	Ile
		35					40					45			
Pro	Leu	Phe	Gly	Ile	Met	Ser	Ser	Asp	Ser	Ala	Asp	Pro	Phe	Tyr	Trp
	50					55					60				
Met	Arg	Val	Ile	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Leu	Met	Glu	Leu	Gly
65				70						75				80	
Ile	Ser	Pro	Ile	Val	Thr	Ser	Gly	Leu	Ile	Met	Gln	Leu	Leu	Ala	Gly
				85					90					95	
Ala	Lys	Ile	Ile	Glu	Val	Gly	Asp	Thr	Pro	Lys	Asp	Arg	Ala	Leu	Phe
				100					105					110	
Asn	Gly	Ala	Gln	Lys	Leu	Phe	Gly	Met	Ile	Ile	Thr	Ile	Gly	Gln	Ser

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145              150              155              160
Ile Val Leu Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly
      165              170              175
Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val
      180              185              190
Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr Gly Arg Gly Thr Glu
      195              200              205
Phe Glu Gly Ala Val Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr
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Asp Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
225              230              235              240
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Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr
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Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile
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305              310              315              320
Leu Gly Gln Trp Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr
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Pro Val Gly Gly Leu Cys Tyr Tyr Leu Ser Pro Pro Glu Ser Phe Gly
      340              345              350
Ser Val Leu Glu Asp Pro Val His Ala Val Val Tyr Ile Val Phe Met
      355              360              365
Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
      370              375              380
Ser Ser Ala Lys Asp Val Ala Lys Gln Leu Lys Glu Gln Gln Met Val
385              390              395              400
Met Arg Gly His Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr
      405              410              415
Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser
      420              425              430
Val Leu Ala Asp Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu
      435              440              445
Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu
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Gln Ser Glu Val Gly Ser Met Gly Ala Leu Leu Phe
465              470              475

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&lt;210&gt; 3803

&lt;211&gt; 345

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3803

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<210> 3804  
 <211> 115  
 <212> PRT  
 <213> Homo sapiens

<400> 3804  
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 Glu Leu Arg Lys Ser Gly Glu Ala Lys Tyr Ala His Leu Ser Asp Glu  
 35 40 45  
 Leu His Val Leu Ile Glu Val Phe Ala Pro Pro Gly Glu Ala Tyr Ser  
 50 55 60  
 Arg Met Ser His Ala Leu Glu Glu Ile Lys Lys Phe Leu Val Pro Asp  
 65 70 75 80  
 Tyr Asn Asp Glu Ile Arg Gln Glu Gln Leu Arg Glu Leu Ser Tyr Leu  
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 Ile Arg Ile  
 115

<210> 3805  
 <211> 1923  
 <212> DNA  
 <213> Homo sapiens

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1923

&lt;210&gt; 3806

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 <213> Homo sapiens

<400> 3806

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Pro Leu Arg Phe Trp Leu Val Ile Asn Gln Glu Gly Asn Met Val Thr
      35           40           45
Ala Arg Gln Glu Pro Arg Leu Val Leu Ile Ser Leu Thr Cys Asp Gly
      50           55           60
Asp Thr Leu Thr Leu Ser Ala Ala Tyr Thr Lys Asp Leu Leu Leu Pro
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Ile Lys Thr Pro Thr Thr Asn Ala Val His Lys Cys Arg Val His Gly
      85           90           95
Leu Glu Ile Glu Gly Arg Asp Cys Gly Glu Ala Ala Ala Gln Trp Ile
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Thr Ser Phe Leu Lys Ser Gln Pro Tyr Arg Leu Val His Phe Glu Pro
      115          120          125
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      130          135          140
Lys Asp Gln Ile Ala Tyr Ser Asp Thr Ser Pro Phe Leu Ile Leu Ser
      145          150          155          160
Glu Ala Ser Leu Ala Asp Leu Asn Ser Arg Leu Glu Lys Lys Val Lys
      165          170          175
Ala Thr Asn Phe Arg Pro Asn Ile Val Ile Ser Gly Cys Asp Val Tyr
      180          185          190
Ala Glu Asp Ser Trp Asp Glu Leu Ile Gly Asp Val Glu Leu Lys
      195          200          205
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      225          230          235          240
Arg Gln Cys Asp Pro Ser Glu Arg Lys Leu Tyr Gly Lys Ser Pro Leu
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<400> 3807

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 35 40 45  
 Ser Tyr His Pro Ala Pro Ser Gly Arg Gly Ser Ala Pro Ser Pro Arg  
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 Ser Ala Pro Gly Trp Leu Arg Pro Phe Trp Ala Phe Ser Phe Trp Pro  
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 <213> Homo sapiens

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 <213> Homo sapiens

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 35 40 45  
 Arg Gly Thr Arg Thr Arg Pro Ser Thr Ser Ser Pro Trp Ser Leu Ala  
 50 55 60  
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<210> 3811  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

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 35 40 45  
 Thr Trp Gly Ala Cys Trp Gln His Cys Leu Asp Ser Arg Ala Ser Leu  
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&lt;210&gt; 3814

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3814

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			20					25					30		
Val	Gly	Leu	Trp	Ile	Leu	Asn	Met	Asp	Ser	Leu	Ser	Ala	Arg	Arg	Thr
		35					40					45			
Leu	His	Thr	Phe	Asp	Leu	Leu	Gly	Phe	Gly	Arg	Ser	Ser	Arg	Pro	Ala
	50					55				60					
Phe	Pro	Arg	Asp	Pro	Glu	Gly	Ala	Glu	Asp	Glu	Phe	Val	Thr	Ser	Ile
65					70				75					80	
Glu	Thr	Trp	Arg	Glu	Thr	Met	Gly	Ile	Pro	Ser	Met	Ile	Leu	Leu	Gly
			85					90					95		
His	Ser	Leu	Gly	Gly	Phe	Leu	Ala	Thr	Ser	Tyr	Ser	Ile	Lys	Tyr	Pro
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Asp	Arg	Val	Lys	His	Leu	Ile	Leu	Val	Asp	Pro	Trp	Gly	Phe	Pro	Leu
		115					120					125			
Arg	Pro	Thr	Asn	Pro	Ser	Glu	Ile	Arg	Ala	Pro	Pro	Ala	Trp	Val	Lys
	130					135					140				
Ala	Val	Ala	Ser	Val	Leu	Gly	Arg	Ser	Asn	Pro	Leu	Ala	Val	Leu	Arg
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<210> 3815
<211> 3669
<212> DNA
<213> Homo sapiens
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2959

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&lt;210&gt; 3816

&lt;211&gt; 707

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3816

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Lys	Tyr	Asp	Pro	Thr	Phe	Lys	Gly	Pro	Ile	Tyr	Asn	Arg	Gly	Cys	Thr
			20					25					30		
Asp	Ile	Ile	Cys	Cys	Val	Phe	Leu	Leu	Ala	Ile	Val	Gly	Tyr	Val	
		35					40				45				
Ala	Val	Gly	Ile	Ile	Ala	Trp	Thr	His	Gly	Asp	Pro	Arg	Lys	Val	Ile

2962

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Arg Ala Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile
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Leu Ala Ile Val Gln Ile Ile Arg Val Ile Leu Glu Tyr Leu Asp Gln
      515              520              525
Arg Leu Lys Ala Ala Glu Asn Lys Phe Ala Lys Cys Leu Met Thr Cys
      530              535              540
Leu Lys Cys Cys Phe Trp Cys Leu Glu Lys Phe Ile Lys Phe Leu Asn
545              550              555              560
Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Thr Asn Phe Cys Thr
      565              570              575
Ser Ala Arg Asn Ala Phe Phe Leu Leu Met Arg Asn Ile Ile Arg Val
      580              585              590
Ala Val Leu Asp Lys Val Thr Asp Phe Leu Phe Leu Leu Gly Lys Leu
      595              600              605
Leu Ile Val Gly Ser Val Gly Ile Leu Ala Phe Phe Phe Phe Thr His
      610              615              620
Arg Ile Arg Ile Val Gln Asp Thr Ala Pro Pro Leu Asn Tyr Tyr Trp
625              630              635              640
Val Pro Ile Leu Thr Val Ile Val Gly Ser Tyr Leu Ile Ala His Gly
      645              650              655
Phe Phe Ser Val Tyr Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe
      660              665              670
Leu Glu Asp Leu Glu Arg Asn Asp Gly Ser Ala Glu Arg Pro Tyr Phe
      675              680              685
Met Ser Ser Thr Leu Lys Lys Leu Leu Asn Lys Thr Asn Lys Lys Ala
      690              695              700
Ala Glu Ser
705

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<210> 3817  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

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<210> 3818  
 <211> 139  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3818

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      20             25             30
Arg Glu Ile Asn Pro Leu Leu Phe Ser Tyr Val Glu Glu Leu Val Glu
      35             40             45
Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
      50             55             60
Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Asp Leu Leu
      65             70             75             80
Asp Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His Thr
      85             90             95
Leu Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys
      100            105            110
Gly Phe Val Cys Glu Leu Cys Arg Glu Gly Asp Val Leu Phe Pro Phe
      115            120            125
Asp Ser His Thr Ser Val Cys Ala Asp Cys Phe
      130            135

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&lt;210&gt; 3819

&lt;211&gt; 1731

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3819

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<212> PRT

<213> Homo sapiens

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&lt;210&gt; 3830

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3830

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			20				25					30			
Val	Glu	Ser	Val	Tyr	Thr	Thr	Phe	Arg	Asp	Arg	Glu	Ile	Met	Phe	His

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 Arg Lys Arg His Ile Gly Asn Asp Ile Val Ala Ile Ile Phe Gln Glu  
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 Ala Tyr Ile Val Val Gln Val Glu Thr Pro Gly Thr Glu Thr Pro Ser  
 100 105 110  
 Tyr Lys Val Ser Val Thr Ala Arg Glu Asp Val Pro Thr Phe Gly Pro  
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 Asp Lys Phe Ala Lys Leu Glu Asp Arg Thr Arg Ala Ala Leu Leu Asp  
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 Asn Leu His Asp Glu Leu His Ala His Thr Gln Ala Met Leu Gly Leu  
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 Gly Pro Glu Glu Asp Lys Phe Glu Asn Gly Gly His Gly Gly Phe Leu  
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 Glu Ser Phe Lys Arg Ala Ile Arg Val Arg Ser His Ser Met Glu Thr  
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 Met Val Gly Gly Gln Lys Lys Ser His Ser Gly Gly Ile Pro Gly Ser  
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 Leu Ser Gly Gly Ile Ser His Asn Ser Met Glu Val Thr Lys Thr Thr  
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 Phe Ser Pro Pro Val Val Ala Ala Thr Val Lys Asn Gln Ser Arg Ser  
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 Pro Ile Lys Arg Arg Ser Gly Leu Phe Pro Arg Leu His Thr Gly Ser  
 275 280 285  
 Glu Gly Gln Gly Asp Ser Arg Ala Arg Cys Asp Ser Thr Ser Ser Thr  
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 Pro Lys Thr Pro Asp Gly Gly His Ser Ser Gln Glu Ile Lys Ser Glu  
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 Thr Ser Ser Asn Pro Ser Ser Pro Glu Ile Cys Pro Asn Lys Glu Lys  
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 Pro Phe Met Lys Leu Lys Glu Asn Gly Arg Ala Ile Ser Arg Ser Ser  
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 Lys Gln Glu Val Phe Val Tyr Ser Pro Ser Pro Ser Ser Glu Ser Pro  
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 Ser Leu Gly Ala Ala Ala Thr Pro Ile Ile Met Ser Arg Ser Pro Thr  
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 Asp Ala Lys Ser Arg Asn Ser Pro Arg Ser Asn Leu Lys Phe Arg Phe  
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&lt;210&gt; 3831

&lt;211&gt; 726



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3831

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gctcag
726

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&lt;210&gt; 3832

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3832

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Phe Ser Pro Glu Thr Asp Pro Leu Xaa Val Ser Gln Ile Pro Ala Ser
20     25     30
Leu Ser Ser Ala Leu Ala Cys Tyr Gly Leu Ser Phe Leu Gln Leu His
35     40     45
Ser Thr Asn Ser His Ile Asp Arg Ile Asn Phe Ser Val Lys Met Val
50     55     60
Ser Ser Ile Leu Gln Ile Pro Lys Leu Ser Tyr Leu Gly Leu Gly Asp
65     70     75     80
Ile Lys Asn Met Glu Gln Lys Tyr Cys Asn Leu Cys Ile Gln Leu Phe
85     90     95
Ile Ser Phe Leu Leu Leu Thr Val Gln Thr Phe
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&lt;210&gt; 3833

&lt;211&gt; 1764

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3833

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<210> 3834

<211> 361

<212> PRT

<213> Homo sapiens

<400> 3834

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			20					25					30		
Val	Ser	Val	Cys	Asp	His	Cys	Lys	Gly	Lys	Met	Gln	Leu	Val	Ala	Asp
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Leu	Leu	Leu	Leu	Ser	Ser	Glu	Ala	Arg	Pro	Val	Leu	Phe	Glu	Gly	Pro
			50			55					60				
Ala	Ser	Ser	Gly	Ala	Gly	Ala	Glu	Ser	Phe	Glu	Gln	Gly	Arg	Asp	Thr
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Ile	Ile	Ala	Arg	Thr	Lys	Gly	Leu	Ser	Ile	Leu	Thr	His	Asp	Val	Gln
			85					90					95		
Ser	Gln	Leu	Asn	Met	Gly	Arg	Phe	Gly	Glu	Ala	Gly	Asp	Ser	Leu	Val
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Glu	Leu	Gly	Asp	Leu	Val	Val	Ser	Leu	Thr	Glu	Cys	Ser	Ala	His	Ala
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Gly	Leu	Val	Asp	Arg	Tyr	Arg	Val	Thr	Arg	Cys	Arg	His	Glu	Val	Glu
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His Arg Glu Arg Leu Arg Asn Ser Ala Cys Ala Val Ser Glu Gly Cys				320
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Thr Leu Leu Ser Gln Ala Leu Arg Glu Arg Ser Ser Pro Arg Thr Leu				
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Pro Pro Val Asn Ser Asn Ser Val Asn				
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&lt;210&gt; 3835

&lt;211&gt; 2366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3835

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&lt;210&gt; 3836

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3836

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Leu Gln Ala Thr Glu Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu
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Gly Leu Thr Ala Ser Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr
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Thr Arg Ala Lys Asp Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg
      130      135      140
Asp Leu Asp Arg Ile Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg
      145      150      155      160
Val Ile Tyr Thr Asn Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser
      165      170      175
Glu Lys Gln Cys Arg Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp
      180      185      190
Ala Leu Leu Phe Met Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu
      195      200      205
Ile Ala Lys Glu Lys Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu
      210      215      220
Leu Asn Lys Arg Val Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr
      225      230      235      240
Arg Glu Leu Gln His Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln
      245      250      255
Lys Val Gln Ala Leu Cys Leu Pro Leu Asp Lys Asp Lys Phe Glu Met
      260      265      270
Asp Leu Arg Asn Leu Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp
      275      280      285
Asn Leu Gly Tyr Asn Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser
      290      295      300
Ile Arg Arg Ala Cys Asp His Met Pro Ser Leu Met Ser Ser Lys Val
      305      310      315      320
Glu Glu Leu Ala Arg Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg
      325      330      335
Glu Asn Ser Asp Leu Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu
      340      345      350
Arg Ala Ser Gln Glu Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala
      355      360      365
Arg Glu Ala Lys Leu Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala
      370      375      380
Leu Glu Glu Lys Ala Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys
      385      390      395      400
Glu Leu Glu Glu Lys Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu
      405      410      415
Ala Ile Arg Asn Ser Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln
      420      425      430
Pro Met Met Pro Val Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln
      435      440      445
Pro Ile Asp Pro Ala Ser Leu Glu Glu Phe Lys Arg Lys Ile Leu Glu
      450      455      460
Ser Gln Arg Pro Pro Ala Gly Ile Pro Val Ala Pro Ser Ser Gly

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465

470

475

&lt;210&gt; 3837

&lt;211&gt; 2084

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3837

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<210> 3838

<211> 468

<212> PRT

<213> Homo sapiens

<400> 3838

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Ile	Lys	Ser	Ile	Leu	Pro	Gly	Arg	Ser	Cys	Asp	Leu	Leu	Gln	Asp	Thr
			20					25					30		
Ser	His	Leu	Pro	Pro	Glu	His	Ser	Asp	Val	Val	Ile	Val	Gly	Gly	Gly
		35					40					45			
Val	Leu	Gly	Leu	Ser	Val	Ala	Tyr	Trp	Leu	Lys	Lys	Leu	Glu	Ser	Arg
	50					55				60					
Arg	Gly	Ala	Ile	Arg	Val	Leu	Val	Val	Glu	Arg	Asp	His	Thr	Tyr	Ser
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Gln	Ala	Ser	Thr	Gly	Leu	Ser	Val	Gly	Gly	Ile	Cys	Gln	Gln	Phe	Ser
				85					90					95	
Leu	Pro	Glu	Asn	Ile	Gln	Leu	Ser	Leu	Phe	Ser	Ala	Ser	Phe	Leu	Arg
			100					105					110		
Asn	Ile	Asn	Glu	Tyr	Leu	Ala	Val	Val	Asp	Ala	Pro	Pro	Leu	Asp	Leu
	115						120					125			
Arg	Phe	Asn	Pro	Ser	Gly	Tyr	Leu	Leu	Leu	Ala	Ser	Glu	Lys	Asp	Ala
	130					135					140				
Ala	Ala	Met	Glu	Ser	Asn	Val	Lys	Val	Gln	Arg	Gln	Glu	Gly	Ala	Lys
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Val	Ser	Leu	Met	Ser	Pro	Asp	Gln	Leu	Arg	Asn	Lys	Phe	Pro	Trp	Ile
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      180      185      190
Trp Phe Asp Pro Trp Cys Leu Leu Gln Gly Leu Arg Arg Lys Val Gln
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Ser Leu Gly Val Leu Phe Cys Gln Gly Glu Val Thr Arg Phe Val Ser
      210      215      220
Ser Ser Gln Arg Met Leu Thr Thr Asp Asp Lys Ala Val Val Leu Lys
      225      230      235      240
Arg Ile His Glu Val His Val Lys Met Asp Arg Ser Leu Glu Tyr Gln
      245      250      255
Pro Val Glu Cys Ala Ile Val Ile Asn Ala Ala Gly Ala Trp Ser Ala
      260      265      270
Gln Ile Ala Ala Leu Ala Gly Val Gly Glu Gly Pro Pro Gly Thr Leu
      275      280      285
Gln Gly Thr Lys Leu Pro Val Glu Pro Arg Lys Arg Tyr Val Tyr Val
      290      295      300
Trp His Cys Pro Gln Gly Pro Gly Leu Glu Thr Pro Leu Val Ala Asp
      305      310      315      320
Thr Ser Gly Ala Tyr Phe Arg Arg Glu Gly Leu Gly Ser Asn Tyr Leu
      325      330      335
Gly Gly Arg Ser Pro Thr Glu Gln Glu Glu Pro Asp Pro Ala Asn Leu
      340      345      350
Glu Val Asp His Asp Phe Phe Gln Asp Lys Val Trp Pro His Leu Ala
      355      360      365
Leu Arg Val Pro Ala Phe Glu Thr Leu Lys Cys Phe Val His Pro Gln
      370      375      380
Val Gln Ser Ala Trp Ala Gly Tyr Tyr Asp Tyr Asn Thr Phe Asp Gln
      385      390      395      400
Asn Gly Val Val Gly Pro His Pro Leu Val Val Asn Met Tyr Phe Ala
      405      410      415
Thr Gly Phe Ser Gly His Gly Leu Gln Gln Ala Pro Gly Ile Gly Arg
      420      425      430
Ala Val Ala Glu Met Val Leu Lys Gly Arg Phe Gln Thr Ile Asp Leu
      435      440      445
Ser Pro Phe Leu Phe Thr Arg Phe Tyr Leu Gly Glu Lys Ile Gln Glu
      450      455      460
Asn Asn Ile Ile
465

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&lt;210&gt; 3839

&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3839

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120
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180
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240
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300

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 600  
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 660  
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<210> 3840

<211> 252

<212> PRT

<213> Homo sapiens

<400> 3840

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		20					25				30				
Met	Glu	Tyr	Leu	Asn	Ser	Arg	Cys	Val	Leu	Phe	Thr	Tyr	Phe	Gln	Gly
	35				40						45				
Asp	Ile	Gly	Ser	Val	Val	Asp	Glu	His	Phe	Ser	Arg	Ala	Leu	Gly	Gln
50					55					60					
Ala	Ile	Thr	Leu	His	Pro	Glu	Ser	Ala	Ile	Ser	Lys	Ser	Lys	Met	Gly
65				70					75					80	
Leu	Thr	Pro	Leu	Trp	Arg	Asp	Ser	Ser	Ala	Leu	Ser	Ser	Gln	Arg	Asn
			85					90					95		
Ser	Phe	Pro	Thr	Ser	Phe	Trp	Thr	Ser	Ser	Tyr	Gln	Pro	Pro	Pro	Ala
		100					105					110			
Pro	Cys	Leu	Gly	Gly	Val	His	Pro	Asp	Phe	Gln	Val	Thr	Gly	Pro	Pro
		115				120				125					
Gly	Thr	Phe	Ser	Ala	Ala	Asp	Pro	Ser	Pro	Trp	Pro	Gly	His	Asn	Leu
130					135					140					
His	Gln	Thr	Gly	Pro	Ala	Pro	Pro	Pro	Ala	Val	Ser	Glu	Ser	Trp	Pro
145				150					155					160	
Tyr	Pro	Leu	Thr	Ser	Gln	Val	Ser	Pro	Ser	Tyr	Ser	His	Met	His	Asp
			165				170					175			
Val	Tyr	Met	Arg	His	His	His	Pro	His	Ala	His	Met	His	His	Arg	His
		180					185				190				
Arg	His	His	His	His	His	His	His	Pro	Pro	Ala	Gly	Ser	Ala	Leu	Asp
		195				200					205				
Pro	Ser	Tyr	Gly	Pro	Leu	Leu	Met	Pro	Ser	Val	His	Ala	Ala	Arg	Ile
	210				215					220					
Pro	Ala	Pro	Gln	Cys	Asp	Ile	Thr	Lys	Thr	Glu	Pro	Thr	Thr	Val	Thr
225				230					235					240	
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245

250

<210> 3841  
 <211> 367  
 <212> DNA  
 <213> Homo sapiens

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 367

<210> 3842  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 3842  
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 Gly Ala Ile Val Ala Ala Met Gly Ile Val Cys Phe Leu Phe Leu Ile  
 35 40 45  
 Glu His Pro Asn Asp Val Arg Cys Ser Ser Thr Leu Val Thr His Ser  
 50 55 60  
 Lys Gly Tyr Glu Asn Gly Thr Asn Arg Leu Ser Leu Pro Lys Pro Ile  
 65 70 75 80  
 Leu Lys Ser Glu Lys Asn Lys Pro Leu Asp Pro Glu Met Gln Cys Leu  
 85 90 95  
 Leu Leu Ser Asp Gly Lys Gly Ser Ile His Pro Asn His Val Val Ile  
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 Leu Pro Gly Asp Gly Gly Ser Gly Pro Ala  
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<210> 3843  
 <211> 712  
 <212> DNA  
 <213> Homo sapiens

<400> 3843  
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712

&lt;210&gt; 3844

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3844

Met	Ala	His	Val	Gly	Ser	Arg	Lys	Arg	Ser	Arg	Ser	Arg	Ser
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Arg	Gly	Arg	Gly	Ser	Glu	Lys	Arg	Lys	Lys	Lys	Ser	Arg	Lys
			20					25				30	Asp
Ser	Arg	Asn	Cys	Ser	Ala	Ser	Thr	Ser	Gln	Gly	Arg	Lys	Ala
			35					40				45	Ser
Ala	Pro	Gly	Ala	Glu	Ala	Ser	Pro	Ser	Pro	Cys	Ile	Thr	Glu
			50					55				60	Arg
Lys	Gln	Lys	Ala	Arg	Arg	Arg	Thr	Arg	Ser	Ser	Ser	Ser	Ser
							70					75	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
												85	
Ser	Ser	Asp	Gly	Arg	Lys	Lys	Arg	Gly	Lys	Tyr	Lys	Asp	Lys
													100
Lys	Lys	Lys	Lys	Lys	Arg	Lys	Lys	Leu	Lys	Lys	Lys	Gly	Lys
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Ala	Glu	Ala	Gln	Gln	Ala	Glu	His	His	Pro	Gln	Gly	Gly	Gly
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													130
													135
													140

&lt;210&gt; 3845

&lt;211&gt; 2302

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3845

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 2302

&lt;210&gt; 3846

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3846

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			20					25					30		
Gly	Pro	Ala	Glu	Pro	Arg	Val	Ala	Gly	Ala	Gly	Ala	Ala	Ala	Ala	Glu
		35					40					45			
Gly	Ala	Ala	Ala	Gly	Ala	Cys	Gly	Pro	Ala	Arg	Cys	Ala	Asp	Gln	Gly
		50				55					60				
Gly	Ala	Arg	Glu	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Ala	Gly	Gly	Gly
65					70					75				80	
Gly	Gly	Ala	His	Gly	His	Phe	Pro	Gln	Arg	Pro	Pro	Gln	Gln	Ala	Gly
			85						90					95	
Gln	Arg	Ala	Ala	Ser	Arg	Ala	Gly	Cys	Gly	His	Arg	Gln	Leu	Gln	Arg
			100					105					110		
Ala	Pro	Ala	Pro	Gly	Leu	Arg	Gln	His	Pro	Cys	Gly	Ser	Gly	Thr	Glu
		115					120					125			
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Pro	His	Thr	Leu	Gln	Arg	His	Leu	Gly	Pro	His	Ala	Thr	Gly	His	Gly
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<210> 3847  
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<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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 50 55 60  
 Lys Arg Leu Pro Cys Asn His Ile Phe His Thr Arg Trp Glu Gly Pro  
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 Trp Gly Ala Cys Pro Ala Gly Pro Arg Pro Gln Lys Ala Gly Pro Lys  
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 <212> DNA  
 <213> Homo sapiens

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<210> 3850

<211> 257

<212> PRT

<213> Homo sapiens

<400> 3850

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			20					25					30		
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Asp	Asp	Pro	Pro	Pro	Ser	Thr	Leu	Leu	Lys	Asp	Tyr	Gln	Asn	Val	Pro
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Gly	Ile	Glu	Lys	Val	Asp	Asp	Val	Val	Lys	Arg	Leu	Leu	Ser	Leu	Glu
				85				90					95		
Met	Ala	Asn	Lys	Lys	Glu	Met	Leu	Lys	Ile	Lys	Gln	Glu	Gln	Phe	Met
		100						105				110			
Lys	Lys	Ile	Val	Ala	Asn	Pro	Glu	Asp	Thr	Arg	Ser	Leu	Glu	Ala	Arg
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Ile	Ile	Ala	Leu	Ser	Val	Lys	Ile	Arg	Ser	Tyr	Glu	Glu	His	Leu	Glu
	130					135					140				
Lys	His	Arg	Lys	Asp	Lys	Ala	His	Lys	Arg	Tyr	Leu	Leu	Met	Ser	Ile
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Asp	Gln	Arg	Lys	Lys	Met	Leu	Lys	Asn	Leu	Arg	Asn	Thr	Asn	Tyr	Asp
				165				170					175		
Val	Phe	Glu	Lys	Ile	Cys	Trp	Gly	Leu	Gly	Ile	Glu	Tyr	Thr	Phe	Pro

	180		185		190										
Pro	Leu	Tyr	Tyr	Arg	Arg	Ala	His	Arg	Arg	Phe	Val	Thr	Lys	Lys	Ala
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Arg	Ala	Leu	Lys	Ala	Ala	Ala	Ala	Gln	Lys	Gln	Ala	Lys	Arg	Arg	
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Gln															

&lt;210&gt; 3851

&lt;211&gt; 1183

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3851

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1080

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<210> 3852

<211> 323

<212> PRT

<213> Homo sapiens

<400> 3852

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			20					25					30		
Trp	Ser	Ile	Ser	Ser	Arg	His	Val	Leu	Leu	Gln	Glu	Glu	Val	Ala	Glu
		35				40						45			
Leu	Gln	Gly	Gln	Val	Gln	Arg	Thr	Glu	Val	Ala	Arg	Gly	Arg	Leu	Glu
	50				55					60					
Lys	Arg	Asn	Ser	Asp	Leu	Leu	Leu	Val	Asp	Thr	His	Lys	Lys	Gln	
65				70					75					80	
Ile	Asp	Gln	Lys	Glu	Ala	Asp	Tyr	Gly	Arg	Leu	Ser	Ser	Arg	Leu	Gln
			85					90					95		
Ala	Arg	Glu	Gly	Leu	Gly	Lys	Arg	Cys	Glu	Asp	Asp	Lys	Val	Lys	Leu
			100					105					110		
Gln	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Ala	Asp	Ile	His	His	Leu	Lys	Glu
	115					120					125				
Gln	Leu	Ala	Glu	Leu	Arg	Gln	Glu	Phe	Leu	Arg	Gln	Glu	Asp	Gln	Leu
	130					135					140				
Gln	Asp	Tyr	Arg	Lys	Asn	Asn	Thr	Tyr	Leu	Val	Lys	Arg	Leu	Glu	Tyr
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Glu	Ser	Phe	Gln	Cys	Gly	Gln	Gln	Met	Lys	Glu	Leu	Arg	Ala	Gln	His
			165					170					175		
Glu	Glu	Asn	Ile	Lys	Lys	Leu	Ala	Asp	Gln	Phe	Leu	Glu	Glu	Gln	Lys
		180						185				190			
Gln	Glu	Thr	Gln	Lys	Ile	Gln	Ser	Asn	Asp	Gly	Lys	Glu	Leu	Asp	Ile
	195					200					205				
Asn	Asn	Gln	Val	Val	Pro	Lys	Asn	Ile	Pro	Lys	Val	Ala	Glu	Asn	Val
	210					215					220				
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225				230					235					240	
Glu	Gln	Ile	Lys	Arg	Gly	Gly	Asp	Ala	Gly	Met	Pro	Gly	Ile	Glu	Glu
			245					250					255		
Asn	Asp	Leu	Ala	Lys	Val	Asp	Asp	Leu	Pro	Pro	Ala	Leu	Arg	Lys	Pro
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Pro	Ile	Ser	Val	Ser	Gln	His	Glu	Ser	His	Gln	Ala	Ile	Ser	His	Leu
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Pro	Thr	Gly	Gln	Pro	Leu	Ser	Pro	Asn	Met	Pro	Pro	Asp	Ser	His	Ile
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 <211> 375  
 <212> DNA  
 <213> Homo sapiens

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<210> 3854  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 3854  
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 Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile Lys  
 35 40 45  
 Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile  
 50 55 60  
 Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser  
 65 70 75 80  
 Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser  
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 Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His  
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 Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser  
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<210> 3855  
 <211> 1377  
 <212> DNA  
 <213> Homo sapiens

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&lt;210&gt; 3856

&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3856

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      100      105      110
Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
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Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Xaa Pro Ala
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      180      185      190
Xaa Gln Pro Thr Glu Thr Arg Phe Val Asp Gly Arg Ala Ile Leu Gln
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Trp Asp Ile Phe Ala Ser Asn Gly Ile Ile His Val Ile Ser Arg Pro
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Leu Lys Ala Pro Pro Ala Pro Val Thr Leu Thr His Thr Gly Leu Gly
  225      230      235      240
Ala Gly Ile Phe Phe Ala Ile Ile Leu Val Thr Gly Ala Val Ala Leu
      245      250      255
Ala Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Arg Thr Ile Gly Phe Gln
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His Phe Glu Ser Glu Glu Asp Ile Asn Val Ala Ala Leu Gly Lys Gln
      275      280      285
Gln Pro Glu Asn Ile Ser Asn Pro Leu Tyr Glu Ser Thr Thr Ser Ala
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Pro Pro Glu Pro Ser Tyr Asp Pro Phe Thr Asp Ser Glu Glu Arg Gln
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&lt;210&gt; 3857

&lt;211&gt; 797

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3857

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&lt;210&gt; 3858

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3858

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			20						25				30		
Ala	Pro	Cys	Ser	Thr	Ser	Ala	Arg	Pro	Ser	Thr	Arg	Ser	Trp	Ala	Arg
			35				40					45			
Ser	Ile	Ser	Ala	Ala	Thr	Trp	Pro	Arg	Pro	Arg	Ala	Thr	Gly	Thr	Leu
	50					55					60				
Ala	Thr	Lys	Thr	Arg	Trp	Pro	Ala	Ser	Arg	Thr	Ala				
65					70						75				

&lt;210&gt; 3859

&lt;211&gt; 1449

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3859

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 tttgaagctc ggagtaaaac tgcttgcaag cacctctgga agtgcagtgt ggaacatcat  
 180  
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 240  
 ggatccatac gttataagca ccgctacagt ggcaggacag ctttgcaaat gagccgagat  
 300  
 ctttctattc agcttccccg gcttgatcag aatgtgacaa gaagtogaag caagacttac  
 360

cctaagcgaa tagcacaaac acagccagct gaatcaaaca ccatcagtag gataactgca  
 420  
 aacatggaaa atggagaaaa tgaaggaaca attaaaatta ttgcaccttc accagtaaaa  
 480  
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 660  
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 720  
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 780  
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 960  
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 1020  
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 1080  
 tagtgcttga cacaagggtga cccaatccgc atcaggcatt ctcatctgcc acgaagttac  
 1140  
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 1320  
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 1440  
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 1449

&lt;210&gt; 3860

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3860

Tyr	Lys	Asn	Lys	Lys	Gln	Val	Gly	Lys	Tyr	Phe	Trp	Pro	Arg	Ile	Thr
1				5					10					15	
Lys	Val	His	Phe	Lys	Glu	Thr	Gln	Phe	Glu	Leu	Arg	Val	Leu	Gly	Lys
			20					25					30		
Asp	Cys	Asn	Glu	Thr	Ser	Phe	Phe	Phe	Glu	Ala	Arg	Ser	Lys	Thr	Ala
		35					40					45			
Cys	Lys	His	Leu	Trp	Lys	Cys	Ser	Val	Glu	His	His	Thr	Phe	Phe	Arg
	50					55					60				
Met	Pro	Glu	Asn	Glu	Ser	Asn	Ser	Leu	Ser	Arg	Lys	Leu	Ser	Lys	Phe



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65          70          75          80
Gly Ser Ile Arg Tyr Lys His Arg Tyr Ser Gly Arg Thr Ala Leu Gln
      85          90          95
Met Ser Arg Asp Leu Ser Ile Gln Leu Pro Arg Pro Asp Gln Asn Val
      100          105          110
Thr Arg Ser Arg Ser Lys Thr Tyr Pro Lys Arg Ile Ala Gln Thr Gln
      115          120          125
Pro Ala Glu Ser Asn Thr Ile Ser Arg Ile Thr Ala Asn Met Glu Asn
      130          135          140
Gly Glu Asn Glu Gly Thr Ile Lys Ile Ile Ala Pro Ser Pro Val Lys
145          150          155          160
Ser Phe Lys Lys Ala Lys Asn Glu Asn Ser Pro Asp Thr Gln Arg Ser
      165          170          175
Lys Ser His Ala Pro Trp Glu Glu Asn Gly Pro Gln Ser Gly Leu Tyr
      180          185          190
Asn Ser Pro Ser Asp Arg Thr Lys Ser Pro Lys Phe Pro Tyr Thr Arg
      195          200          205
Arg Arg Asn Pro Ser Cys Gly Ser Asp Asn Asp Ser Val Gln Pro Val
      210          215          220
Arg Arg Arg Lys Ala His Asn Ser Gly Glu Asp Ser Asp Leu Lys Gln
225          230          235          240
Arg Arg Arg Ser Arg Ser Arg Cys Asn Thr Ser Ser Gly Ser Glu Ser
      245          250          255
Glu Asn Ser Asn Arg Glu His Arg Lys Lys Arg Asn Arg Ile Arg Gln
      260          265          270
Glu Asn Asp Met Val Asp Ser Ala Pro Gln Trp Glu Ala Val Leu Arg
      275          280          285
Arg Gln Lys Glu Lys Asn Gln Ala Asp Pro Asn Asn Arg Arg Ser Arg
      290          295          300
His Arg Ser Arg Ser Arg Ser Pro Asp Ile Gln Ala Lys Glu Glu Leu
305          310          315          320
Trp Lys His Ile Gln Lys Glu Leu Val Asp Pro Ser Gly Leu Ser Glu
      325          330          335
Glu Gln Leu Lys Glu Ile Pro Tyr Thr Lys Ile Glu
      340          345

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&lt;210&gt; 3861

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3861

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120
ggagagggca gctactccaa ggtgaaggtg gccacatcca agaagtacaa gggtagcgtg
180
gccatcaagg tggtggaccg gcggcgagcg ccccgaggact tcgtcaacaa gttcctgccg
240
cgagagctgt ccactctgcg gggcgtgcga caccgcaca tcgtgcacgt ctcgagttc
300
atcgaggtgt gcaacgggaa actgtacatc gtgatggaag cggccgccac cgacctgctg
360

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 480  
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 540  
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 600  
 acccgagtca tgcatttctt gagcacctac tgtctgcccag gccccagagc tcattggcgaa  
 660  
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 720  
 atgacatgga aataaaaaaaaa aaaaaaaaa  
 748

&lt;210&gt; 3862

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3862

Met Ser Gly Asp Lys Leu Leu Ser Glu Leu Gly Tyr Lys Leu Gly Arg  
 1 5 10 15  
 Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys  
 20 25 30  
 Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala  
 35 40 45  
 Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu  
 50 55 60  
 Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu  
 65 70 75 80  
 Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp  
 85 90 95  
 Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala  
 100 105 110  
 Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp  
 115 120 125  
 His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser  
 130 135 140  
 Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln  
 145 150 155 160  
 Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Val  
 165 170 175  
 Arg Val Thr Arg Val Met His Phe Leu Ser Thr Tyr Cys Leu Pro Gly  
 180 185 190  
 Pro Arg Ala His Gly Glu Glu Thr Trp Ala His Pro Cys Arg Lys Arg  
 195 200 205  
 Asp Asn  
 210

&lt;210&gt; 3863

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 120  
 agttttgctc tcagttggga ctctgggaaa aaaactgtgt ggctgatctc cacgaggttc  
 180  
 ttctggtcga ggctccccga gaaccatctg gccatgggct ggcagccgag ttctcgagc  
 240  
 gtccaggctg acggtacatt ccaggctagc catcctatca taatcgaatc tgagtagatt  
 300  
 tttatcaatc gcttgggaca agccattgaa ttttcggaga g  
 341

<210> 3864  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 3864  
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 Ile Gly Trp Leu Ala Trp Asn Val Pro Ser Ala Trp Thr Leu Arg Glu  
 20 25 30  
 Leu Gly Cys Gln Pro Met Ala Arg Trp Phe Ser Gly Ser Leu Asp Gln  
 35 40 45  
 Lys Asn Leu Val Glu Ile Ser His Thr Val Phe Phe Pro Glu Ser Gln  
 50 55 60  
 Leu Arg Ala Lys Leu Lys Cys Pro Gly Gly Ser Cys Thr Pro Gly Leu  
 65 70 75 80  
 Lys Lys Ile Gly Ser Leu Lys Val Ser Cys Glu Glu Phe Leu Leu Met  
 85 90 95  
 Gly Leu Arg Tyr Gln His Leu Asp Pro Pro Ser Arg  
 100 105

<210> 3865  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

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 aatcaggaat tgacgataag cttactacat tttgaaatta tctgactttc ctcatgaaat  
 120  
 gagacctatg tgaagccac ttaattttct gaaacttcac atcatgtacc ttcattgtaa  
 180  
 tattctgaca cttgtttcat gcagccatac cagtcacaac tttaaatttt tagtcagact  
 240  
 ttgctcaciaa ggtttcagga taattaatac aaatggtttg ggccagccat cacacagcag  
 300  
 tctcctatctt acttcactac aactacagct ttcattcttc attacattac tttttctgag  
 360

tagtctgggt caaatagtag aaactgaata ttccttaacc aaaatgcttg gaagtaggcc  
 420  
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 480  
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<210> 3866

<211> 109

<212> PRT

<213> Homo sapiens

<400> 3866

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Ser	His	Asn	Phe	Lys	Phe	Leu	Val	Arg	Leu	Cys	Ser	Gln	Gly	Phe	Arg
			20					25					30		
Ile	Ile	Asn	Thr	Asn	Gly	Leu	Gly	Gln	Pro	Ser	His	Ser	Ser	Leu	Leu
		35				40					45				
Phe	Thr	Ser	Leu	Gln	Leu	Gln	Leu	Ser	Phe	Phe	Ile	Thr	Leu	Leu	Phe
	50				55					60					
Leu	Ser	Ser	Leu	Gly	Gln	Ile	Val	Gln	Thr	Glu	Tyr	Ser	Leu	Thr	Lys
65				70					75					80	
Met	Leu	Gly	Ser	Arg	Pro	Gly	Ala	Ala	Ala	His	Pro	Cys	Asn	Pro	Ser
				85				90						95	
Ile	Leu	Gly	Gly	Gln	Ser	Arg	Gln	Ile	Thr	Gln	Gly	Gln			
			100					105							

<210> 3867

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 3867

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 120  
 ctggacagtg caaagcgatc ggaggacagg gagaaggag ctctgattga ggagctctta  
 180  
 caggcaaac aggatcttca agatctgctg attgccaaag aggagcaaga agacctcttg  
 240  
 agaaagcgag agcgtgaact caccgccctg aaggagagccc tgaaagaaga ggtttccagc  
 300  
 catgatcagg agatggacaa gctgaaggag caatatgatg ctgagttgca ggccctgagg  
 360  
 gagagtgtgg aagaagcaac caagaatgtc gaggtcttgg cgagcaggag caacacttca  
 420  
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 480  
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 540  
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cgacagttag aggagggcct tgtgcacgcc agaaaggaag aaaaagaagc tgtgtcagcc  
 660  
 agaagggccc tggagaatga actggaggct gctcagggaa atctgagtca gactacccag  
 720  
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 780  
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 840  
 cagaaggaga tggcagacat tgttgaggcc tcccgtacct caaccctgga gctccagaac  
 900  
 cagctggatg agtataagga gaaaaaccgc agggagctcg cagaaatgca aagacagttg  
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<210> 3868

<211> 344

<212> PRT

<213> Homo sapiens

<400> 3868

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Lys	Met	Glu	Arg	Glu	Gln	His	Gln	Thr	Glu	Ile	Arg	Asp	Leu	Gln	Asp
		20						25					30		
Gln	Leu	Ser	Glu	Met	His	Asp	Glu	Leu	Asp	Ser	Ala	Lys	Arg	Ser	Glu
	35						40					45			
Asp	Arg	Glu	Lys	Gly	Ala	Leu	Ile	Glu	Glu	Leu	Leu	Gln	Ala	Lys	Gln
50					55					60					
Asp	Leu	Gln	Asp	Leu	Leu	Ile	Ala	Lys	Glu	Glu	Gln	Glu	Asp	Leu	Leu
65				70					75					80	
Arg	Lys	Arg	Glu	Arg	Glu	Leu	Thr	Ala	Leu	Lys	Gly	Ala	Leu	Lys	Glu
			85					90					95		
Glu	Val	Ser	Ser	His	Asp	Gln	Glu	Met	Asp	Lys	Leu	Lys	Glu	Gln	Tyr
		100						105					110		
Asp	Ala	Glu	Leu	Gln	Ala	Leu	Arg	Glu	Ser	Val	Glu	Glu	Ala	Thr	Lys
	115					120					125				
Asn	Val	Glu	Val	Leu	Ala	Ser	Arg	Ser	Asn	Thr	Ser	Glu	Gln	Asp	Gln
130					135					140					
Ala	Gly	Thr	Glu	Met	Arg	Val	Lys	Leu	Leu	Gln	Glu	Glu	Asn	Glu	Lys
145				150				155						160	
Leu	Gln	Gly	Arg	Ser	Glu	Glu	Leu	Glu	Arg	Arg	Val	Ala	Gln	Leu	Gln
			165					170					175		
Arg	Gln	Ile	Glu	Asp	Leu	Lys	Gly	Asp	Glu	Ala	Lys	Ala	Lys	Glu	Thr
		180						185					190		
Leu	Lys	Lys	Tyr	Glu	Gly	Glu	Ile	Arg	Gln	Leu	Glu	Glu	Ala	Leu	Val
	195					200						205			
His	Ala	Arg	Lys	Glu	Glu	Lys	Glu	Ala	Val	Ser	Ala	Arg	Arg	Ala	Leu
210					215					220					
Glu	Asn	Glu	Leu	Glu	Ala	Ala	Gln	Gly	Asn	Leu	Ser	Gln	Thr	Thr	Gln
225				230					235					240	
Glu	Gln	Lys	Gln	Leu	Ser	Glu	Lys	Leu	Lys	Glu	Glu	Ser	Glu	Gln	Lys

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<400> 3869
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120
tgatgcacac acattccaga aatgcagagg tatgctgctg ccacggggta ggggtgcggg
180
aggcggcctg gcctcatggc cgcagaccgt gcccagccc gggcctggca ggtagctggc
240
cactgataaa tgccactggg atcctaggag aagctgggga ccatgctga ggtactgaag
300
gggaccatgg tggatggcat cctgggcact ttgtagcttg tctgaggga aggcctctgc
360
tgccatagaa aagctggaca catgtcacc tggggccctg acatcctaaa atgccccact
420
gactaccagt cactaggaga aaggtctccg gctatgccct tcccagtgat gcttgcccc
480
gagtgactgg tcacaggtgg gggacaggtt tgctccagaa accgtaggcc tttcttgtct
540
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600
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660
gcctgaggtt ctgcctggac cgaaggaggc ctgcctcaca gcacctctgt gaggggactg
720
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780
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840
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900
caccaccca tctgcctctg gccccagtg aagtcagaag aggcaggagc cccgcaggct
960
gtgagcctgg cgcaggtcgg ctgacagcga gcttctcatc tgcttgggtg tagagcggac
1020

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gctctcggca gcctgcacgg cccggctcag ggccttggtg agctcctcta ggtcgcccag  
1080  
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1140  
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<210> 3870

<211> 100

<212> PRT

<213> Homo sapiens

<400> 3870

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Ala	Ile	His	His	Gly	Pro	Leu	Gln	Tyr	Leu	Thr	His	Gly	Pro	Gln	Leu
			20					25					30		
Leu	Leu	Gly	Ser	Gln	Trp	His	Leu	Ser	Val	Ala	Ser	Tyr	Leu	Pro	Gly
		35					40					45			
Pro	Gly	Trp	Gly	Thr	Val	Cys	Gly	His	Glu	Ala	Arg	Pro	Pro	Pro	Ala
	50					55					60				
Pro	Leu	Pro	Arg	Gly	Ser	Ser	Ile	Pro	Leu	His	Phe	Trp	Asn	Val	Cys
65					70					75				80	
Ala	Ser	Met	Met	Phe	Val	Tyr	Leu	Arg	His	Leu	Lys	Ile	Tyr	Phe	Arg
				85					90					95	
Tyr	Glu	Gly	Lys												
			100												

<210> 3871

<211> 473

<212> DNA

<213> Homo sapiens

<400> 3871

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120  
tgggatggtt gagttgacag ctctgaatcc cagaaacctt aattttggct tatcttttga  
180  
taggctgagg gaaaatacaa agatgatcct gttgatctcc gccttgatat tgaacgtcgt  
240  
aaaaaacata aggagagaga tcttaaacga ggtaaatcga gagaatcagt ggattcccga  
300  
gactccagtc actcaaggga aaggctcagct gaaaaaacag agaaaactca taaaggatca  
360  
aagaaacaga agaaagacct ctgagagccg agacaagctg ggagcgaaag gagattttcc  
420  
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473

<210> 3872

<211> 66  
 <212> PRT  
 <213> Homo sapiens

<400> 3872  
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 Glu Arg Arg Lys Lys His Lys Glu Arg Asp Leu Lys Arg Gly Lys Ser  
 20 25 30  
 Arg Glu Ser Val Asp Ser Arg Asp Ser Ser His Ser Arg Glu Arg Ser  
 35 40 45  
 Ala Glu Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys  
 50 55 60  
 Asp Leu  
 65

<210> 3873  
 <211> 869  
 <212> DNA  
 <213> Homo sapiens

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 aggaggcaga agtcgtccga ggcccctgtg cagtccccgc agcgctccgt ggactccatc  
 180  
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 240  
 accaagaagg actacagaga ggtagaaaaa cttttgagag cagttgctga tggagatcta  
 300  
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 360  
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 420  
 gtcagaaga ggctggcgaa ggctcctgcc agtgggcttg gtgtgaacgt gaccagccag  
 480  
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 720  
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 780  
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 840  
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 869

<210> 3874



&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3874

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Asp Ile Ala Ala Glu Arg Ser Val His Arg Asp Pro Glu Gln Thr Glu
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Gly Asp Pro Leu Lys Cys Ala Leu Asn Ser Lys Ile Leu Ser Val Met
           20           25           30
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Pro Val Gln Ser Pro Gln Arg Ser Val Asp Ser Ile Ser Gln Glu Ser
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Ser Thr Ser Ser Phe Ser Ser Met Ser Ala Gly Ser Arg Gln Glu Glu
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Thr Lys Lys Asp Tyr Arg Glu Val Glu Lys Leu Leu Arg Ala Val Ala
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Asp Gly Asp Leu Glu Met Val Arg Tyr Leu Leu Glu Trp Thr Glu Glu
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Asp Leu Glu Asp Ala Glu Asp Thr Val Ser Ala Ala Asp Pro Glu Phe
           115          120          125
Cys His Pro Leu Cys Gln Cys Pro Lys Cys Ala Pro Ala Gln Lys Arg
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Leu Ala Lys Val Pro Ala Ser Gly Leu Gly Val Asn Val Thr Ser Gln
145          150          155          160
Asp Gly Ser Ser Pro Leu His Val Ala Ala Leu His Gly Arg Ala Asp
           165          170          175
Leu Ile Arg Leu Leu Leu Lys His Gly Ala Asn Ala Gly Ala Arg Asn
           180          185          190
Ala Asp Gln Ala Val Pro Leu His Leu Ala Cys Gln Gln Gly His Phe
           195          200          205
Gln Val Val Lys Cys Leu Leu Asp Ser Asn Ala Lys Pro Asn Lys Lys
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Asp Leu Ser Gly Asn Thr Pro Leu Ile Tyr Ala Cys Ser Gly Gly His
225          230          235          240Glu Leu
Val Ala Leu Leu Leu Gln His Gly Ala Ser Ile Asn Ala
           245          250          255
Leu Thr Ile Arg Gly Asn Thr Ala Leu His Glu Ala Val Ile Glu Lys
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His Val Phe Val Val Glu Leu Leu Leu Leu His Gly Ala Ser Val Arg
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Cys

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&lt;210&gt; 3875

&lt;211&gt; 2640

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3875

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<210> 3876

<211> 824

<212> PRT

<213> Homo sapiens

<400> 3876

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			20					25					30		
Pro	Pro	Ala	Ala	Leu	Gly	Leu	Val	Ser	Ser	Arg	Thr	Ser	Gly	Ala	Val
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His	Gly	Leu	His	Ser	Val	Leu	Glu	Glu	Trp	Phe	Val	Glu	Val	Leu	Gln
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Asn	Asp	Leu	Gln	Ala	Asn	Ile	Ser	Pro	Glu	Phe	Trp	Asn	Ala	Ile	Ser
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Gln	Cys	Glu	Asn	Ser	Ala	Asp	Glu	Pro	Gln	Cys	Leu	Leu	Leu	Leu	Leu
			100				105				110				
Asp	Ala	Phe	Gly	Leu	Leu	Glu	Ser	Arg	Leu	Asp	Pro	Tyr	Leu	Arg	Ser
		115				120					125				
Leu	Glu	Leu	Leu	Glu	Lys	Trp	Thr	Arg	Leu	Gly	Leu	Leu	Met	Gly	Thr

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Leu Phe Phe Ser Thr Pro Arg Thr Phe Gln Glu Met Ile Gln Arg Leu		
	165	170
Tyr Gly Cys Phe Leu Arg Val Tyr Met Gln Ser Lys Arg Lys Gly Glu		
	180	185
Gly Gly Thr Asp Pro Glu Leu Glu Gly Glu Leu Asp Ser Arg Tyr Ala		
	195	200
Arg Arg Arg Tyr Tyr Arg Leu Leu Gln Ser Pro Leu Cys Ala Gly Cys		
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Ser Ser Asp Lys Gln Gln Cys Trp Cys Arg Gln Ala Leu Glu Gln Phe		
225	230	235
His Gln Leu Ser Gln Val Leu His Arg Leu Ser Leu Leu Glu Arg Val		
	245	250
Ser Ala Glu Ala Val Thr Thr Thr Leu His Gln Val Thr Arg Glu Arg		
	260	265
Met Glu Asp Arg Cys Arg Gly Glu Tyr Glu Arg Ser Phe Leu Arg Glu		
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Phe His Arg Trp Ile Glu Arg Val Val Gly Trp Leu Gly Lys Val Phe		
290	295	300
Leu Gln Asp Gly Pro Ala Arg Pro Ala Ser Pro Glu Ala Gly Asn Thr		
305	310	315
Leu Arg Arg Trp Arg Cys His Val Gln Arg Phe Phe Tyr Arg Ile Tyr		
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	340	345
Asp Ser Arg Pro Ala Ile Glu Asp Leu Lys Tyr Cys Leu Glu Arg Thr		
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370	375	380
Arg Leu Leu His Pro Gly Val Asn Thr Cys Asp Ile Ile Thr Leu Tyr		
385	390	395
Ile Ser Ala Ile Lys Ala Leu Arg Val Leu Asp Pro Ser Met Val Ile		
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Asp Thr Val Arg Gln Ile Val Ala Gly Leu Thr Gly Asp Ser Asp Gly		
	435	440
Thr Gly Asp Leu Ala Val Glu Leu Ser Lys Thr Asp Pro Ala Ser Leu		
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Glu Thr Gly Gln Asp Ser Glu Asp Asp Ser Gly Glu Pro Glu Asp Trp		
465	470	475
Val Pro Asp Pro Val Asp Ala Asp Pro Gly Lys Ser Ser Ser Lys Arg		
	485	490
Arg Ser Ser Asp Ile Ile Ser Leu Leu Val Ser Ile Tyr Gly Ser Lys		
	500	505
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His Gln Phe Ser Phe Ser Pro Glu Arg Glu Ile Arg Asn Val Glu Leu		
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Leu Lys Leu Arg Phe Gly Glu Ala Pro Met His Phe Cys Glu Val Met		
545	550	555
Leu Lys Asp Met Ala Asp Ser Arg Arg Ile Asn Ala Asn Ile Arg Glu		

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 580 585 590  
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 675 680 685  
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 690 695 700  
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 Tyr Arg Leu Pro Lys Asn Cys Ser  
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&lt;210&gt; 3877

&lt;211&gt; 1112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3877

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<210> 3878

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<212> PRT

<213> Homo sapiens

<400> 3878

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			20					25					30		
His	Ala	Lys	Lys	Ala	Asn	Gly	Pro	Asn	Tyr	Ile	Gln	Pro	Gln	Lys	Arg
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Gln	Thr	Thr	Phe	Glu	Ser	Gln	Asp	Arg	Lys	Ala	Val	Ser	Pro	Ser	Ser
	50					55					60				
Ser	Glu	Lys	Arg	Ser	Lys	Asn	Pro	Ile	Ser	Arg	Pro	Leu	Glu	Gly	Lys
65					70					75				80	
Lys	Ser	Leu	Ser	Leu	Ser	Ala	Lys	Thr	His	Asn	Ile	Gly	Phe	Asp	Lys
				85					90					95	
Asp	Ser	Cys	His	Ser	Thr	Thr	Lys	Thr	Glu	Ala	Ser	Gln	Glu	Glu	Arg
		100						105					110		
Ser	Asp	Ser	Ser	Gly	Leu	Thr	Ser	Leu	Lys	Lys	Ser	Pro	Lys	Val	Ser
	115						120					125			
Ser	Lys	Asp	Thr	Arg	Glu	Ile	Lys	Thr	Asp	Phe	Ser	Leu	Ser	Ile	Ser
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Asn	Ser	Ser	Asp	Val	Ser	Ala	Lys	Asp	Lys	His	Ala	Glu	Asp	Asn	Glu
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Lys	Arg	Leu	Ala	Ala	Leu	Glu	Ala	Arg	Gln	Lys	Ala	Lys	Glu	Val	Gln
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Lys	Lys	Leu	Val	His	Asn	Ala	Leu	Ala	Asn	Leu	Asp	Gly	His	Pro	Glu

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225      230      235      240
Asp Glu Glu Ser Asp Ser Glu Asp Asp Ser Asn Arg Phe Lys Ile Lys
      245      250      255
Pro Gln Phe Glu Gly Arg Ala Gly Gln Lys Leu Met Asp Leu Gln Ser
      260      265      270
His Phe Gly Thr Asp Asp Arg Phe Arg Met Asp Ser Arg Phe Leu Glu
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Thr Asp Ser Glu Glu Glu Gln Glu Glu Val Asn Glu Lys Lys Thr Ala
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Gln Ser Val Leu Gln Ile Asn Leu Ser Asn Ser Thr Asn Arg Gly Ser
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Val Ala Ala Lys Lys Phe Lys Asp Ile Ile His Tyr Asp Pro Thr Lys
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Ser Lys
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&lt;210&gt; 3879

&lt;211&gt; 2769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3879

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&lt;210&gt; 3880

&lt;211&gt; 116

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3880

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Phe	Leu	His	Arg	Leu	Pro	Ser	Glu	Val	Ser	Ala	Leu	Gln	His	Leu	Lys
			20					25					30		
Ala	Ile	Asp	Leu	Ser	Arg	Asn	Gln	Phe	Gln	Asp	Phe	Pro	Glu	Gln	Leu
		35					40					45			
Thr	Ala	Leu	Pro	Ala	Leu	Glu	Thr	Ile	Asn	Leu	Glu	Glu	Asn	Glu	Ile
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Val	Asp	Val	Pro	Val	Glu	Lys	Leu	Ala	Ala	Met	Pro	Ala	Leu	Arg	Ser
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Ile	Asn	Leu	Arg	Phe	Asn	Pro	Leu	Asn	Ala	Glu	Val	Arg	Val	Ile	Ala
			85					90					95		
Pro	Pro	Leu	Ile	Lys	Phe	Asp	Met	Leu	Met	Ser	Pro	Glu	Gly	Ala	Arg
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Ala	Pro	Leu	Pro												
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&lt;210&gt; 3881

&lt;211&gt; 1393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3881

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&lt;210&gt; 3882

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3882

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			20				25					30			
Gln	Met	Pro	Ser	Leu	Asn	Trp	Pro	Glu	Ala	Leu	Pro	Pro	Pro	Pro	Pro

35 40 45  
 Ser Cys Glu Leu Ser Cys Leu Glu Gly Pro Glu Glu Glu Leu Glu Gly  
 50 55 60  
 Ser Ser Glu Pro Glu Glu Trp Cys Pro Pro Met Pro Glu Arg Ser His  
 65 70 75 80  
 Leu Thr Glu Pro Ser Ser Gly Gly Trp Leu Val Thr Pro Ser Arg  
 85 90 95  
 Arg Glu Thr Pro Ser Pro Thr Pro Ser Tyr Gly Gln Gln Ser Thr Ala  
 100 105 110  
 Thr Leu Thr Pro Ser Pro Pro Asp Pro Pro Gln Pro Pro Thr Asp Met  
 115 120 125  
 Pro His Leu His Gln Met Pro Arg Arg Val Pro Leu Gly Pro Ser Ser  
 130 135 140  
 Pro Leu Ser Val Ser Gln Pro Met Leu Gly Ile Arg Glu Ala Arg Pro  
 145 150 155 160  
 Ala Gly Leu Gly Ala Gly Pro Ala Ala Ser Pro His Leu Ser Pro Ser  
 165 170 175  
 Pro Ala Pro Ser Thr Ala Ser Ser Ala Pro Gly Arg Thr Trp Gln Gly  
 180 185 190  
 Asn Gly Glu Met Thr Pro Pro Leu Gln Gly Pro Arg Ala Arg Phe Arg  
 195 200 205  
 Lys Lys Pro Lys Ala Leu Pro Tyr Arg Arg Glu Asn Ser Pro Gly Asp  
 210 215 220  
 Leu Pro Pro Pro Pro Leu Pro Pro Pro Glu Xaa Arg Gly Glu Leu Gly  
 225 230 235 240  
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&lt;210&gt; 3883

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3883

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&lt;210&gt; 3884

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3884

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			20					25					30		
Lys	Ala	Arg	Arg	Arg	Thr	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
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Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
	50					55				60					
Asp	Gly	Arg	Lys	Lys	Arg	Gly	Lys	Tyr	Lys	Asp	Lys	Arg	Arg	Lys	Lys
65					70					75				80	
Lys	Lys	Lys	Arg	Lys	Lys	Leu	Lys	Lys	Lys	Gly	Lys	Glu	Lys	Ala	Glu
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Ala	Gln	Gln	Val	Glu	Ala	Leu	Pro	Gly	Pro	Ser	Leu	Asp	Gln	Trp	His
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Arg	Ser	Ala	Gly	Glu	Glu	Glu	Asp	Gly	Pro	Val	Leu	Thr	Asp	Glu	Gln
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Val	Pro	Asn	Pro	Gly	His	Glu	Ala	His	Asp	Gln	Gly	Gly	Trp	Asp	Ala
		130				135					140				
Arg	Gln	Ser	Val	Ile	Arg	Lys	Val	Val	Asp	Pro	Glu	Thr	Gly	Arg	Thr
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Arg	Leu	Ile	Lys	Gly	Asp	Gly	Glu	Val	Leu	Glu	Glu	Ile	Val	Thr	Lys
			165					170					175		
Glu	Arg	His	Arg	Glu	Ile	Asn	Lys	Val	Gly	Val	Ala	Pro	Leu	Pro	Ala
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&lt;210&gt; 3885

&lt;211&gt; 1671

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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<211> 277

<212> PRT

<213> Homo sapiens

<400> 3886

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Gln	Val	Leu	Ala	Ala	Thr	Tyr	Asn	Gln	Ala	Ala	Gln	Leu	Trp	Lys
	50					55				60				
Gly	Glu	Ala	Gln	Ser	Lys	Glu	Thr	Leu	Ser	Gly	His	Lys	Asp	Lys
65				70						75				80
Thr	Ala	Ala	Lys	Phe	Lys	Leu	Thr	Arg	His	Gln	Ala	Val	Thr	Gly
			85					90					95	
Arg	Asp	Arg	Thr	Val	Lys	Glu	Trp	Asp	Leu	Gly	Arg	Ala	Tyr	Cys
	100							105				110		
Arg	Thr	Ile	Asn	Val	Leu	Ser	Tyr	Cys	Asn	Asp	Val	Val	Xaa	Trp
	115						120					125		
Pro	Tyr	His	His	Xaa	Ser	Gly	His	Asn	Asp	Gln	Lys	Ile	Arg	Phe
	130					135				140				
Asp	Ser	Xaa	Gly	Gly	Pro	Thr	Ala	Pro	Arg	Ser	Ser	Leu	Xaa	Gln
145				150						155				160
Arg	Val	Thr	Ser	Leu	Ser	Leu	Ser	Xaa	Arg	Pro	Thr	Xaa	His	Leu
			165					170					175	
Ser	Cys	Ser	Arg	Asp	Asn	Thr	Leu	Lys	Val	Ile	Asp	Leu	Arg	Val
			180					185				190		
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Trp	Thr	Lys	Ala	Val	Phe	Ser	Pro	Asp	Arg	Ser	Tyr	Ala	Leu	Ala
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Ser	Cys	Asp	Gly	Ala	Leu	Tyr	Ile	Trp	Asp	Val	Asp	Thr	Gly	Lys
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Glu	Ser	Arg	Leu	Gln	Gly	Pro	His	Cys	Ala	Ala	Val	Asn	Ala	Val
			245					250				255		
Trp	Cys	Tyr	Ser	Gly	Ser	His	Met	Val	Ser	Val	Asp	Gln	Gly	Arg
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<212> DNA

<213> Homo sapiens

<400> 3887

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&lt;210&gt; 3888

&lt;211&gt; 1230

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3888

Met	Ala	Ser	Ala	Ser	Tyr	His	Ile	Ser	Asn	Leu	Leu	Glu	Lys	Met	Thr
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Ser	Ser	Asp	Lys	Asp	Phe	Arg	Phe	Met	Ala	Thr	Asn	Asp	Leu	Met	Thr
		20						25					30		
Glu	Leu	Gln	Lys	Asp	Ser	Ile	Lys	Leu	Asp	Asp	Asp	Ser	Glu	Arg	Lys
		35					40					45			
Val	Val	Lys	Met	Ile	Leu	Lys	Leu	Leu	Glu	Asp	Lys	Asn	Gly	Glu	Val
		50				55					60				
Gln	Asn	Leu	Ala	Val	Lys	Cys	Leu	Gly	Pro	Leu	Val	Ser	Lys	Val	Lys
		65			70					75				80	
Glu	Tyr	Gln	Val	Glu	Thr	Ile	Val	Asp	Thr	Leu	Cys	Thr	Asn	Met	Leu
			85					90					95		
Ser	Asp	Lys	Glu	Gln	Leu	Arg	Asp	Ile	Ser	Ser	Ile	Gly	Leu	Lys	Thr
		100						105					110		
Val	Ile	Gly	Glu	Leu	Pro	Pro	Ala	Ser	Ser	Gly	Ser	Ala	Leu	Ala	Ala
		115					120					125			
Asn	Val	Cys	Lys	Lys	Ile	Thr	Gly	Arg	Leu	Thr	Ser	Ala	Ile	Ala	Lys
		130				135					140				
Gln	Glu	Asp	Val	Ser	Val	Gln	Leu	Glu	Ala	Leu	Asp	Ile	Met	Ala	Asp
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Met	Leu	Ser	Arg	Gln	Gly	Gly	Leu	Leu	Val	Asn	Phe	His	Pro	Ser	Ile

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Leu Thr Cys Leu Leu Pro Gln Leu Thr Ser Pro Arg Leu Ala Val Arg
180      185      190
Lys Arg Thr Ile Ile Ala Leu Gly His Leu Val Met Ser Cys Gly Asn
195      200      205
Ile Val Phe Val Asp Leu Ile Glu His Leu Leu Ser Glu Leu Ser Lys
210      215      220
Asn Asp Ser Met Ser Thr Thr Arg Thr Tyr Ile Gln Cys Ile Ala Ala
225      230      235      240
Ile Ser Arg Gln Ala Gly His Arg Ile Gly Glu Tyr Leu Glu Lys Ile
245      250      255
Ile Pro Leu Val Val Lys Phe Cys Asn Val Asp Asp Asp Glu Leu Arg
260      265      270
Glu Tyr Cys Ile Gln Ala Phe Glu Ser Phe Val Arg Arg Cys Pro Lys
275      280      285
Glu Val Tyr Pro His Val Ser Thr Ile Ile Asn Ile Cys Leu Lys Tyr
290      295      300
Leu Thr Tyr Asp Pro Asn Tyr Asn Tyr Asp Asp Glu Asp Glu Asp Glu
305      310      315      320
Asn Ala Met Asp Ala Asp Gly Gly Asp Asp Asp Asp Gln Gly Ser Asp
325      330      335
Asp Glu Tyr Ser Asp Asp Asp Asp Met Ser Trp Lys Val Arg Arg Ala
340      345      350
Ala Ala Lys Cys Leu Asp Ala Val Val Ser Thr Arg His Glu Met Leu
355      360      365
Pro Glu Phe Tyr Lys Thr Val Ser Pro Ala Leu Ile Ser Arg Phe Lys
370      375      380
Glu Arg Glu Glu Asn Val Lys Ala Asp Val Phe His Ala Tyr Leu Ser
385      390      395      400
Leu Leu Lys Gln Thr Arg Pro Val Gln Ser Trp Leu Cys Asp Pro Asp
405      410      415
Ala Met Glu Gln Gly Glu Thr Pro Leu Thr Met Leu Gln Ser Gln Val
420      425      430
Pro Asn Ile Val Lys Ala Leu His Lys Gln Met Lys Glu Lys Ser Val
435      440      445
Lys Thr Arg Gln Cys Cys Phe Asn Met Leu Thr Glu Leu Val Asn Val
450      455      460
Leu Pro Gly Ala Leu Thr Gln His Ile Pro Val Leu Val Pro Gly Ile
465      470      475      480
Ile Phe Ser Leu Asn Asp Lys Ser Ser Ser Ser Asn Leu Lys Ile Asp
485      490      495
Ala Leu Ser Cys Leu Tyr Val Ile Leu Cys Asn His Ser Pro Gln Val
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Phe His Pro His Val Gln Ala Leu Val Pro Pro Val Val Ala Cys Val
515      520      525
Gly Asp Pro Phe Tyr Lys Ile Thr Ser Glu Ala Leu Leu Val Thr Gln
530      535      540
Gln Leu Val Lys Val Ile Arg Pro Leu Asp Gln Pro Ser Ser Phe Asp
545      550      555      560
Ala Thr Pro Tyr Ile Lys Asp Leu Phe Thr Cys Thr Ile Lys Arg Leu
565      570      575
Lys Ala Ala Asp Ile Asp Gln Glu Val Lys Glu Arg Ala Ile Ser Cys
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Met Gly Gln Ile Ile Cys Asn Leu Gly Asp Asn Leu Gly Ser Asp Leu

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Arg Leu Thr Thr Val Lys Ala Leu Thr Leu Ile Ala Gly Ser Pro Leu		
625	630	635
Lys Ile Asp Leu Arg Pro Val Leu Gly Glu Gly Val Pro Ile Leu Ala		640
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Ser Phe Leu Arg Lys Asn Gln Arg Ala Leu Lys Leu Gly Thr Leu Ser		655
	660	665
Ala Leu Asp Ile Leu Ile Lys Asn Tyr Ser Asp Ser Leu Thr Ala Ala		670
	675	680
Met Ile Asp Ala Val Leu Asp Glu Leu Pro Pro Leu Ile Ser Glu Ser		685
	690	695
Asp Met His Val Ser Gln Met Ala Ile Ser Phe Leu Thr Thr Leu Ala		700
705	710	715
Lys Val Tyr Pro Ser Ser Leu Ser Lys Ile Ser Gly Ser Ile Leu Asn		720
	725	730
Glu Leu Ile Gly Leu Val Arg Ser Pro Leu Leu Gln Gly Gly Ala Leu		735
	740	745
Ser Ala Met Leu Asp Phe Phe Gln Ala Leu Val Val Thr Gly Thr Asn		750
	755	760
Asn Leu Gly Tyr Met Asp Leu Leu Arg Met Leu Thr Gly Pro Val Tyr		765
	770	775
Ser Gln Ser Thr Ala Leu Thr His Lys Gln Ser Tyr Tyr Ser Ile Ala		780
785	790	795
Lys Cys Val Ala Ala Leu Thr Arg Ala Cys Pro Lys Glu Gly Pro Ala		800
	805	810
Val Val Gly Gln Phe Ile Gln Asp Val Lys Asn Ser Arg Ser Thr Asp		815
	820	825
Ser Ile Arg Leu Leu Ala Leu Leu Ser Leu Gly Glu Val Gly His His		830
	835	840
Ile Asp Leu Ser Gly Gln Leu Glu Leu Lys Ser Val Ile Leu Glu Ala		845
	850	855
Phe Ser Ser Pro Ser Glu Glu Val Lys Ser Ala Ala Ser Tyr Ala Leu		860
865	870	875
Gly Ser Ile Ser Val Gly Asn Leu Pro Glu Tyr Leu Pro Phe Val Leu		880
	885	890
Gln Glu Ile Thr Ser Gln Pro Lys Arg Gln Tyr Leu Leu Leu His Ser		895
	900	905
Leu Lys Glu Ile Ile Ser Ser Ala Ser Val Val Gly Leu Lys Pro Tyr		910
	915	920
Val Glu Asn Ile Trp Ala Leu Leu Leu Lys His Cys Glu Cys Ala Glu		925
	930	935
Glu Gly Thr Arg Asn Val Val Ala Glu Cys Leu Gly Lys Leu Thr Leu		940
945	950	955
Ile Asp Pro Glu Thr Leu Leu Pro Arg Leu Lys Gly Tyr Leu Ile Ser		960
	965	970
Gly Ser Ser Tyr Ala Arg Ser Ser Val Val Thr Ala Val Lys Phe Thr		975
	980	985
Ile Ser Asp His Pro Gln Pro Ile Asp Pro Leu Leu Lys Asn Cys Ile		990
	995	1000
Gly Asp Phe Leu Lys Thr Leu Glu Asp Pro Asp Leu Asn Val Arg Arg		1005
	1010	1015
Val Ala Leu Val Thr Phe Asn Ser Ala Ala His Asn Lys Pro Ser Leu		1020

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 Ile Arg Asp Leu Leu Asp Thr Val Leu Pro His Leu Tyr Asn Glu Thr  
                                  1045                      1050                      1055  
 Lys Val Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys  
                                  1060                      1065                      1070  
 His Thr Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys  
                                  1075                      1080                      1085  
 Met Tyr Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu  
                                  1090                      1095                      1100  
 Phe Leu Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys  
 1105                      1110                      1115                      1120  
 Met Leu Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser  
                                  1125                      1130                      1135  
 Ala Val Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr  
                                  1140                      1145                      1150  
 Cys Thr Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys  
                                  1155                      1160                      1165  
 Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu  
                                  1170                      1175                      1180  
 Thr Ile Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser  
 1185                      1190                      1195                      1200  
 Gln Ile Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln  
                                  1205                      1210                      1215  
 Lys Asp Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser  
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&lt;210&gt; 3889

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3889

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&lt;210&gt; 3890

<211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 3890

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Glu	Glu	Asp	Gly	Pro	Val	Leu	Thr	Asp	Glu	Gln	Val	Pro	Asn	Pro	Gly
			20					25					30		
His	Glu	Ala	His	Asp	Gln	Gly	Gly	Trp	Asp	Ala	Arg	Gln	Ser	Ile	Ile
			35				40					45			
Arg	Lys	Val	Val	Asp	Pro	Glu	Thr	Gly	Arg	Thr	Arg	Leu	Ile	Lys	Gly
	50					55				60					
Asp	Gly	Glu	Val	Leu	Glu	Glu	Ile	Val	Thr	Lys	Glu	Arg	His	Arg	Glu
65					70					75				80	
Ile	Asn	Lys	Gln	Ala	Thr	Arg	Gly	Asp	Cys	Leu	Ala	Phe	Gln	Met	Arg
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<210> 3891  
 <211> 1687  
 <212> DNA  
 <213> Homo sapiens

<400> 3891

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840

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 1680  
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&lt;210&gt; 3892

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3892

Val	Arg	Val	Leu	Asn	Ile	Trp	Pro	Tyr	Pro	Gln	Gln	Glu	Cys	Leu	His
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Ser	Pro	Asn	Trp	Gln	His	Gln	Thr	Gly	His	Gly	Thr	Glu	Ser	Ser	Gly
			20					25					30		
Ser	Gly	Leu	Phe	Ala	Leu	Cys	Thr	Leu	Asp	Gly	Thr	Leu	Lys	Leu	Met
		35					40					45			
Glu	Glu	Met	Glu	Glu	Ala	Asp	Lys	Leu	Leu	Trp	Ser	Val	Gln	Val	Asp
	50					55					60				
His	Gln	Leu	Phe	Ala	Leu	Glu	Lys	Leu	Asp	Val	Thr	Gly	Asn	Gly	His
65					70					75				80	
Glu	Glu	Val	Val	Ala	Cys	Ala	Trp	Asp	Gly	Gln	Thr	Tyr	Ile	Ile	Asp
			85					90					95		
His	Asn	Arg	Thr	Val	Val	Arg	Phe	Gln	Val	Asp	Glu	Asn	Ile	Arg	Ala
			100					105					110		
Phe	Cys	Ala	Gly	Leu	Tyr	Ala	Cys	Lys	Glu	Gly	Arg	Asn	Ser	Pro	Cys
	115						120					125			
Leu	Val	Tyr	Val	Thr	Phe	Asn	Gln	Lys	Ile	Tyr	Val	Tyr	Trp	Glu	Val

130		135		140
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr				
145		150		155
Lys Pro Ser Thr Thr Ala Cys Cys Arg Ser Trp Ala Trp Ile Leu Thr				
	165		170	175
Thr Ser Leu				

&lt;210&gt; 3893

&lt;211&gt; 1591

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3893

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<210> 3894

<211> 334

<212> PRT

<213> Homo sapiens

<400> 3894

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		20						25					30		
Gly	Glu	Ser	Phe	Val	Met	Tyr	Tyr	Lys	Ser	Lys	Glu	Asn	Cys	Val	Val
		35					40					45			
Asp	Asn	Ile	Lys	Val	Cys	Ser	Asn	Asp	Thr	Gly	Ser	Gly	Lys	Phe	Lys
	50					55				60					
Cys	Val	Cys	Ile	Thr	Met	Arg	Val	Pro	Arg	Asn	Pro	Thr	Ile	Gly	Asp
65					70				75					80	
Lys	Phe	Ala	Ser	Arg	His	Gly	Gln	Lys	Gly	Ile	Leu	Ser	Arg	Leu	Trp
				85				90						95	
Pro	Ala	Glu	Asp	Met	Pro	Phe	Thr	Glu	Ser	Gly	Met	Val	Pro	Asp	Ile
		100						105					110		
Leu	Phe	Asn	Pro	His	Gly	Phe	Pro	Ser	Arg	Met	Thr	Ile	Gly	Met	Leu
		115					120					125			
Ile	Glu	Ser	Met	Ala	Gly	Lys	Ser	Ala	Ala	Leu	His	Gly	Leu	Cys	His
	130					135				140					
Asp	Ala	Thr	Pro	Phe	Ile	Phe	Ser	Glu	Glu	Asn	Ser	Ala	Leu	Glu	Tyr
145					150					155				160	
Phe	Gly	Glu	Met	Leu	Lys	Ala	Ala	Gly	Tyr	Asn	Phe	Tyr	Gly	Thr	Glu
			165					170					175		
Arg	Leu	Tyr	Ser	Gly	Ile	Ser	Gly	Leu	Glu	Leu	Glu	Ala	Asp	Ile	Phe
		180					185					190			
Ile	Gly	Val	Tyr	Tyr	Gln	Arg	Leu	Arg	His	Met	Val	Ser	Asp	Lys	
	195					200					205				
Phe	Gln	Val	Arg	Thr	Thr	Gly	Ala	Arg	Asp	Arg	Val	Thr	Asn	Gln	Pro
	210					215					220				
Ile	Gly	Gly	Arg	Asn	Val	Gln	Gly	Gly	Ile	Arg	Phe	Gly	Glu	Met	Glu
225				230					235					240	
Arg	Asp	Ala	Leu	Leu	Ala	His	Gly	Thr	Ser	Phe	Leu	Leu	His	Asp	Arg
			245					250					255		
Leu	Phe	Asn	Cys	Ser	Asp	Arg	Ser	Val	Ala	His	Val	Cys	Val	Lys	Cys



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<210> 3896

<211> 346

<212> PRT

<213> Homo sapiens

<400> 3896

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 35 40 45  
 Ile Glu Ser Thr Ser Pro Ile Ser Arg Thr Asp Glu Ile Arg Lys Asn  
 50 55 60  
 Thr Tyr Arg Thr Leu Asp Ser Leu Glu Gln Thr Ile Lys Gln Leu Glu  
 65 70 75 80  
 Asn Thr Ile Ser Glu Met Ser Pro Lys Ala Leu Val Asp Thr Ser Cys  
 85 90 95  
 Ser Ser Asn Arg Asp Ser Val Ala Ser Ser Ser His Ile Ala Gln Glu  
 100 105 110  
 Ala Ser Pro Arg Pro Leu Leu Val Pro Asp Glu Gly Pro Thr Ala Leu  
 115 120 125  
 Glu Pro Pro Thr Ser Ile Pro Ser Ala Ser Arg Lys Gly Ser Ser Gly  
 130 135 140  
 Ala Pro Gln Thr Ser Arg Met Pro Val Pro Met Ser Ala Lys Asn Arg  
 145 150 155 160  
 Pro Gly Thr Leu Asp Lys Pro Gly Lys Gln Ser Lys Leu Gln Asp Pro  
 165 170 175  
 Arg Gln Tyr Arg Gln Ala Asn Gly Ser Ala Lys Lys Ser Gly Gly Asp  
 180 185 190  
 Phe Lys Pro Thr Ser Pro Ser Leu Pro Ala Ser Lys Ile Pro Ala Leu  
 195 200 205  
 Ser Pro Ser Ser Gly Lys Ser Ser Ser Leu Pro Ser Ser Ser Gly Asp  
 210 215 220  
 Ser Ser Asn Leu Pro Asn Pro Pro Ala Thr Lys Pro Ser Ile Ala Ser  
 225 230 235 240  
 Asn Pro Leu Ser Pro Gln Thr Gly Pro Pro Ala His Ser Ala Ser Leu  
 245 250 255  
 Ile Pro Ser Val Ser Asn Gly Ser Leu Lys Phe Gln Ser Leu Thr His  
 260 265 270  
 Thr Gly Lys Gly His His Leu Ser Phe Ser Pro Gln Ser Gln Asn Gly  
 275 280 285  
 Arg Ala Pro Pro Pro Leu Ser Phe Ser Ser Ser Pro Pro Ser Pro Ala  
 290 295 300  
 Ser Ser Val Ser Leu Asn Gln Gly Ala Lys Gly Thr Arg Thr Ile His  
 305 310 315 320  
 Thr Pro Ser Leu Thr Ser Tyr Lys Ala Gln Asn Gly Ser Ser Ser Lys  
 325 330 335  
 Ala Thr Pro Ser Thr Ala Lys Glu Thr Ser

340

345

&lt;210&gt; 3897

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3897

gccctgtggt ccggtccaga ccagggtgag gcatggagga ggctctgcac agccatttgc  
 60  
 agctcagcca gcaccgggtg atggcagga ggcctgggct tctgcactgg cttctggcct  
 120  
 cttctgggca cccacgcttt gtccatgaat ggaaagcaat gctgacggct gcccaatgtg  
 180  
 tccaggacgt ttctgaaact cctgttcctc tcccgtccc tctctctgtc ccactgtcca  
 240  
 cctcagtac ctctctctt cgtggctctc accccacact ctgccactgc cacattttcc  
 300  
 tctgcgcca gcctctgcct ccacctgaaa ctttcctgga aatctcaaaa tgtaattcca  
 360  
 ggtccc  
 366

&lt;210&gt; 3898

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3898

Met	Glu	Glu	Ala	Leu	His	Ser	His	Leu	Gln	Leu	Ser	Gln	His	Arg	Val
1				5				10					15		
Met	Ala	Gly	Arg	Pro	Gly	Leu	Leu	His	Trp	Leu	Leu	Ala	Ser	Ser	Gly
			20					25				30			
His	Pro	Arg	Phe	Val	His	Glu	Trp	Lys	Ala	Met	Leu	Thr	Ala	Ala	Gln
			35				40					45			
Cys	Val	Gln	Asp	Val	Ser	Glu	Thr	Pro	Val	Pro	Leu	Pro	Val	Pro	Leu
	50				55					60					
Ser	Val	Pro	Leu	Ser	Thr	Ser	Val	Thr	Ser	Ser	Leu	Arg	Gly	Ser	His
65				70				75				80			
Pro	Thr	Leu	Cys	His	Cys	His	Ile	Phe	Leu	Cys	Ala	Gln	Pro	Leu	Pro
			85				90					95			
Pro	Pro	Glu	Thr	Phe	Leu	Glu	Ile	Ser	Lys	Cys	Asn	Ser	Arg	Ser	
			100				105					110			

&lt;210&gt; 3899

&lt;211&gt; 1092

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3899

ngaaacggta accagccctg ggaagccgc aagaggcctc agcgggtggcc gtccgagcgc  
 60  
 cgagaggtga ggggtgcccc gcctcacctg cagaggggccc gttccgggct cgaaccggc  
 120

accttccgga aaatggcggc tgccaggccc agcctgggccc gagtcctccc aggatcctct  
 180  
 gtccctgttcc tgtgtgacat gcaggagaag ttccgccaca acatcgccta cttcccacag  
 240  
 atcgtctcag tggctgcccc catgctcaag gtggccccggc tgcttgaggt gccagtcagt  
 300  
 ctgacggagc agtaccacaca aggcctgggc ccacagggtgc ccgagctggg gactngaggg  
 360  
 ccttcgggccc ctggccaaga cctgcttcag catgggtgcct gcctgcagca ggagctggac  
 420  
 agtcggcccc agctgcgctc tgtgctgctc tgtggcattg aggcacaggc ctgcatcttg  
 480  
 aacacgaccc tggacctcct agaccggggg ctgcagggtcc atgtggtggt ggacgcctgc  
 540  
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 600  
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 660  
 ttcaaggaga tccagaaact catcaaggag cccgccccag acagcggact gctgggcctc  
 720  
 ttccaaggcc agaactccct cctccactga actccaaccc tgccttgagg gaagaccacc  
 780  
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 900  
 gacagctgct cccggaaatg caaatgagac tcctggaaac tgggtgggaa ttggctgagc  
 960  
 caagatggag gcggggctcg gccccgggcc acttcacggg gcgggaaggg gaggggaaga  
 1020  
 agagtctcag actgtgggac acggactcgc agaataaaca tatatgtggc tgtgaaaaaa  
 1080  
 aaaaaaaaaa aa  
 1092

&lt;210&gt; 3900

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3900

Xaa	Asn	Gly	Asn	Gln	Pro	Trp	Glu	Ala	Arg	Lys	Arg	Pro	Gln	Arg	Trp
1			5					10					15		
Pro	Ser	Glu	Arg	Arg	Glu	Val	Arg	Val	Pro	Pro	Pro	His	Leu	Gln	Arg
			20					25					30		
Gly	Arg	Ser	Gly	Leu	Glu	Pro	Gly	Thr	Phe	Arg	Lys	Met	Ala	Ala	Ala
			35				40					45			
Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu	Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu
			50			55					60				
Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg	His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln
65					70					75				80	
Ile	Val	Ser	Val	Ala	Ala	Arg	Met	Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu
				85					90					95	
Val	Pro	Val	Met	Leu	Thr	Glu	Gln	Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr

```

      100      105      110
Val Pro Glu Leu Gly Thr Xaa Gly Pro Ser Ala Ala Gly Gln Asp Leu
      115      120      125
Leu Gln His Gly Ala Cys Leu Gln Gln Glu Leu Asp Ser Arg Pro Gln
      130      135      140
Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln Ala Cys Ile Leu
      145      150      155      160
Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln Val His Val Val
      165      170      175
Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg Leu Val Ala Leu
      180      185      190
Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr Ser Glu Gly Leu
      195      200      205
Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln Phe Lys Glu Ile
      210      215      220
Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly Leu Leu Gly Leu
      225      230      235      240
Phe Gln Gly Gln Asn Ser Leu Leu His
      245

```

&lt;210&gt; 3901

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3901

```

nncctagggg aggtgggcgg ggagctgggg acagatggcc ttggtttggg agcatagcct
60
ctgatcagca tctctgtgtt tggacagaac ctgctgggac tacagaacat cccagggccg
120
ttcttcctgc aggtgtacca caccttcctc aggattgcag agaccagggt aggtgacgcc
180
gtcctggggc tggctctgcat gctgctgctg ctggtgctga agctgatgcg ggaccacgtg
240
cctcccgtcc accccagat gcccctgggt gtgcggctca gccgtgggct ggtctgggct
300
gccacgacag ctgcgaacgc cctgggtggc tccttcgcag ccctgggtgc gtactccttc
360
gaggtgactg gataccagcc ttctatccta acaggggaga cagctgaggg gctccctcca
420
gtccggatcc cgcccttctc agtgaccaca gccaacggga cgatctcctt caccgagatg
480
gtgcaggaca tgggagccgg gctggccgtg gtgccctga tgggcctcct ggagagcatt
540
gcggtggcca aagccttcgc atctcagaat aattaccgca tcgatgccaa ccaggagctg
600
ctggccatcg gtctcaccaa catgttgggc tcctcgtct cctcctacce ggtcacaggc
660
agctttggac ggacagccgt gaacgctcag tcgggggtgt gcaccccggc ggggggcctg
720
gtgacgggag tgctggtgct gctgtctctg gactacctga cctcactgtt ctactacatc
780
cccaagtctg ccctggetgc cgatcatc atggccgtgg cccgctgtt cgacaccaag
840

```

atcttcagga cgctctggcg tgtaagagg ctggacctgc tgccctgtg cgtgaccttc  
 900  
 ctgctgtgct tctgggaggt gcagtacggc atcctggccg gggccctggt gtctctgctc  
 960  
 atgctcctgc actctgcagc caggcctgag accaaggtgt cagagggggc ggttctggtc  
 1020  
 ctgcagccgg ccagcgccct gtccttccct gtcctctgcc cccactccc tgctgttcag  
 1080  
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 ggctggaccg tcctctgtgg gcctcagcca gtgggtgctgc agcaagggg gtggctcccc  
 1200  
 acatatcact ccttccctgc ccctaaagtc cggttcctgt ttctgggggg ttgatttag  
 1260  
 gggagctaag ggctgtgag tcctagt  
 1287

<210> 3902

<211> 312

<212> PRT

<213> Homo sapiens

<400> 3902

Met	Leu	Leu	Leu	Leu	Val	Leu	Lys	Leu	Met	Arg	Asp	His	Val	Pro	Pro
1				5					10					15	
Val	His	Pro	Glu	Met	Pro	Pro	Gly	Val	Arg	Leu	Ser	Arg	Gly	Leu	Val
			20				25						30		
Trp	Ala	Ala	Thr	Thr	Ala	Arg	Asn	Ala	Leu	Val	Val	Ser	Phe	Ala	Ala
		35					40					45			
Leu	Val	Ala	Tyr	Ser	Phe	Glu	Val	Thr	Gly	Tyr	Gln	Pro	Phe	Ile	Leu
	50					55					60				
Thr	Gly	Glu	Thr	Ala	Glu	Gly	Leu	Pro	Pro	Val	Arg	Ile	Pro	Pro	Phe
65					70					75				80	
Ser	Val	Thr	Thr	Ala	Asn	Gly	Thr	Ile	Ser	Phe	Thr	Glu	Met	Val	Gln
				85					90					95	
Asp	Met	Gly	Ala	Gly	Leu	Ala	Val	Val	Pro	Leu	Met	Gly	Leu	Leu	Glu
			100						105				110		
Ser	Ile	Ala	Val	Ala	Lys	Ala	Phe	Ala	Ser	Gln	Asn	Asn	Tyr	Arg	Ile
		115					120					125			
Asp	Ala	Asn	Gln	Glu	Leu	Leu	Ala	Ile	Gly	Leu	Thr	Asn	Met	Leu	Gly
		130					135				140				
Ser	Leu	Val	Ser	Ser	Tyr	Pro	Val	Thr	Gly	Ser	Phe	Gly	Arg	Thr	Ala
145					150					155				160	
Val	Asn	Ala	Gln	Ser	Gly	Val	Cys	Thr	Pro	Ala	Gly	Gly	Leu	Val	Thr
			165						170				175		
Gly	Val	Leu	Val	Leu	Leu	Ser	Leu	Asp	Tyr	Leu	Thr	Ser	Leu	Phe	Tyr
		180						185					190		
Tyr	Ile	Pro	Lys	Ser	Ala	Leu	Ala	Ala	Val	Ile	Ile	Met	Ala	Val	Ala
		195					200					205			
Pro	Leu	Phe	Asp	Thr	Lys	Ile	Phe	Arg	Thr	Leu	Trp	Arg	Val	Lys	Arg
	210					215					220				
Leu	Asp	Leu	Leu	Pro	Leu	Cys	Val	Thr	Phe	Leu	Leu	Cys	Phe	Trp	Glu
225					230					235				240	
Val	Gln	Tyr	Gly	Ile	Leu	Ala	Gly	Ala	Leu	Val	Ser	Leu	Leu	Met	Leu

```

                245                250                255
Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val Ser Glu Gly Pro Val
                260                265                270
Leu Val Leu Gln Pro Ala Ser Gly Leu Ser Phe Pro Val Leu Cys Pro
                275                280                285
Pro Leu Pro Ala Val Gln Asp Pro Lys Thr Leu Ser Pro Thr Leu Ser
                290                295                300
Ser Pro Gln Gly Cys Arg His Leu
305                310

```

&lt;210&gt; 3903

&lt;211&gt; 598

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3903

```

gcgcgccggg gagcgcgcgt ggtgctggcc tgccgcagcc aggagcgcgg ggaggcggct
60
gccttcgacc tccgccagga gagggggaac aatgaggtca tcttcattggc cttggacttg
120
gccagtctgg cctcgggtcg ggcctttgcc actgcctttc tgagctctga gccacgggtg
180
gacatcctca tccacaatgc cggatatcagt tctgtgggcc ggaccctga gccgtttaac
240
ctgctgcttc ggggtgaacca tatcggtccc tttctgctga cacatctgct gctgccttgc
300
ctgaaggcat gtgcccctag ccgcgtggtg gtggtagcct cagctgcccc ctgtcgggga
360
cgtcttgact tcaaacgcct ggaccgcccc gtggtgctgg cggcaggagc tgcggcatat
420
gctgacacta agctggctaa tgtactgttt gcccgggagc tcgccaacca gcttgaggcc
480
actggcgta cctgctatgc agcccaccca gggcctgtga actcggagct gttcctgcgc
540
catgttcctg gatggctgcg cccacttttg cgcccattgg cttggctggt gccccggg
598

```

&lt;210&gt; 3904

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3904

```

Ala Arg Arg Gly Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg
1      5      10      15
Gly Glu Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu
20     25     30
Val Ile Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala
35     40     45
Phe Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
50     55     60
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe Asn
65     70     75     80
Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr His Leu

```



```

      85              90              95
Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val Val Val Val
      100              105              110
Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe Lys Arg Leu Asp
      115              120              125
Arg Pro Val Val Leu Ala Ala Gly Ala Ala Ala Tyr Ala Asp Thr Lys
      130              135              140
Leu Ala Asn Val Leu Phe Ala Arg Glu Leu Ala Asn Gln Leu Glu Ala
      145              150              155              160
Thr Gly Val Thr Cys Tyr Ala Ala His Pro Gly Pro Val Asn Ser Glu
      165              170              175
Leu Phe Leu Arg His Val Pro Gly Trp Leu Arg Pro Leu Leu Arg Pro
      180              185              190
Leu Ala Trp Leu Val Pro Arg
      195

```

&lt;210&gt; 3905

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3905

```

ggatcctctg agctgcgctc ggccttctcg gcggcacgca ccacccccct ggagggcacg
60
tcggagatgg cggtgacctt cgacaagggtg tacgtgaaca tcgggggcca ctctgatgtg
120
gccaccggcc agtttcgctg ccgcgtgccc ggcgcctact tcttctcctt cacggctggc
180
aaggccccgc acaagagccc gtcggtgatg ctggtgcgaa accgcgacga ggtgcaggcg
240
ctggccttcg acgagcagcg gcggccaggc gcgcggcgcg cagccagcca gagcgccatg
300
ctgcagctcg actacggcga cacagtgtgg ctgcggctgc atggcgcccc gcagtacgcg
360
ctaggcgcgc
370

```

&lt;210&gt; 3906

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3906

```

Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro
1          5          10          15
Leu Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val
20        25        30
Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg
35        40        45
Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His
50        55        60
Lys Ser Pro Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala
65        70        75        80
Leu Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser

```

	85		90		95
Gln Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg					
	100		105		110
Leu His Gly Ala Pro Gln Tyr Ala Leu Gly Ala					
	115		120		

&lt;210&gt; 3907

&lt;211&gt; 4474

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3907

```

gcgcgccgga accggaaccg acctgcgccg gaaccggaac ggagagcggg ttgccagggc
60
ccgaagaggg ctggctgcgg cggctctcgt cggctgtccg ttccttgctg gagaatttgg
120
ccacaaagag ctgccaagat agctggggcca ggaagaaagc gccgcagccc tgaccagac
180
gctgttgccg accccggggc actctggctg tcgaccaagc ggctcaagat gtctggcggg
240
gccagtgcc aaggcccaag gagagggccc ccaggactgg aggacaccac tagtaagaag
300
aagcagaagg atcgagcaaa ccaggagagc aaggatggag atcctaggaa agagacaggg
360
tctcgatatg ttgccaggc tggctctttaa cctctggcct caggatgatcc ttctgcctca
420
gcctcccatg cagctgggat cacaggctca cgccaccgta cccggctgtt ctttcttca
480
tcgtcagggc cagcatccac tcctcaagag gagcagacca aagagggagc ttgtgaagac
540
cctcatgatc tcttggtac tccactcca gagttgttgc tcgattggag gcagagtgc
600
gaagaggtga ttgtcaagct tcgtgtggga gtaggtcccc tgcagctgga ggatgtagat
660
gctgctttca cagatacaga ctgtgtgggt cggtttgag gtggtcagca gtggggtggg
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1080
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1140
gtgaaggaga tctgcaggga cacctcaaga gtacttttcc gtgagcagga cttcacgctc
1200
atcttccaga ccagggatgg aaacttcctg aggctgcacc cgggctgtgg gcccacacc
1260

```

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1380  
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2580  
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2940  
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3060  
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3120  
gagaggggtgt cccgaccoga agctgctgtg cctgggtacc agcatccaag tgaagctatg  
3180  
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&lt;210&gt; 3908

&lt;211&gt; 1373

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3908

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Ser Pro Asp Pro Asp Ala Val Ala Asp Pro Gly Ala Leu Trp Leu Ser
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Thr Lys Arg Leu Lys Met Ser Gly Gly Ala Ser Ala Thr Gly Pro Arg
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Arg Gly Pro Pro Gly Leu Glu Asp Thr Thr Ser Lys Lys Lys Gln Lys
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Asp Arg Ala Asn Gln Glu Ser Lys Asp Gly Asp Pro Arg Lys Glu Thr
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Gly Ser Arg Tyr Val Ala Gln Ala Gly Leu Glu Pro Leu Ala Ser Gly
      100          105          110
Asp Pro Ser Ala Ser Ala Ser His Ala Ala Gly Ile Thr Gly Ser Arg
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His Arg Thr Arg Leu Phe Phe Pro Ser Ser Ser Gly Ser Ala Ser Thr
      130          135          140
Pro Gln Glu Glu Gln Thr Lys Glu Gly Ala Cys Glu Asp Pro His Asp
      145          150          155          160
Leu Leu Ala Thr Pro Thr Pro Glu Leu Leu Leu Asp Trp Arg Gln Ser
      165          170          175
Ala Glu Glu Val Ile Val Lys Leu Arg Val Gly Val Gly Pro Leu Gln
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Leu Glu Asp Val Asp Ala Ala Phe Thr Asp Thr Asp Cys Val Val Arg
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Phe Ala Gly Gly Gln Gln Trp Gly Gly Val Phe Tyr Ala Glu Ile Lys
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Ser Ser Cys Ala Lys Val Gln Thr Arg Lys Gly Ser Leu Leu His Leu
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Val Pro Pro Gly Asn Asp Pro Val Ser Pro Ala Met Val Arg Ser Arg
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Asn Pro Gly Lys Asp Asp Cys Ala Lys Glu Glu Met Ala Val Ala Ala
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      325          330          335
Leu Ala Phe Val Lys Asn Asp Ser Tyr Glu Lys Gly Pro Asp Ser Val
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Val Val His Val Tyr Val Lys Glu Ile Cys Arg Asp Thr Ser Arg Val
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Leu Phe Arg Glu Gln Asp Phe Thr Leu Ile Phe Gln Thr Arg Asp Gly

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Cys Phe Thr Ala Ser Arg	Ile Asp Ile Cys	Leu Arg Lys Arg	Gln Ser	
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Gln Arg Trp Gly Gly Leu	Glu Ala Pro Ala	Ala Arg Val Gly	Gly Ala	
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His Leu Ala Ser Pro Lys	Pro Thr Cys Met	Val Pro Pro Met	Pro His	
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Ser Pro Val Ser Gly Asp	Ser Val Glu Glu	Glu Glu Glu Glu	Lys	
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Lys Val Cys Leu Pro Gly	Phe Thr Gly Leu	Val Asn Leu Gly	Asn Thr	
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Cys Phe Met Asn Ser Val	Ile Gln Ser Leu	Ser Asn Thr Arg	Glu Leu	
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Leu Lys Ala Ile Val Ala	Ser Lys Ala Ser	Gln Phe Thr Gly	Tyr Ala	
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Gln His Asp Ala Gln Glu	Phe Met Ala Phe	Leu Leu Asp Gly	Leu His	
	645	650	655	
Glu Asp Leu Asn Arg Ile	Gln Asn Lys Pro	Tyr Thr Glu Thr	Val Asp	
	660	665	670	
Ser Asp Gly Arg Pro Asp	Glu Val Val Ala	Glu Glu Ala Trp	Gln Arg	
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His Lys Met Arg Asn Asp	Ser Phe Ile Val	Asp Leu Phe Gln	Gly Gln	
	690	695	700	
Tyr Lys Ser Lys Leu Val	Cys Pro Val Cys	Ala Lys Val Ser	Ile Thr	
705	710	715	720	
Phe Asp Pro Phe Leu Tyr	Leu Pro Val Pro	Leu Pro Gln Lys	Gln Lys	
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Val Leu Pro Val Phe Tyr	Phe Ala Arg Glu	Pro His Ser Lys	Pro Ile	
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Lys Phe Leu Val Ser Val	Ser Lys Glu Asn	Ser Thr Ala Ser	Glu Val	
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Leu Asp Ser Leu Ser Gln	Ser Val His Val	Lys Pro Glu Asn	Leu Arg	
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&lt;210&gt; 3909

&lt;211&gt; 2704

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3909

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<212> PRT

<213> Homo sapiens

<400> 3910

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Asp	Leu	Tyr	Arg	His	Pro	Gln	Leu	Asp	Ala	Asp	Ile	Glu	Ala	Val	Lys
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Glu	Ile	Tyr	Ser	Glu	Asn	Ser	Val	Ser	Ile	Arg	Glu	Tyr	Gly	Thr	Ile
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Asp	Asp	Val	Asp	Ile	Asp	Leu	His	Ile	Asn	Ile	Ser	Phe	Leu	Asp	Glu
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Glu	Val	Ser	Thr	Ala	Trp	Lys	Val	Leu	Arg	Thr	Glu	Pro	Ile	Val	Leu
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Arg	Leu	Arg	Phe	Ser	Leu	Ser	Gln	Tyr	Leu	Asp	Gly	Pro	Glu	Pro	Ser
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